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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:06:00 ; Search time 188.365 Seconds
(without alignments)
4355.452 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPRCVTRTPPLRGSAR.....KXDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	12028	100.0	2287	4	AAB66475	Aab66475 Rat alpha
2	11657	96.9	2254	2	AAAY14590	Aay14590 Rat T-typ
3	11626	96.7	2272	2	AAAY14592	Aay14592 Rat T-typ
4	11610.5	96.5	2265	2	AAAY14591	Aay14591 Rat T-typ
5	11606.5	96.5	2247	2	AAAY14593	Aay14593 Rat T-typ
6	11542.5	96.0	2428	3	AAAY70720	Aay70720 Rat pancr
7	10857	90.3	2250	2	AAAY14586	Aay14586 Human T-t
8	10833	90.1	2268	2	AAAY14588	Aay14588 Human T-t
9	10820.5	90.0	2273	4	AAAE01019	Aae01019 Human T-t
10	10810.5	89.9	2261	2	AAAY14587	Aay14587 Human T-t
11	10806.5	89.8	2243	2	AAAY14589	Aay14589 Human T-t
12	10806.5	89.8	2243	7	ADJ68819	Adj68819 Human hea
13	10533	87.6	2266	4	AAB66481	Aab66481 Human alp
14	6226.5	51.8	2359	4	AAB66476	Aab66476 Rat alpha
15	6222	51.7	2353	2	AAAY06299	Aay06299 Human act
16	6222	51.7	2353	6	ABP72254	Abp72254 Human T-t
17	6222	51.7	2353	7	ADJ69322	Adj69322 Human hea
18	6221	51.7	2353	2	AAAY06298	Aay06298 Human act
19	6195.5	51.5	2353	5	ABG30840	Abg30840 Human vol
20	5872	48.8	1207	4	AAU00474	Aau00474 Human T-t
21	5835	48.5	2044	2	AAAY14594	Aay14594 Human T-t
22	5827	48.4	2038	2	AAAY14595	Aay14595 Human T-t
23	5718.5	47.5	2034	2	AAAY06300	Aay06300 Human act
24	5409	45.0	2175	5	AAU10535	Aau10535 Human T-t
25	5409	45.0	2175	6	ABU08511	Abu08511 Human T-t

26	5409	45.0	2175	8	ADH69265	Adh69265 Human TCC
27	5405.5	44.9	2188	5	AAU10536	Aau10536 Human T-t
28	5405.5	44.9	2188	6	ABU08512	Abu08512 Human T-t
29	5405.5	44.9	2188	8	ADH69267	Adh69267 Human TCC
30	5345	44.4	1835	2	AAAY14597	Aay14597 Rat T-typ
31	5345	44.4	1835	8	ADH69268	Adh69268 Rat T-typ
32	5342.5	44.4	1823	2	AAAY14596	Aay14596 Human T-t
33	5179.5	43.1	1792	4	AAB66477	Aab66477 Rat brain
34	4807	40.0	982	4	AAAM23743	Aam23743 Human EST
35	3950	32.8	1854	2	AAW79161	Aaw79161 Human cal
36	3950	32.8	1854	4	AAB66472	Aab66472 Protein e
37	3397	28.2	2435	4	ABB60448	Abb60448 Drosophil
38	3125	26.0	644	4	AAB66478	Aab66478 Human alp
39	2975	24.7	1859	4	ABG10954	Abg10954 Novel hum
40	1911.5	15.9	853	4	AAAM93437	Aam93437 Human pol
41	1911.5	15.9	853	8	ADL31041	Adl31041 Human pro
42	1686.5	14.0	518	4	AAB66479	Aab66479 Human alp
43	1682	14.0	2339	2	AAAR33549	Aar33549 Sequence
44	1680.5	14.0	2264	8	ADM31026	Adm31026 Human cal
45	1678	14.0	2343	2	AAAY31809	Aay31809 N-type ca

ALIGNMENTS

RESULT 1
AAB66475
ID AAB66475 standard; protein; 2287 AA.

XX AAB66475;

XX 09-APR-2001 (first entry)

XX Rat alpha-IG calcium channel protein.

KW Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
KW hypotensive; cardiant; nootropic; T-type calcium channel subunit;
KW cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
KW epilepsy; alpha-IG calcium channel.

OS Rattus sp.

XX WO200102561-A2.

PN 11-JAN-2001.

PD 04-JUL-2000; 2000WO-CA000794.

XX 02-JUL-1999; 99US-00346794.

PR (NEUR-) NEUROMED TECHNOLOGIES INC.

XX Snutch TP, Baillie DL;

DR WPI; 2001-123111/13.

DR N-PSDB; AAF31677.

XX Novel T-type calcium channel alpha-1 subunit gene useful for treating cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and epilepsy.

PS Disclosure; Page 63-72; 103pp; English.

XX The present sequence is given in a specification providing sequences and partial sequences for three types of mammalian (human and rat) T-type calcium channel subunits. An expression cassette has been generated which comprises a nucleotide sequence encoding a T-type calcium channel alpha_1 subunit operably linked to control sequences to effect its expression. The novel calcium channel nucleic acids and proteins are useful for treating conditions characterised by undesirable levels of T-type calcium channel activity such as cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and epilepsy

SQ		Sequence 2287 AA;					
		Query Match	100.0%;	Score 12028;	DB 4;	Length 2287;	
		Best Local Similarity	100.0%;	Pred. No. 0;			
		Matches 2287;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	MLPHRVPRCVRTPPLRGSRPSSDPPGPRRLARGTWTRRRMERAPRSRDS	SPVASRSSTTC	PG	60		
DB	1	MLPHRVPRCVRTPPLRGSRPSSDPPGPRRLARGTWTRRRMERAPRSRDS	SPVASRSSTTC	PG	60		
QY	61	PGAAGAGSTKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWF	RVSM	120			
DB	61	PGAAGAGSTKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWF	RVSM	120			
QY	121	LVILLNCVTLMGFRPCEDIAQDSQRCRILQAFDDFIAPFAFVEMVVKWALGIFGK	KCYL	180			
DB	121	LVILLNCVTLMGFRPCEDIAQDSQRCRILQAFDDFIAPFAFVEMVVKWALGIFGK	KCYL	180			
QY	181	GDTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILV	TL	240			
DB	181	GDTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILV	TL	240			
QY	241	PMLGNVLLCFFVFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQ	TENEDSP	300			
DB	241	PMLGNVLLCFFVFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQ	TENEDSP	300			
QY	301	FICSQPRENGMRSCHSVPTLRGEGGGPPCSDLDETYNSSNTTCVWNQY	TNCSAGEH	360			
DB	301	FICSQPRENGMRSCHSVPTLRGEGGGPPCSDLDETYNSSNTTCVWNQY	TNCSAGEH	360			
QY	361	NPFKGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFYNFIYFILLI	IVGSFFMIN	420			
DB	361	NPFKGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFYNFIYFILLI	IVGSFFMIN	420			
QY	421	LCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFPSEPGSCYEEL	LKYLVI	480			
DB	421	LCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFPSEPGSCYEEL	LKYLVI	480			
QY	481	RRLAQVSRAIGVRAGLLSSPVARSQEQPSGSCSTRHRRLSVHHLVHHHHHH	HHYHLG	540			
DB	481	RRLAQVSRAIGVRAGLLSSPVARSQEQPSGSCSTRHRRLSVHHLVHHHHHH	HHYHLG	540			
QY	541	NGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPRGAESVHSFYHAD	CHLEP	600			
DB	541	NGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPRGAESVHSFYHAD	CHLEP	600			
QY	601	QAPPPRCPSAEGRTVGSKVYPTVHTSPPEILKDKALVEVAPSPGPTLT	SFNIPGP	660			
DB	601	QAPPPRCPSAEGRTVGSKVYPTVHTSPPEILKDKALVEVAPSPGPTLT	SFNIPGP	660			
QY	661	FSSMHKLLTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGE	PE	720			
DB	661	FSSMHKLLTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGE	PE	720			
QY	721	DSEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLLC	DTFRKI	780			
DB	721	DSEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLLC	DTFRKI	780			
QY	781	GIMIAILVNTLSMGIEYHEQPEELTNALEISNIVETSLFALEMLLKLV	YGPFGYIKNPY	840			
DB	781	GIMIAILVNTLSMGIEYHEQPEELTNALEISNIVETSLFALEMLLKLV	YGPFGYIKNPY	840			
QY	841	NIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPALORQLV	LMKTMNVAT	900			
DB	841	NIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKVRFLPALORQLV	LMKTMNVAT	900			
QY	901	FCMLLMFIFIFISILGMHLFGCKFASERDGTLDPRKNFDSLLWAI	VTVFQIL	960			
DB	901	FCMLLMFIFIFISILGMHLFGCKFASERDGTLDPRKNFDSLLWAI	VTVFQIL	960			
QY	961	VLYNGMASTSSWAALYFIALMTFGNYLVFLNLLVAILVEGFQAE	GATKSESE	1020			
DB	961	VLYNGMASTSSWAALYFIALMTFGNYLVFLNLLVAILVEGFQAE	GATKSESE	1020			

[illegible]

QY 1142 LLSGEGSQDEEESSEEDRASAGSDHRRGSLEREAKSFDLPDRTLQVPLHRTASGR 1201
Db |||||
QY 1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRES 1261
Db |||||
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSAERIFL 1321
Db |||||
QY 1322 TLSNYIFTAVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSG 1381
Db |||||
QY 1382 TKILGMLRVLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
Db |||||
QY 1442 VOLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKYNFENLQALMSLFVLASKDGWVD 1501
Db |||||
QY 1502 IMYDGLDAVGVDQQPIMNHNPMWLLYFISFLLI VAFVLMNFVGVVVENFHKCRHQEEEE 1561
Db |||||
QY 1562 EARRREEKRLRLLEKRRSKEKQMAEACKPYSDYSRFRLLVHHLCTSHYLDLFTIGVI 1621
Db |||||
QY 1622 GLNVVTWAMEHYQQPQILDEALKICNVIFTVIFVESVFKLVAFAFRFFQDRWNQDLA 1681
Db |||||
QY 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKVAVGMRALHHTVMQALP 1741
Db |||||
QY 1742 QVGNLGLLFMLFFIFAALGVLELFGDLECDETHPCEGLGRHATFRNFGMAFLTFRVSTG 1801
Db |||||
QY 1802 DNWNGIMKPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1861
Db |||||
QY 1862 KEEAELEAELEEMKTLSPQSPHSPGLSPGLPWPGEVGNSTSPKPGAPHTTAAHIGAAASGF 1921
Db |||||
QY 1922 SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCMNGSTAERSLGHGHWGL 1981
Db |||||
QY 1982 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAI PKLPPPGRSPLAQRPLR 2041
Db |||||
QY 2042 RQAAIRTDSDLVQGLGSREDLLSEVSGPSCPLTRSSSFVGGSSIQVQQRSGIQSKVSKHI 2101
Db |||||
QY 2102 RLPAPCPGLEPSNAKDPPEPTRSSLELDTLSWISGDLLPSSQEEELFPRDLKKCYSVETQ 2161
Db |||||
QY 2162 SCRRRPGFWLDEQRHRSIAVSCLDGSGQPRLCPSPSLLGGQPLGGPGSRPKKLSPPPSIS 2221
Db |||||

QY 2222 IDPPESQGSRRPPCSPGVCLRRRAPASDSKOPSVSSPLDSTAASPSPKKDTLSLSGLSSDP 2281
Db |||||
QY 2282 TDMDP 2286
Db |||||
QY 2250 TDMDP 2254
Db |||||
RESULT 3
AAAY14592
ID AAY14592 standard; protein; 2272 AA.
XX AAY14592;
XX 07-DEC-1999 (first entry)
XX Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1c).
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX Rattus sp.
XX WO9929847-A1.
XX 17-JUN-1999.
XX 30-OCT-1998; 98WO-US023161.
XX 05-DEC-1997; 97US-00985809.
XX (LOYO) UNIV LOYOLA CHICAGO.
XX Perez-Reyes E, Cribbs LL;
PI WPI; 1999-394972/33.
XX N-PSDB; AAX83487.
PT New T-type voltage-gated calcium channels.
XX Disclosure; Page 85-94; 138pp; English.
CC This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC alpha-1-G designated rCavT1c. Voltage gated channels are membrane bound
CC glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC -channels contains a putative IVS4 region comprising the amino acid
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium
CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel nucleic
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 2272 AA;
Query Match 96.7%; Score 11626; DB 2; Length 2272;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2217; Conservative 0; Mismatches 8; Indels 18; Gaps 1;
QY 62 GAAGAGSTEKDPGSAADSEAEGLPYPALAPVFFVYLSQDSRPSWCLRTVCNPFVRSML 121
Db |||||
QY 122 VILLNCVTLMFRPCEDIACDSQRCRLQAFDDFIFAFFAEMVVMVALGIFGKKCYLG 181
|||

Db 90 VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIAFFAFAVMMVKMVALGIFGKKCYLG 149

QY 182 DTWNRLDFFIVIAGMLEYSLDLQNVFSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTP 241

Db 150 DTWNRLDFFIVIAGMLEYSLDLQNVFSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTP 209

QY 242 MLGNVLLCFFVFFIFGIVGVQLWAGLLRNCFLPENFSPLSVLEPYQYQTENEDESPF 301

Db 210 MLGNVLLCFFVFFIFGIVGVQLWAGLLRNCFLPENFSPLSVLEPYQYQTENEDESPF 269

QY 302 ICSQPRENGMRCRSVPTLRGEGGPPPCSLDYETYNSSNTTCVNNQYNTNCSAGEHN 361

Db 270 ICSQPRENGMRCRSVPTLRGEGGPPPCSLDYETYNSSNTTCVNNQYNTNCSAGEHN 329

QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL 421

Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL 389

QY 422 CLVVIATQFSETKQRESQLMREQRVRLFSNASTLASFSEPGSCYEELLKYLVILRKAAR 481

Db 390 CLVVIATQFSETKQRESQLMREQRVRLFSNASTLASFSEPGSCYEELLKYLVILRKAAR 449

QY 482 RLAQVSAIGVRAGLLSSPVARSQEPQPSGCTSRSHRRLSVHLLVHHHHHHHHYHLGN 541

Db 450 RLAQVSAIGVRAGLLSSPVARSQEPQPSGCTSRSHRRLSVHLLVHHHHHHHHYHLGN 509

QY 542 GTLRVPRAPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601

Db 510 GTLRVPRAPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

QY 602 APPPRCPSEASGRTVGSKVYPTVHTSPPPPEILKDKALVEVAPSPGPTLTSTNIPPGPF 661

Db 570 APPPRCPSEASGRTVGSKVYPTVHTSPPPPEILKDKALVEVAPSPGPTLTSTNIPPGPF 629

QY 662 SSMKLLTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 721

Db 630 SSMKLLTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 689

QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDPAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781

Db 690 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDPAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

QY 782 IMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841

Db 750 IMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809

QY 842 IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVREPLPALQRLVLMKTMNDNVATF 901

Db 810 IFDGVIVVISWEIVGQQGGGLSVLRTFRLMRVLKLVREPLPALQRLVLMKTMNDNVATF 869

QY 902 CMLLMFIFIFISILGMHLFGCKFASERDGTDLPRKNFDSLWAIIVTVFQILTQEDWNKV 961

Db 870 CMLLMFIFIFISILGMHLFGCKFASERDGTDLPRKNFDSLWAIIVTVFQILTQEDWNKV 929

QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021

Db 930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 989

QY 1022 GDGRKRLALVALGEHAELRKSLLPPLIIHTAATPMHPKSSSTGVGEALGSGSRRTS 1081

Db 990 GDGRKRLALVALGEHAELRKSLLPPLIIHTAATPMHPKSSSTGVGEALGSGSRRTS 1049

QY 1082 SGSAEPGAAHHEMKCPPSARSPPSWSAASSWTSRSTRSRNSLGRAPSLKRSPSGERRS 1141

Db 1050 SGSAEPGAAHHEMKCPPSARSPPSWSAASSWTSRSTRSRNSLGRAPSLKRSPSGERRS 1109

QY 1142 LLSGEGQESQDEESSEEDRASGSDHRHRSGLERAKSSFDPDPTLQVPLHRTASGR 1201

Db 1110 LLSGEGQESQDEESSEEDRASGSDHRHRSGLERAKSSFDPDPTLQVPLHRTASGR 1169

QY 1202 SSASEHQDCNGKASGRLARTLTDDPQLDGGDDNDDEGNLSKGERIQAWVRSLPACCRES 1261

Db 1170 SSASEHQDCNGKASGRLARTLTDDPQLDGGDDNDDEGNLSKGERIQAWVRSLPACCRES 1229

QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFL 1321

Db 1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFL 1289

QY 1322 TLSNYIFTAVFLAEMTVKVVVALGWCAGEQAYLRSSMNVDLGLLVLSVIDILVSMVSDSG 1381

Db 1290 TLSNYIFTAVFLAEMTVKVVVALGWCAGEQAYLRSSMNVDLGLLVLSVIDILVSMVSDSG 1349

QY 1382 TKILGMLRVLRLLRTLRLPLRVISRAQGLKLVETLMSILKPIGNIVVICCAFFIIFGILG 1441

Db 1350 TKILGMLRVLRLLRTLRLPLRVISRAQGLKLVETLMSILKPIGNIVVICCAFFIIFGILG 1409

QY 1442 VOLFKGKFFVCOGEDTRNITNKSDCAEASRVRVRHKYNFNDLGOALMSLFVLASKDGWVD 1501

Db 1410 VOLFKGKFFVCOGEDTRNITNKSDCAEASRVRVRHKYNFNDLGOALMSLFVLASKDGWVD 1469

QY 1502 IMYDGLDAVGVDQOQIMNHNPMWLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEE 1561

Db 1470 IMYDGLDAVGVDQOQIMNHNPMWLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEE 1529

QY 1562 EARRBEKRLRLEKKRRSKEKQMA-----EAQCKPYYSYRFRLL 1603

Db 1530 EARRBEKRLRLEKKRRSKEKQMA DMLDDVIASSSSASAASEAQCKPYYSYRFRLL 1589

QY 1604 VHLCCTSHYLDLFTIGVIGLNVVTMAMEHYQQOQILDEALKICNYIFTVIFVESVFKLV 1663

Db 1590 VHLCCTSHYLDLFTIGVIGLNVVTMAMEHYQQOQILDEALKICNYIFTVIFVESVFKLV 1649

QY 1664 AFAFRFFQDRWNQDLAIIVLLSIMGITLEEIEVNLISLPINPTIIRIMRVLRIRARVLKLL 1723

Db 1650 AFGFRFFQDRWNQDLAIIVLLSIMGITLEEIEVNLISLPINPTIIRIMRVLRIRARVLKLL 1709

QY 1724 KMAVGMRALLHTVMQALPOVGNLGLLFMLLFFIFAALGVELFGDLECEDETHCEGLGRHA 1783

Db 1710 KMAVGMRALLHTVMQALPOVGNLGLLFMLLFFIFAALGVELFGDLECEDETHCEGLGRHA 1769

QY 1784 TERNFGMAFLTFRVSTGDNWNGIMKDPSPRDCDQESTCYNTVISPIYFVSFVLTQAQFVLV 1843

Db 1770 TERNFGMAFLTFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTQAQFVLV 1829

QY 1844 NVVIAVLMKHLEESNKEAEAELEAELEMKTLSPQPHSPGLSPFLWPGEVGNSTDS 1903

Db 1830 NVVIAVLMKHLEESNKEAEAELEAELEMKTLSPQPHSPGLSPFLWPGEVGNSTDS 1889

QY 1904 PKPGAPHTTAHGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYM 1963

Db 1890 PKPGAPHTTAHGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYM 1949

QY 1964 CRNGSTAERSLHGRGWGLPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGA 2023

Db 1950 CRNGSTAERSLHGRGWGLPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGA 2009

QY 2024 IPKLPPGRSPLAQRPLRQAARTDSDLVQGLGSRDLDLSEVSGPSCPLTRSSSFWGG 2083

Db 2010 IPKLPPGRSPLAQRPLRQAARTDSDLVQGLGSRDLDLSEVSGPSCPLTRSSSFWGG 2069

QY 2084 SIQVQORSQISQVSKHIRLPAPCPGLEPSWAKDPPETRSSLLELDTLSWISGDLPLSSQ 2143

Db 2070 SIQVQORSQISQVSKHIRLPAPCPGLEPSWAKDPPETRSSLLELDTLSWISGDLPLSSQ 2129

QY 2144 EEPLFPRDLKKCYSVETOSCRRRPGFWLDEORRHSAIVSCLDSGQPRCPSPSSLGQP 2203

Db 2130 EEPLFPRDLKKCYSVETOSCRRRPGFWLDEORRHSAIVSCLDSGQPRCPSPSSLGQP 2189

QY 2204 LGGPGSRPKKLSPPSISIDPPESQSRPPCPGVCLRRRAPASDSKDPSSVSPLDSTAA 2263

Db 2190 LGGPGSRPKKLSPPSISIDPPESQSRPPCPGVCLRRRAPASDSKDPSSVSPLDSTAA 2249

QY 2264 SPSPKDRTLSSLGLSSDPTDMDP 2286

Db 2250 SPSPKDRTLSSLGLSSDPTDMDP 2272

QY 1382 TKILGMLRVLRLRLTLRPLRVISRAOGLKLVVETLMSSSLKPIGNIIVVICCAFFIIFGILG 1441
Db |||||
QY 1350 TKILGMLRVLRLRLTLRPLRVISRAOGLKLVVETLMSSSLKPIGNIIVVICCAFFIIFGILG 1409
Db |||||
QY 1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASVRWRHKYNFDNLGQALMSLFVLASKDQWVD 1501
Db |||||
QY 1410 VQLFKGKFFVCQGEDTRNITNKSDCAEASVRWRHKYNFDNLGQALMSLFVLASKDQWVD 1469
QY 1502 IMYDGLDAVGVDQDQPIIMNHNPMWMLLYFISFELLIVAFVFLNMFVGVVVENFHKCRHQHEE 1561
Db |||||
QY 1470 IMYDGLDAVGVDQDQPIIMNHNPMWMLLYFISFELLIVAFVFLNMFVGVVVENFHKCRHQHEE 1529
QY 1562 EARRREKRLRLEKKRR-----SKEQMAEAQCKPYSDYSRFRLLVHHLCTS 1610
Db |||||
QY 1530 EARRREKRLRLEKKRRNMLDDVIASSSSASAASEAQCKPYSDYSRFRLLVHHLCTS 1589
QY 1611 HYLDLFIITGVLNVVTMAMEHYQQQILDEALKICNYIFTVIFVFESVFKLVAFARRF 1670
Db |||||
QY 1590 HYLDLFIITGVLNVVTMAMEHYQQQILDEALKICNYIFTVIFVFESVFKLVAFARRF 1649
QY 1671 FQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1730
Db |||||
QY 1650 FQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1709
QY 1731 ALLHTVMQALPOVGNLGLLFFLFFIFAALGVLELFGDLECDTHCEGLGRHATERNFGM 1790
Db |||||
QY 1710 ALLHTVMQALPOVGNLGLLFFLFFIFAALGVLELFGDLECDTHCEGLGRHATERNFGM 1769
QY 1791 AFLTLFRVSTGDNWNGIMKOPSRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVI AVL 1850
Db |||||
QY 1770 AFLTLFRVSTGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVI AVL 1829
QY 1851 MKHLEESNKEAKEAELEAELEMKTLSPQPHSPLGSPFLWPGEVGNSTDSPKGAPH 1910
Db |||||
QY 1830 MKHLEESNKEAKEAELEAELEMKTLSPQPHSPLGSPFLWPGEVGNSTDSPKGAPH 1889
QY 1911 TTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA 1970
Db |||||
QY 1890 TTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA 1949
QY 1971 ERSGLHRGWGLPKAQSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPP 2030
Db |||||
QY 1950 ERSGLHRGWGLPKAQSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPP 2009
QY 2031 GRSPLAQRLRRQAAIRTDSDLVQGLGSRDRLLESEVSGPSCPLTRSSSFWGSSIQVQOR 2090
Db |||||
QY 2010 GRSPLAQRLRRQAAIRTDSDLVQGLGSRDRLLESEVSGPSCPLTRSSSFWGSSIQVQOR 2069
QY 2091 SGIQSVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLPSSQBEPLFPR 2150
Db |||||
QY 2070 SGIQSVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLPSSQBEPLFPR 2129
QY 2151 DLKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGPSR 2210
Db |||||
QY 2130 DLKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGPSR 2189
QY 2211 PKKKLSPPSISIDPPESQSGSRPPCPGVCLRRRAPADSKDPSVSSPLDSTAASPSPKKD 2270
Db |||||
QY 2190 PKKKLSPPSISIDPPESQSGSRPPCPGVCLRRRAPADSKDPSVSSPLDSTAASPSPKKD 2249
QY 2271 TLSLSGLSSDPTDMDP 2286
Db |||||
QY 2250 TLSLSGLSSDPTDMDP 2265

RESULT 5
AAV14593
ID AAY14593 standard; protein; 2247 AA.
XX
AC AAY14593;
XX
DT 07-DEC-1999 (first entry)

XX Rat T-type voltage-gated Ca channel alpha-1-G (rCavTld).
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
KW Rattus sp.
XX WO9929847-A1.
XX 17-JUN-1999.
XX 30-OCT-1998; 98WO-US023161.
PF 05-DEC-1997; 97US-00985809.
PR (LOYO) UNIV LOYOLA CHICAGO.
XX Perez-Reyes E, Cribbs LL;
XX WPI; 1999-394972/33.
DR N-PSDB; AAX83488.
XX New T-type voltage-gated calcium channels.
PT Disclosure; Page 94-103; 138pp; English.
XX This sequence represents a rat T-type voltage-gated calcium (Ca) channel
PS alpha-1-G designated rCavTld. Voltage gated channels are membrane bound
XX glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC -channels contains a putative IVS4 region comprising the amino acid
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium
CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel nucleic
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 2247 AA;

Query Match 96.5%; Score 11606.5; DB 2; Length 2247;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2211; Conservative 1; Mismatches 6; Indels 7; Gaps 1;
QY 62 GAAGAGSTEKDPGSADSEAGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPFVRSML 121
Db |||||
QY 30 GRQPGSTEKDPGSADSEAGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPFVRSML 89
QY 122 VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
Db |||||
QY 90 VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149
QY 182 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLTLP 241
Db |||||
QY 150 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMRILVTLTLP 209
QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPSVDLEPYQTENEDESPF 301
Db |||||
QY 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPSVDLEPYQTENEDESPF 269
QY 302 ICSQPRENGMRSCRSVPTLRGEGGGPPCPSLDYETYNSSNTTCVNNQYTNCSAGEHN 361
Db |||||
QY 270 ICSQPRENGMRSCRSVPTLRGEGGGPPCPSLDYETYNSSNTTCVNNQYTNCSAGEHN 329
QY 362 PFKGAINFDNIGYAWIAFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 421
|||

Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

QY 422 CLVVIATQFSETKQRESQLMREQVRFLSNASTILASFSEPGSCYEELLKYLVIYLRKAAR 481

Db 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTILASFSEPGSCYEELLKYLVIYLRKAAR 449

QY 482 RLAQVRAIGVRAGLLSSPVARSQEPQPSGSCSTRSHRRLSVHHLVHHHHHHHHVHLGN 541

Db 450 RLAQVRAIGVRAGLLSSPVARSQEPQPSGSCSTRSHRRLSVHHLVHHHHHHHHVHLGN 509

QY 542 GTLRVPRAASPEIQDRDANGSRRLMLPPPSTPTSPGGPPRGAESVHSFYHADCHLEPVRQ 601

Db 510 GTLRVPRAASPEIQDRDANGSRRLMLPPPSTPTSPGGPPRGAESVHSFYHADCHLEPVRQ 569

QY 602 APPPRCPSEASGRVTGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSTNIPPGPF 661

Db 570 APPPRCPSEASGRVTGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSTNIPPGPF 629

QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 721

Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 689

QY 722 SEAVYEFTQDAQHSDLRDPHSRRRRQSLGPDPAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781

Db 690 SEAVYEFTQDAQHSDLRDPHSRRRRQSLGPDPAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

QY 782 IMIAILVNILSMGIEYHEQPEELTNALEISNIVETSLFALEMLLKLLVYGPFYIKNPYN 841

Db 750 IMIAILVNILSMGIEYHEQPEELTNALEISNIVETSLFALEMLLKLLVYGPFYIKNPYN 809

QY 842 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRFPAQORQLVLMKTMNDVATF 901

Db 810 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRFPAQORQLVLMKTMNDVATF 869

QY 902 CMLLMFLIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTOEDWNKV 961

Db 870 CMLLMFLIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTOEDWNKV 929

QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEQDATKSESEPDFFSVD 1021

Db 930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEQDATKSESEPDFFSVD 989

QY 1022 GDGDRKKRLALVALGEHAELRKSLPLLIHTAATPM SHPKSSSTGVGEALGSGSRTSS 1081

Db 990 GDGDRKKRLALVALGEHAELRKSLPLLIHTAATPM SHPKSSSTGVGEALGSGSRTSS 1049

QY 1082 SGSAEPGAAHHEMKPPSARSSPHSPWSAASSWTSSRRSSRNSLGRAPSLKRRSPSGERRS 1141

Db 1050 SGSAEPGAAHHEMKPPSARSSPHSPWSAASSWTSSRRSSRNSLGRAPSLKRRSPSGERRS 1109

QY 1142 LLSGEGQESQDEESSEEDRASPGSDHHRHGSGLEREAQSSFDLPDTLOVPLHRTASGR 1201

Db 1110 LLSGEGQESQDEESSEEDRASPGSDHHRHGSGLEREAQSSFDLPDTLOVPLHRTASGR 1169

QY 1202 SSASEHQDCNGKSASGRRLARTLRDTPQLDGGDDNDENGLSKGERIQAWVRSRLPACCRE 1261

Db 1170 SSASEHQDCNGKSASGRRLARTLRDTPQLDGGDDNDENGLSKGERIQAWVRSRLPACCRE 1229

QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321

Db 1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289

QY 1322 TLSNVIYFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSG 1381

Db 1290 TLSNVIYFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSG 1349

QY 1382 TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441

Db 1350 TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409

QY 1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKYNFDNLGQALMSLFLVASKDGWVD 1501

Db 1410 VQLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKYNFDNLGQALMSLFLVASKDGWVD 1469

QY 1502 IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFVFLNMVFGVVVENFHKRQHQHEE 1561

Db 1470 IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFVFLNMVFGVVVENFHKRQHQHEE 1529

QY 1562 EARRREKRLRLLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFTITGVI 1621

Db 1530 EARRREKRLRLLEKKRR :-----KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFTITGVI 1582

QY 1622 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFARFRFFQDRWNQDLA 1681

Db 1583 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGRFRFFQDRWNQDLA 1642

QY 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALHHTVMQALP 1741

Db 1643 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALHHTVMQALP 1702

QY 1742 QVGNLGLLFMLLFFIFAALGVLEFGDLECEDETHPCCEGLGRHATFRNFGMAFLTILFRVSTG 1801

Db 1703 QVGNLGLLFMLLFFIFAALGVLEFGDLECEDETHPCCEGLGRHATFRNFGMAFLTILFRVSTG 1762

QY 1802 DNWNGIMKDPSTRDCQESTCYNTVISP IYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEA 1861

Db 1763 DNWNGIMKDTLRDCQESTCYNTVISP IYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEA 1822

QY 1862 KEEAELEAELEEMKTLSPQHPSPGLSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921

Db 1823 KEEAELEAELEEMKTLSPQHPSPGLSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAASGF 1882

QY 1922 SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHGWGL 1981

Db 1883 SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHGWGL 1942

QY 1982 PKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQPLR 2041

Db 1943 PKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQPLR 2002

QY 2042 RQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101

Db 2003 RQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2062

QY 2102 RLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLPSQEPFLPRDLKKCYSVETQ 2161

Db 2063 RLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLPSQEPFLPRDLKKCYSVETQ 2122

QY 2162 SCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGPSRPPKKLSPPSIS 2221

Db 2123 SCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGPSRPPKKLSPPSIS 2182

QY 2222 IDPPESQGSRRPCCSPGVCLRRRAPASDSKDPSSVSSPLDSTAASPSPKKDTLSLGLSSDP 2281

Db 2183 IDPPESQGSRRPCCSPGVCLRRRAPASDSKDPSSVSSPLDSTAASPSPKKDTLSLGLSSDP 2242

QY 2282 TDMDP 2286

Db 2243 TDMDP 2247

RESULT 6
AAY70720

ID AAY70720 standard; protein; 2428 AA.

XX AAY70720;

XX AC

XX DT 18-JUL-2000 (first entry)

XX DE Rat pancreatic T-type calcium channel.

XX DE Rat; pancreatic T-type calcium channel alpha1 subunit; insulin;
KW pancreatic beta cell; alpha1G; low voltage activated Ca2+ channel family;
KW antidiabetic; calcium influx; L type calcium channel; NIDDM;
KW type II diabetes; non-insulin dependent diabetes mellitus.

XX

OS Rattus sp.

XX Key Location/Qualifiers

FT 1. 52

FT /note= "Region upstream to pancreatic T-type calcium

FT channel protein"

FT Misc-difference 4

FT /note= "Encoded by in-frame stop codon TGA"

FT Protein 53. 2428

FT /label= Pancreatic T-type calcium channel_alphal_subunit

FT /note= "This region is claimed as SEQ ID NO: 2"

FT 53. 86

FT /note= "Unique region that differs from amino acid

FT sequence of neuronal T-type calcium channel_alphal

FT subunit (alpha1G)"

FT 1023. 1046

FT /label= Intracellular_loop_I(II-III)

FT /note= "Unique region that differs from amino acid

FT sequence of neuronal T-type calcium channel_alphal

FT subunit (alpha1G)"

FT 1622. 1640

FT /label= Intracellular_loop_L(III-IV)

FT /note= "Unique region that differs from amino acid

FT sequence of neuronal T-type calcium channel_alphal

FT subunit (alpha1G)"

FT Misc-difference 2341

FT /note= "Encoded by in-frame stop codon TGA"

FT Misc-difference 2371

FT /note= "Encoded by in-frame stop codon TAA"

XX WO200015845-A1.

PN 23-MAR-2000.

XX 26-AUG-1999; 99WO-US019675.

XX 26-AUG-1998; 98US-0098004P.

PR 27-JAN-1999; 99US-0117399P.

XX (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.

PA

XX Li M;

PI

XX WPI; 2000-271475/23.

DR N-PSDB; AAZ52309.

DR

XX Novel nucleic acids encoding pancreatic T-type calcium channels used for

PT regulation of T-type calcium channels and treatment of type II diabetes.

XX

PS Example 1; Page 120; 124pp; English.

XX

CC The present sequence is a protein that includes pancreatic T-type calcium

CC channel alphasubunit derived from rat insulin secreting beta cell line,

CC INS-1. The protein shows 96.3 % identity to the neuronal T-type calcium

CC channel alphasubunit (alpha1G). The T-type Ca2+ channel from INS-1

CC (alpha1G-INS) and neuronal alphasubunit are alternative splice isoforms of the

CC same gene. The INS-1 isoform is also expressed in brain, neonatal heart

CC and kidney besides pancreatic beta cells. T-type Ca2+ channel belongs to

CC the family of low voltage activated Ca2+ channels. The present sequence

CC is used for treating diseases associated with abnormal expression or

CC function of T-type calcium channels. They are especially used for

CC treating type II diabetes. Modulators of pancreatic T-type Ca2+ channel

CC e.g. antisense oligonucleotides, ribozymes and inhibitors are used in

CC methods for modifying insulin secretion by pancreatic beta cells, basal

CC calcium levels, potential L type calcium channel activity, pancreatic

CC cell death, pancreatic beta cell proliferation and calcium influx through

CC L type calcium channels in cells

XX

SQ Sequence 2428 AA;

Query Match 96.0%; Score 11542.5; DB 3; Length 2428;

Best Local Similarity 95.4%; Pred. No. 0;

Matches 2219; Conservative 3; Mismatches 54; Indels 51; Gaps 4;

QY 3 PHRVPRCVRTPPPLRGSARPSSDPPGPRLARGWTRRRMERAPSRSDSPVASRS----- 54

Db 22 PTGVPRLRREDTSSEGLRSLPLFGPPGAPAG-----QRMDEEDGAGAEESGQPRSTQ 73

QY 55 -STTCPGGAAGAGSTEKOPGSADEAEGLPYPALAPVVFYLSQDSRPSWCLRTVCNP 113

Db 74 LNDLSGAGGRQPGSTKOPGSADEAEGLPYPALAPVVFYLSQDSRPSWCLRTVCNP 133

QY 114 WFERVSMVLVLLNCVTGLMFRPCEDIACDSORCRILQAFDDFIFAFFAVEMVVMVALGI 173

Db 134 WFERVSMVLVLLNCVTGLMFRPCEDIACDSORCRILQAFDDFIFAFFAVEMVVMVALGI 193

QY 174 FGKCCYLGDWTNRLDFFIVIAAGMLEYSLDLQNVSFSAVTRVRLPLRAINRVPSMRILV 233

Db 194 FGKCCYLGDWTNRLDFFIVIAAGMLEYSLDLQNVSFSAVTRVRLPLRAINRVPSMRILV 253

QY 234 TLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVDLEPYQT 293

Db 254 TLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVDLEPYQT 313

QY 294 ENEDESPFICSPRENGMRSCSVPTLRGEGGGPPCSLDIYETYNSSNTTCVNWNQYVT 353

Db 314 ENEDESPFICSPRENGMRSCSVPTLRGEGGGPPCSLDIYETYNSSNTTCVNWNQYVT 373

QY 354 NCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYFILLIIV 413

Db 374 NCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYFILLIIV 433

QY 414 GSFFMINCLVVIATQFSETKQRESQLMREQVRVFNASTLASFSEPGSCYEELLKYLIV 473

Db 434 GSFFMINCLVVIATQFSETKQRESQLMREQVRVFNASTLASFSEPGSCYEELLKYLIV 493

QY 474 YILRKAARRLAQVSRRAIGVRAGLLSSPVARSGQEPQSGSCSTRSHRRLSVHHLVHHHHH 533

Db 494 YILRKAARRLAQVSRRAIGVRAGLLSSPVARSGQEPQSGSCSTRSHRRLSVHHLVHHHHH 553

QY 534 HHYHLGNGTLRVPRASPEIQDRDANGSRRLLMLPPSTPTPSGGPPRGAEVSFYHAD 593

Db 554 HHYHLGNGTLRVPRASPEIQDRDANGSRRLLMLPPSTPTPSGGPPRGAEVSFYHAD 613

QY 594 HLEPVRCQAPPPRCPEASGRVTGSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTS 653

Db 614 HLEPVRCQAPPPRCPEASGRVTGSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTS 673

QY 654 ENTPPGPFSSMHKLLTOSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESA 713

Db 674 ENTPPGPFSSMHKLLTOSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESA 733

QY 714 DHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQSRSLGPDAPSSVLAFWRLICDTRKIV 773

Db 734 DHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQSRSLGPDAPSSVLAFWRLICDTRKIV 793

QY 774 DSKYFGRGIMIALVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLLKLLVYGP 833

Db 794 DSKYFGRGIMIALVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLLKLLVYGP 853

QY 834 GYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMK 893

Db 854 GYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMK 913

QY 894 TMDNVATFCMLLMFIFISILGMHLFGCKFASERDGTLPDRKNPDSLLWAIIVTFQIL 953

Db 914 TMDNVATFCMLLMFIFISILGMHLFGCKFASERDGTLPDRKNPDSLLWAIIVTFQIL 973

QY 954 TQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAE----- 1003

Db 974 TQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEIIGKREDASG 1033

QY 1004 -----GDATKSESEPDFFSPSVGDGDRKKRLALVALGEHAELRKSLLPPLI 1050

Db 1034 QLSCIQLPVNSQGGDATKSESEPDFFSPSVGDGDRKKRLALVALGEHAELRKSLLPPLI 1093

QY 1051 IHTAATPMShPKSSSTGVGEALGSGRRRTSSGSAEPGAHHEMKCPPSARSSPHSPWSA 1110
Db 1094 IHTAATPMSLpKSSSTGVGEALGSGRRRTSSGSAEPGAHHEMKSPPSARSSPHSPWSA 1153
QY 1111 ASSWTSRRSSRNSLGRAPSLKRSPSGERRSLLSGEGQESODEEESSEEDRASPGSDHR 1170
Db 1154 ASSWTSRRSSRNSLGRAPSLKRSPSGERRSLLSGEGQESODEEESSEEDRASPGSDHR 1213
QY 1171 HRGSLEREAKSSFDPDLPTLQVPLGHLRTASGRSSASEHQDCNGKSASGRLARTLRITDDPQL 1230
Db 1214 HRGSLEREAKSSFDPDLPTLQVPLGHLRTASGRSSASEHQDCNGKSASGRLARTLRITDDPQL 1273
QY 1231 DGDDNDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMF 1290
Db 1274 DGDDNDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMF 1333
QY 1291 HVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFFGEQ 1350
Db 1334 HVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFFGEQ 1393
QY 1351 AYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTRLRPLRVISRAQGLK 1410
Db 1394 AYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTRLRPLRVISRAQGLK 1453
QY 1411 LVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEAS 1470
Db 1454 LVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEAS 1513
QY 1471 YRWVRHKYNFDNLGQALMSLFLVASKDGWVDIMYDGLDAVGVDQOOPIMNHNPWMLLYFIS 1530
Db 1514 YRWVRHKYNFDNLGQALMSLFLVASKDGWVDIMYDGLDAVGVDQOOPIMNHNPWMLLYFIS 1573
QY 1531 FLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREKLRRLRLEKRR----- 1579
Db 1574 FLLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREKLRRLRLEKRRMLDDVIASG 1633
QY 1580 SKEQMAEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQIL 1639
Db 1634 SSASAASEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQIL 1693
QY 1640 DEALKICNYIFTVIFVFESVFKLVAFAFERFFQDRWNQDLAIVLLSIMGITLEEIEVN 1699
Db 1694 DEALKICNYIFTVIFVFESVFKLVAFAFERFFQDRWNQDLAIVLLSIMGITLEEIEVNA 1753
QY 1700 SLPINPTIIRMRVLRARVLKLLKMAVGMRALHTHTVMQALPQVGNLGLLFFLFFIFAA 1759
Db 1754 SLPINPTIIRMRVLRARVLKLLKMAVGMRALHTHTVMQALPQVGNLGLLFFLFFIFAA 1813
QY 1760 LGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSCRDCQES 1819
Db 1814 LGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCQES 1873
QY 1820 TCYNTVISPIYFVSFVLTAQFVLNVNVTIAVLMKHLEESNKEAEAELEAEELEMKTILS 1879
Db 1874 TCYNTVISPIYFVSFVLTAQFVLNVNVTIAVLMKHLEESNKEAEAELEAEELEMKTILS 1933
QY 1880 PQPHSPLGSPFLWPGEVGNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPL 1939
Db 1934 PQPHSPLGSPFLWPGEVGNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPL 1993
QY 1940 GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHGWGLPKAQSGSILSVHSQPADT 1999
Db 1994 GPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHGWGLPKAQSGSILSVHSQPADT 2053
QY 2000 SCILQLPKDVHYLLQPHGAPTGWAI PKLPPPGESPLAQRLRRQAIRTDSL DVQGLGSR 2059
Db 2054 SCILQLPKDVHYLLQPHGAPTGWAI PKLPPPGESPLAQRLRRQAIRTDSL DVQGLGSR 2113
QY 2060 EDLLSEVSGPSCPLTRSSFWGGSSIQVQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPP 2119
Db 2114 EDLLSEVSGPSCPLTRSSFWGGSSIQVQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPP 2173
QY 2120 ETRSSLELDTLSWISGDLPLSSQEEPLFPRDLKKCYSVETQSCRRRPPGFWLDEQRRHSI 2179

Db 2174 ETRSSLELDTLSWISGDLPLSSQEEPLSPRDLKKCYSVETQSCRRRPPGSWLDEQRRHSI 2233
QY 2180 AVSCLDSGSGPRLCPSSSLGGQPLGGGSRPKKKLSPPSISIDPPESQGSRRPPCSPGVC 2239
Db 2234 AVSCLDSGSGPRLCPSSSLGGQPLGGGSRPKKKLSPPSISIDPPESQGSRRPPCSPGVC 2293
QY 2240 LRRRAPASDSKDPVSSPLDSTAASPSPKKDTLSLSGLSSDPTMDP 2286
Db 2294 LRRRAPASDSKDPVSSPLDSTAASPSPKKDTLSLSGLSSDPTMDP 2340
RESULT 7
AAY14586
ID AAY14586 standard; protein; 2250 AA.
XX AAY14586;
AC AAY14586;
XX 07-DEC-1999 (first entry)
DT 07-DEC-1999 (first entry)
XX Human T-type voltage-gated Ca channel alpha-1-G (hCavT1a).
DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
KW Homo sapiens.
XX OS
XX WO9929847-A1.
PN 17-JUN-1999.
XX 30-OCT-1998; 98WO-US023161.
PF 05-DEC-1997; 97US-00985809.
XX (LOYO) UNIV LOYOLA CHICAGO.
PA Perez-Reyes E, Cribbs LL;
XX WPI; 1999-394972/33.
DR N-PSDB; AAX83481.
XX New T-type voltage-gated calcium channels.
PT Disclosure; Page 31-40; 138pp; English.
XX This sequence represents a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCavT1a. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

SQ Sequence 2250 AA;

Query Match 90.3%; Score 10857; DB 2; Length 2250;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 2084; Conservative 32; Mismatches 104; Indels 6; Gaps 4;

QY 62 GAAGAGSTKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSCLRVCNPNWFERVSM 121
Db 30 GRPGGSAEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSCLRVCNPNWFERISML 89

QY 122 VILLNCVTLGMFRCEDIACDSQRCRILQAFDDFIFAFAVEMVVMVALGIFGKKCYLG 181
Db 90 VILLNCVTLGMFRCEDIACDSQRCRILQAFDDFIFAFAVEMVVMVALGIFGKKCYLG 149
QY 182 DTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTP 241
Db 150 DTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTP 209
QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNCFLPENFSLPLSDLEPYQ TENEDESP 301
Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNCFLPENFSLPLSDLEPYQ TENEDESP 269
QY 302 ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSNTTCVNMNQY YTNCSAGEHN 361
Db 270 ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSNTTCVNMNQY YTNCSAGEHN 329
QY 362 PFKGAINEDNIGYAWIAIFQVITLEGVVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL 421
Db 330 PFKGAINEDNIGYAWIAIFQVITLEGVVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL 389
QY 422 CLVVIATQFSETKQRESQOLMREQVRFLSNASTLASFSEPGSCYEELLYLVILRKAAR 481
Db 390 CLVVIATQFSETKQRESQOLMREQVRFLSNASTLASFSEPGSCYEELLYLVILRKAAR 449
QY 482 RLAQVSRAIGVRAGLLSSPVARSQGEQPPSGSCTRSHRRLSVHHLVHHHHHHYHLGN 541
Db 450 RLAQVSRAIGVRAGLLSSPVARSQGEQPPSGSCTRSHRRLSVHHLVHHHHHHYHLGN 509
QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
Db 510 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569
QY 602 APPRCPSEASGRVSGKVYPTVHTSPPPPEILKDKALVEVAPSPGPTLTSENIPPGPF 661
Db 570 APPRCPSEASGRVSGKVYPTVHTSPPPPEILKDKALVEVAPSPGPTLTSENIPPGPF 629
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHVMPDSD 721
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHVMPDSD 689
QY 722 SEAVYEFTQDAQHSDLRDPHRRRQSRSLGPDPAEPSVLAFWRLICDTFRKIVDSKYFGRG 781
Db 690 SEAVYEFTQDAQHSDLRDPHRRRQSRSLGPDPAEPSVLAFWRLICDTFRKIVDSKYFGRG 748
QY 782 IMIAILVNTLSMGIYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFYIKNPYN 841
Db 749 IMIAILVNTLSMGIYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFYIKNPYN 808
QY 842 IFDGVIVVSWEIVGQGGGLSVLRTFRLMRVLKLVRELPAQRLVLMKTMNDVATF 901
Db 809 IFDGVIVVSWEIVGQGGGLSVLRTFRLMRVLKLVRELPAQRLVLMKTMNDVATF 868
QY 902 CMLLMFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAI VTFVQILTQEDWNKV 961
Db 869 CMLLMFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAI VTFVQILTQEDWNKV 928
QY 962 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEDPFFSPSD 1021
Db 929 LYNMGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEDPFFSPSD 988
QY 1022 GDGDRKRLALVALGEHAELRKSLLPPLI IHTAATPM SHPKSSSTGVGEALGSGRR TSS 1081
Db 989 GDGDRKRLALVALGEHAELRKSLLPPLI IHTAATPM SHPKSSSTGVGEALGSGRR TSS 1048
QY 1082 SGSAEPGA AHMKCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRS 1141
Db 1049 SGSAEPGAA -HEMKSPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRS 1107
QY 1142 LLSGEGQESQDEEESSEEDRASGAGSDHRRGSLEREA KSFDLPDTLQVPGHLRTASGR 1201
Db 1108 LLSGEGQESQDEEESSEEDRASGAGSDHRRGSLEREA KSFDLPDTLQVPGHLRTASGR 1167

QY 1202 SSASEHQDCNGKSASGRRLARTLRTDDPQLDGGDDNDDEGNLSKGERIQAWVRSRLPACC RE 1261
Db 1168 GSASEHQDCNGKSASGRRLARALRPDDPLDGGDDADDEGNLSKGERVRAWIRARLPAC CLE 1227
QY 1262 RDSWSAYIFPPQSRPRLCHR IITHKMFHDVVVLV IIFLNCITIAMERPKIDPHSAERIFL 1321
Db 1228 RDSWSAYIFPPQSRPRLCHR IITHKMFHDVVVLV IIFLNCITIAMERPKIDPHSAERIFL 1287
QY 1322 TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLVLISVIDILVSMVSDSG 1381
Db 1288 TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLVLISVIDILVSMVSDSG 1347
QY 1382 TKILGMLRVLRLLRTLRLRVISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILG 1441
Db 1348 TKILGMLRVLRLLRTLRLRVISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILG 1407
QY 1442 VQLFKGKFFVCOGEDTRNITNKSDCAEASRYWRVVRHKYNFNDLGOALMSL FVLASKDGWVD 1501
Db 1408 VQLFKGKFFVCOGEDTRNITNKSDCAEASRYWRVVRHKYNFNDLGOALMSL FVLASKDGWVD 1467
QY 1502 IMYDGLDAVGVDQQPIMNHNPMWLLYFISFLLIIVAFFVLNMFGVVVENFHKCRHQE EEE 1561
Db 1468 IMYDGLDAVGVDQQPIMNHNPMWLLYFISFLLIIVAFFVLNMFGVVVENFHKCRHQE EEE 1527
QY 1562 EARRREEKRLRLEKKRRSKEKQMAEAOCKPYYSYDYSRPRLLVHHLCTSHYLDLFTGVI 1621
Db 1528 EARRREEKRLRLEKKRRSKEKQMAEAOCKPYYSYDYSRPRLLVHHLCTSHYLDLFTGVI 1587
QY 1622 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVKLVAFARFRFFQDRWNQDLA 1681
Db 1588 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVKLVAFARFRFFQDRWNQDLA 1647
QY 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1741
Db 1648 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1707
QY 1742 QVGNLGLLFMLLFFIFAALGVLELFGDLECEDETHPCCEGLGRHATFRNFGMAFLTLFRVSTG 1801
Db 1708 QVGNLGLLFMLLFFIFAALGVLELFGDLECEDETHPCCEGLGRHATFRNFGMAFLTLFRVSTG 1767
QY 1802 DNWNKIMKDPSCDCQESTCVNTVISPIYFVSFVLTAQFVLNVVVI AVLKMHLEESNKEA 1861
Db 1768 DNWNKIMKDLRDCQESTCVNTVISPIYFVSFVLTAQFVLNVVVI AVLKMHLEESNKEA 1827
QY 1862 KEEAELEAELEEMKTLSPQHPSPGLSPFLWPVGVEGVNSTDSPKPGAPHTTAHICAASGF 1921
Db 1828 KEEAELEAELEEMKTLSPQHPSPGLSPFLWPVGVEGVNSTDSPKPGALHPAAHARSASHF 1887
QY 1922 SLEHPTMVPHPEEVPVPLGPDLTVRKSGVSRTHSLPNDSYMCRNGSTAE RSLGHRGWGL 1981
Db 1888 SLEHPTMQPHPTLP ---GPDLTVRKSGVSRTHSLPNDSYMCRHGSTAEGLGHRGWGL 1944
QY 1982 PKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPGGRSPLAQRP L 2041
Db 1945 PKAQSGSVLSVHSQPADTSYILQPKDAPHLLOPHSAPTWTGTIPKLPPGGRSPLAQRP L 2004
QY 2042 RQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSIGIQSKVSKHI 2101
Db 2005 RQAAIRTDSDLVQGLGSRREDLLAEVSGPSPPLARAYFWGQSSTQAQHSRSHSKISKHM 2064
QY 2102 RLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDL -PSSQEEPLFPRDLKKCYSVET 2160
Db 2065 TTPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSVEA 2124
QY 2161 QSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPLSGQPLGGPSRPPKKLSPPSI 2220
Db 2125 QSCRRRPTWLDEQRRHSIAVSCLDGSGQPHLGTDPNLSGGQPLGGPSRPPKKLSPPSI 2184
QY 2221 SIDPPESQGSRRPPCSPGVCLRRRAPASDSKDPVSYPDLSTAA SPSPKXDTLSLGLSSD 2280
Db 2185 TIDPPESQGPRTPPSPGICLRRRAPSSDSKDFLASGPPDMSAASPSPKDVLSLGLSSD 2244
QY 2281 PTMDMP 2286

Db 30 GRPCGSAEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNWPFERISML 89

QY 122 VILLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIAPFAFVEMVVKMVALGFGKKCYLG 181

Db 90 VILLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIAPFAFVEMVVKMVALGFGKKCYLG 149

QY 182 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRULPLRAINRVPSMRILVTLLDTP 241

Db 150 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRULPLRAINRVPSMRILVTLLDTP 209

QY 242 MLGNVLLLCFFVFFIFIGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQ TENEDESP 301

Db 210 MLGNVLLLCFFVFFIFIGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYQ TENEDESP 269

QY 302 ICSPRENMRSCRSVPTLRGEGGGPPCSDLYETXNSSNTTCVNWNQYTNCSAGEHN 361

Db 270 ICSPRENMRSCRSVPTLRGEGGGPPCGLDYEAYNSSNTTCVNWNQYTNCSAGEHN 329

QY 362 PFKGAINFDNIGYAWIAIFQVITLLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSPFMINL 421

Db 330 PFKGAINFDNIGYAWIAIFQVITLLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSPFMINL 389

QY 422 CLVVIATQSETKQRESQOLMREQVRFLSNASTLASFSEPGSCYEELLYLKYLVILRKAAR 481

Db 390 CLVVIATQSETKQRESQOLMREQVRFLSNASTLASFSEPGSCYEELLYLKYLVILRKAAR 449

QY 482 RLAQVSRAIGVRAGLLSSPVARSQGEPPQSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 541

Db 450 RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLGN 509

QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601

Db 510 GTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQ 569

QY 602 APPRCPSEASGRTVSGKVYPTVHTSPPEILKOKALVEVAPSPGPPTLTSTFNIPPGPF 661

Db 570 APPRSPSEASGRTVSGKVYPTVHTSPPETLKEKALVEVAASSGPPTLTSLNIPPGPY 629

QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 721

Db 630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689

QY 722 SEAVYEFTQDAQHSDLRDPHSRRRRQORSLGPDPAEPSSVLAFWRLICDTERKIVDSKYFGRG 781

Db 690 SEAVYEFTQDAQHSDLRDPHS - RRQRS LGPDPAEPSSVLAFWRLICDTERKIVDSKYFGRG 748

QY 782 IMIAILVNTLSMGIBYHEQPEELTNALEISNIVFTSLFALEM LKLLVYGPFGYIKNPNYN 841

Db 749 IMIAILVNTLSMGIBYHEQPEELTNALEISNIVFTSLFALEM LKLLVYGPFGYIKNPNYN 808

QY 842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALORQLVVLKMTMDNVATF 901

Db 809 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALORQLVVLKMTMDNVATF 868

QY 902 CMLLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSL LWAIVTVFQILTQEDWNKV 961

Db 869 CMLLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSL LWAIVTVFQILTQEDWNKV 928

QY 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLIVAILVEGFQAE ----- 1003

Db 929 LYNGMASTSSWAALYFIALMTFGNYVLFNLIVAILVEGFQAEISKREDASGQLSCIQLP 988

QY 1004 -----GDATKSESEPDFFSPVDGDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPM 1058

Db 989 VDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGEHPELRKSLLPPLIHTAATPM 1048

QY 1059 SHPKSSSTGVGEALGSGRRTSSSGSAEPGAHHHEMKCPPSARSSPHSPWSAASSWTSRR 1118

Db 1049 SLPKSTSTGLGEALGPASRRTSSSGSAEPGAA -HEMKSPSARSSPHSPWSAASSWTSRR 1107

QY 1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHHRGSLERE 1178

Db 1108 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQSQDEEESSEERASPGSDHHRGSLERE 1167

QY 1179 AKSSFDLPDTLOVPGLHRTASGRSSASEHQDCNGKSASGRLARTLRDTPQLDGGDDNDE 1238

Db 1168 AKSSFDLPDTLOVPGLHRTASGRSSASEHQDCNGKSASGRLARLPDDPPLDGGDDADDE 1227

QY 1239 GNLSKGERIOAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLIIF 1298

Db 1228 GNLSKGERVRAWIRARLPACCLERDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLIIF 1287

QY 1299 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGQAYLRSSWN 1358

Db 1288 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGQAYLRSSWN 1347

QY 1359 VLDGLLVLIISVIDILVSMVSDSGTKILGMLRVLRLRLRPLRVISRAQGLKLVVETLMS 1418

Db 1348 VLDGLLVLIISVIDILVSMVSDSGTKILGMLRVLRLRLRPLRVISRAQGLKLVVETLMS 1407

QY 1419 SLKPIGNIWVICCAFFIIFGILGVQLFKGKFFVCQGBDTRNITNKSDCAEASVWRVHKY 1478

Db 1408 SLKPIGNIWVICCAFFIIFGILGVQLFKGKFFVCQGBDTRNITNKSDCAEASVWRVHKY 1467

QY 1479 NFDNLGQALMSLFLVASKDGWVDIMYDGLDAVGVDQOPIMNHNPMWMLLYFISFLLIIVAFF 1538

Db 1468 NFDNLGQALMSLFLVASKDGWVDIMYDGLDAVGVDQOPIMNHNPMWMLLYFISFLLIIVAFF 1527

QY 1539 VLNMFVGVVVENFHKCRQHQBEEBARRREKRLRLEKKRRSKEKQMAEAQCKPYSDYS 1598

Db 1528 VLNMFVGVVVENFHKCRQHQBEEBARRREKRLRLEKKRRSKEKQMAEAQCKPYSDYS 1587

QY 1599 RFRLLVHHLCTSHYLDLFIITGVILNVVTMAMEHYQQPQILDDEALKICNYIFTVIFVLES 1658

Db 1588 RFRLLVHHLCTSHYLDLFIITGVILNVVTMAMEHYQQPQILDDEALKICNYIFTVIFVLES 1647

QY 1659 VFKLVAFAFERFFQDRWNQDLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIAR 1718

Db 1648 VFKLVAFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIAR 1707

QY 1719 VLKLLKMAVGMRAALLHTVMQALPQVGNLGLLFLMLFFIFAALGVELFGDLECEDETHPCEG 1778

Db 1708 VLKLLKMAVGMRAALLHTVMQALPQVGNLGLLFLMLFFIFAALGVELFGDLECEDETHPCEG 1767

QY 1779 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPDRDCDQESTCYNTVISPIYFVSFVLTA 1838

Db 1768 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTA 1827

QY 1839 QFVLNVNVVIAVLMKHLEESNKEAEAELEAELEEMTKTILSPQSPHSPGSPFLWPGEV 1898

Db 1828 QFVLNVNVVIAVLMKHLEESNKEAEAELEAELEEMTKTILSPQSPHSPGSPFLWPGEV 1887

QY 1899 NSTDSPKPGAPHTTAHGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGSVRTHSLP 1958

Db 1888 DSPDSPKPGALHPAAHARSASHFSLHPTMQPHTPELP ---GPDLLTVRKSGSVRTHSLP 1944

QY 1959 NDSYMCNRNGSTAERSLGHARGWGLPKAQSGSILSVHSQPADTSCITLQLPKDVHYLLQPHGA 2018

Db 1945 NDSYMCNRHGSTAEGPLGHRGWLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSA 2004

QY 2019 PTWGAIPKLPPPGKRSPLAQRPLRRQAAINTDSDVQGLSREDLLSEVSGPSCPLTRSSS 2078

Db 2005 PTWGTIPKLPPPGKRSPLAQRPLRRQAAINTDSDVQGLSREDLLAEVSGPSPPLARAYS 2064

QY 2079 FWGSSSIQVQORSQISQKSVSKHIRLPAPCPGLEPSPWAKOPPETRSSLELDTELSWISGDL 2138

Db 2065 FWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDL 2124

QY 2139 L-PSSQEEPLFPRDLKKCYSVETQSCRRRPPFWLDEQRRHSIAVSCLDSGSQPRLCPSPS 2197

Db 2125 LPPGGQEEPPSPRDLKKCYSEVAQSCQRRRTSWLDEQRRHSIAVSCLDSGSQPHLGTDP 2184

QY 2198 SLGGQPLGGPSRPPKKLSPPSISIDPPESQSRPPCSPGVCLRRRAPASDSDKPSVSSP 2257

Db 2185 NLGGQPLGGPSRPPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSDKPLASGP 2244

QY 2258 LDSTAASPKKDTLSLSGLSSDPTMDP 2286
Db 2245 PDSMAASPKKDVLSLSGLSSDPADLDP 2273

RESULT 10
AAY14587
ID AAY14587 standard; protein; 2261 AA.
XX
AC AAY14587;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human T-type voltage-gated Cc channel alpha-1-G (hCavT1b).
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy.

OS Homo sapiens.
XX
PN WO9929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
XX
DR N-PSDB; AAX83482.

PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 40-49; 138pp; English.

CC This sequence represents a human T-type voltage-gated calcium (Ca)
CC channel alpha-1-G designated hCavT1b. Voltage gated channels are membrane
CC bound glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC -channels contains a putative IVS4 region comprising the amino acid
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium
CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel nucleic
XX acid, e.g. to treat cardiomyopathy, epilepsy, etc

SQ Sequence 2261 AA;

Query Match 89.9%; Score 10810.5; DB 2; Length 2261;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 2078; Conservative 33; Mismatches 109; Indels 17; Gaps 5;

QY 62 GAAGAGSTEKDPGSADSEAGLPALAPVFFYLSQDSRPRSWCLRTVCNPFERVSML 121
Db 30 GRPGSGAEKDPGSADSEAGLPALAPVFFYLSQDSRPRSWCLRTVCNPFERISML 89
QY 122 VILLNCVTGLMFRPCEDIACDQRCRILQAFDDFIAPFAFVEMVVKMVALGFGKCYLG 181
Db 90 VILLNCVTGLMFRPCEDIACDQRCRILQAFDDFIAPFAFVEMVVKMVALGFGKCYLG 149
QY 182 DTWNRLDFFIAGMLEYSLDLQNVSFSAVRTVRLPLRAINRVPSMRILVTLTLLDTP 241

Db 150 DTWNRLDFFIAGMLEYSLDLQNVSFSAVRTVRLPLRAINRVPSMRILVTLTLLDTP 209
QY 242 MLGNVLLLCFFVFFIFIGVQLWAGLLNRCFLPENFSLPLSDLEFYQTENEDESPP 301
Db 210 MLGNVLLLCFFVFFIFIGVQLWAGLLNRCFLPENFSLPLSDLEFYQTENEDESPP 269
QY 302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSDLYETYNSSNTTCVWNQYTYNCSAGEHN 361
Db 270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCGLDYAYNSSNTTCVWNQYTYNCSAGEHN 329
QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYFILLIIVGSFFMINL 421
Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYFILLIIVGSFFMINL 389
QY 422 CLVVIATQFSETKQRESQRLMREQRVRFSLNASTLASFSEPGSCVEELLKYLVIYLKKAAR 481
Db 390 CLVVIATQFSETKQRESQRLMREQRVRFSLNASTLASFSEPGSCVEELLKYLVIYLKKAAR 449
QY 482 RLAQVSRAGIVRAAGLLSSPVARSQEQPPSGSCTRSRRRLSVHHLVHHHHHHHHYHLGN 541
Db 450 RLAQVSRAGIVRAAGLLSSPVARSQEQPPSGSCTRSRRRLSVHHLVHHHHHHHHYHLGN 509
QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPPTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 601
Db 510 GTLRVPRASPEIQDRDANGSRRLMLPPPTPALSGAPPGGAESVHSFYHADCHLEPVRQ 569
QY 602 APPPRCPSEASGRTVSGKVYPTVHTSPPPEILKDKALVEVAPSPGPTLTSTFNIPPGPF 661
Db 570 APPPRCPSEASGRTVSGKVYPTVHTSPPPEILKDKALVEVAPSPGPTLTSTFNIPPGPY 629
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHVPDSD 721
Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHVPDSD 689
QY 722 SEAVYEFTQDAQHSDDLDPHSRRRQSLGPDPAEPSSVLAPWRLICDTRKIVDSKYFGRG 781
Db 690 SEAVYEFTQDAQHSDDLDPHSRRRQSLGPDPAEPSSVLAPWRLICDTRKIVDSKYFGRG 748
QY 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVYGPFGYIKNPYN 841
Db 749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVYGPFGYIKNPYN 808
QY 842 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF 901
Db 809 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF 868
QY 902 CMLLMFIFIFISILGMHLFGCKFASERDGTDLPRKNFDSLWAIIVTFQILTQEDWNKV 961
Db 869 CMLLMFIFIFISILGMHLFGCKFASERDGTDLPRKNFDSLWAIIVTFQILTQEDWNKV 928
QY 962 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPPFSPSVD 1021
Db 929 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPPFSPSVD 988
QY 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMShPKSSSTGVGEALGSGSRRTSS 1081
Db 989 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMShPKSSSTGVGEALGSGSRRTSS 1048
QY 1082 SGSAPFGAAHEMKCPPSPSPSPSWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1141
Db 1049 SGSAPFGAAHEMKCPPSPSPSPSWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRS 1107
QY 1142 LLSGEGQESQDEEESSEEDRASPGSDHRRHRSGLEREAKSSFDLPDTLQVPLHRTASGR 1201
Db 1108 LLSGEGQESQDEEESSEEDRASPGSDHRRHRSGLEREAKSSFDLPDTLQVPLHRTASGR 1167
QY 1202 SSASEHQDCNGKSGASGRILARTLRTDDPQLDGGDDNDNDEGNLSKGERIQAWVRSRLPACC 1261
Db 1168 GSASEHQDCNGKSGASGRILARALRPDDPPLDGGDDADDEGNLSKGERVRAWIRARLPAC 1227
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVHVLVLIIFLNCITIAMERPKIDPHSAERIFL 1321
Db 1228 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVHVLVLIIFLNCITIAMERPKIDPHSAERIFL 1287

QY	1322	TLSNVIFTAVFLAEMTVKVVVALGWCFCGEQAYLRSSNVNLDGLLVLSVIDILVSMVSDSG	1381	XX	AAY14589;
Db	1288	TLSNVIFTAVFLAEMTVKVVVALGWCFCGEQAYLRSSNVNLDGLLVLSVIDILVSMVSDSG	1347	XX	07-DEC-1999 (first entry)
QY	1382	TKILGMLRVLRLLRTLRLPRVISRAOGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG	1441	DE	Human T-type voltage-gated Ca channel alpha-1-G (hCavT1d).
Db	1348	TKILGMLRVLRLLRTLRLPRVISRAOGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG	1407	XX	Human; T-type voltage-gated calcium channel; membrane; pore; ion;
QY	1442	VQLFKGKFVVCQGEDTRNITNKSDCAEASRYWRVHRKYNFDNLGOALMSLFLASKDGWVD	1501	KW	activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
Db	1408	VQLFKGKFVVCQGEDTRNITNKSDCAEASRYWRVHRKYNFDNLGOALMSLFLASKDGWVD	1467	XX	Homo sapiens.
QY	1502	IMYDGLDAVGVDQOPIMNHNPMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEE	1561	XX	WC9929847-A1.
Db	1468	IMYDGLDAVGVDQOPIMNHNPMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEE	1527	PD	17-JUN-1999.
QY	1562	EARRREEKRLRLEKRR-----SKEKQMAEAQCKPYSDYSRFRLLVHHLCTS	1610	XX	30-OCT-1998; 98WO-US023161.
Db	1528	EARRREEKRLRLEKRRNMLDDVIASGSSASAASEAQCKPYSDYSRFRLLVHHLCTS	1587	PR	05-DEC-1997; 97US-00985809.
QY	1611	HYLDLFIITGVLNVVTMAMEHYQOQILDEALKICNYIFTVIFVFESVFKLVAFAPRRF	1670	XX	(LOYO) UNIV LOYOLA CHICAGO.
Db	1588	HYLDLFIITGVLNVVTMAMEHYQOQILDEALKICNYIFTVIFVLESVFKLVAFAPRRF	1647	PI	Perez-Reyes E, Cribbs LL;
QY	1671	FQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR	1730	XX	WPI; 1999-394972/33.
Db	1648	FQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR	1707	DR	N-PSDB; AAX83484.
QY	1731	ALLHTVMQALPQVGNLGLLFLMLFFIPAALGVLELFGDLECDTHPCCEGLGRHATFRNFGM	1790	PT	New T-type voltage-gated calcium channels.
Db	1708	ALLDTVMQALPQVGNLGLLFLMLFFIPAALGVLELFGDLECDTHPCCEGLGRHATFRNFGM	1767	XX	Disclosure; Page 58-67; 138pp; English.
QY	1791	AFLTFRVSTGDNWNGIMKDPDRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVI AVL	1850	CC	This sequence represents a human T-type voltage-gated calcium (Ca)
Db	1768	AFLTFRVSTGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVI AVL	1827	CC	channel alpha-1-G designated hCavT1d. Voltage gated channels are membrane
QY	1851	MKHLEESNKEAKEAEAELEAELEMKTLSPQPHSPLGSPFLWPGEVGNSTDSPKPGAPH	1910	CC	bound glycosylated proteins formed of several subunits. The large alpha
Db	1828	MKHLEESNKEAKEAEAELEAELEMKTLSPQPHSPLGSPFLWPGEVGNSTDSPKPGALH	1887	CC	subunits form a pore in the membrane that is selective for a given ionic
QY	1911	TTAHIGAAAGFSLHPTMVPHEEVPVPLPGDILLTVRKSGVSRTHSLPNDSYMCRNGSTA	1970	CC	species. Each alpha subunit contains 4 domains (I, II, III and IV) and
Db	1888	PAAHARSASHFSLHPTMQPHTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTA	1944	CC	each domain contains 6 putative transmembrane helical segments (S1-S6). T
QY	1971	ERSLHRGWGLPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHCAPTWGAIPKLPPP	2030	CC	-type Ca channels are activated at a lower voltage than L- or N-type
Db	1945	EGPLHRGWGLPKAQSGSVLSVHSQPADTSVILQPKDAPHLQLQPHSAPTGTIPKLPPP	2004	CC	channels. Characteristics of T-type channels include short current time,
QY	2031	GRSPLAQRPLRROAIRTDSLVDVQGLGSRREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQR	2090	CC	slow activation kinetics near threshold, fast inactivation kinetics and
Db	2005	GRSPLAQRPLRROAIRTDSLVDVQGLGSRREDLLAEVSGPSPPLARAYSFWGQSSTQAQQH	2064	CC	slow tail current. The sequences AAX83481-X83492 represent novel T-type
QY	2091	SGIQSVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLI-PSSQEEPLFP	2149	CC	voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
Db	2065	SRSHSKISKHMTTPPAPCPGEPNWKGPPEPTRSSLELDTLSWISGDLIPLPGGQEEPPSP	2124	CC	-channels contains a putative IVS4 region comprising the amino acid
QY	2150	RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSFSSLGQPLGGPGS	2209	CC	sequence AAY14598. Cells expressing the T-type voltage-gated calcium
Db	2125	RDLKKCYSVQAQSCRRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPNSNLGGQPLGGPGS	2184	CC	channel proteins can be used to screen for drugs which affect calcium
QY	2210	RPKKLSPPSISIDPPESQSGSRPPCSPGVCLRRRAPASDSKDPSSVSSPLDSTAASPSPKK	2269	CC	channels. Methods are also disclosed for treating a disease or disorder
Db	2185	RPKKLSPPSITIDPPESQSGRPTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKK	2244	CC	associated with a deficiency in a native T-type calcium channel nucleic
QY	2270	DTLSLSGLSSDPTDMDP 2286		CC	acid, e.g. to treat cardiomyopathy, epilepsy, etc
Db	2245	DVLSLSGLSSDPADLDP 2261		XX	
RESULT 11					SQ
AAY14589					Sequence 2243 AA;
ID AAY14589 standard; protein; 2243 AA.					Query Match 89.8%; Score 10806.5; DB 2; Length 2243;
					Best Local Similarity 93.3%; Pred. No. 0;
					Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;
QY	62	GAAGAGSTKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERVSM	121	QY	62 GAAGAGSTKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERVSM
Db	30	GRPGGSAEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERISML	89	Db	30 GRPGGSAEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERISML
QY	122	VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKCYLG	181	QY	122 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKCYLG
Db	90	VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKCYLG	149	Db	90 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKCYLG
QY	182	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVTRVRLPLRAINRVFSMRILVTLLDITLP	241	QY	182 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVTRVRLPLRAINRVFSMRILVTLLDITLP
Db	150	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVTRVRLPLRAINRVFSMRILVTLLDITLP	209	Db	150 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVTRVRLPLRAINRVFSMRILVTLLDITLP
QY	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLENFSLPLSVDLEPYQTENEDESPF	301	QY	242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLENFSLPLSVDLEPYQTENEDESPF
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLENFSLPLSVDLEPYQTENEDESPF	269	Db	210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLENFSLPLSVDLEPYQTENEDESPF
QY	302	ICSQPRENGMRSCRSVPTLRGEGGGGPPCSDLYETYNSSNTTCVNMNQYVYTNCSAGEHN	361	QY	302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSDLYETYNSSNTTCVNMNQYVYTNCSAGEHN

Db 270 ICSQPRENGMRSCRSVPTLRGDGGGPPCGLDYEAYNSSNTTCVNWNQYTYTNCAGEHN 329

QY 362 PFKGAINFNDIGYAWIAIFQVITILEGWVDIMYFVMDAHSFYNYFIYFILLIIVGSPFMINL 421

Db 330 PFKGAINFNDIGYAWIAIFQVITILEGWVDIMYFVMDAHSFYNYFIYFILLIIVGSPFMINL 389

QY 422 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLYLVYLKKAAR 481

Db 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLYLVYLKKAAR 449

QY 482 RLAQVSRALGVRAGLLSSPVARSQGPQPSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 541

Db 450 RLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLGN 509

QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 601

Db 510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVHSFYHADCHLEPVRQ 569

QY 602 APPPRCPSEASGRTVSGKVYPTVHTSPPPPEILKOKALVEVAPSPGPPTLTSTFNIPPGPF 661

Db 570 APPPRSPSEASGRTVSGKVYPTVHTSPPPPETLKEKALVEVAASSGPPTLTSLNIPPGPY 629

QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHWPDS 721

Db 630 SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPCYARAGAGEVELADREMPDS 689

QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLLICDTFRKIVDSKYFGRG 781

Db 690 SEAVYEFTQDAQHSDLRDPHS-RRQSLGPDAPSSVLAFWRLLICDTFRKIVDSKYFGRG 748

QY 782 IMIAILVNTLSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841

Db 749 IMIAILVNTLSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 808

QY 842 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF 901

Db 809 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF 868

QY 902 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 961

Db 869 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 928

QY 962 LYNGMASTSSWAALYFIALMTFNGYVLFNLLVAILVEGFAEGDATKSESEPDFSPSVD 1021

Db 929 LYNGMASTSSWAALYFIALMTFNGYVLFNLLVAILVEGFAEGDANKSESEPDFSPSLD 988

QY 1022 GDGDRKKRLALVALGEAEELRKSLLPPLIIHTAATPMSPHKSSSTGVGEALGSGSRRTSS 1081

Db 989 GDGDRKKCLALVSLGEHPRLKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRTSS 1048

QY 1082 SGSAPFGAAHEMKCPPSARSPPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141

Db 1049 SGSAPFGAA-HEMKSPPSARSPPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1107

QY 1142 LLSGEGQESQDEEESSEEDRASPAGSDHRRHRSLEERAKSSFDLPDTLQVPLHRTASGR 1201

Db 1108 LLSGEGQESQDEEESSEERASAPAGSDHRRHRSLEERAKSSFDLPDTLQVPLHRTASGR 1167

QY 1202 SSASEHQDCNGKSASGRRLARTLRTDDPQLDGDNDNDEGNLSKGERIQAWVRSLPACC 1261

Db 1168 GSASEHQDCNGKSASGRRLARLPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACCLE 1227

QY 1262 RDSWAYIFPPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFL 1321

Db 1228 RDSWAYIFPPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFL 1287

QY 1322 TLSNVIPTAVFLAEMTVKVVALGWCFCGEQAYLRSSNVNLDGLLVLSIVDILVSMVSDSG 1381

Db 1288 TLSNVIPTAVFLAEMTVKVVALGWCFCGEQAYLRSSNVNLDGLLVLSIVDILVSMVSDSG 1347

QY 1382 TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICAFFIIFGILG 1441

Db 1348 TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICAFFIIFGILG 1407

QY 1442 VOLFKGKFFVCQGEDTRNITNKSDCAEASRYRVRHKYNFNDLQALMSLVASKDGWVD 1501

Db 1408 VOLFKGKFFVCQGEDTRNITNKSDCAEASRYRVRHKYNFNDLQALMSLVASKDGWVD 1467

QY 1502 IMYDGLDAVGVDQQPIMNHNPMWLLYFISFLLIIVAFFVLMNFMVGVVVENFHKCRHQHEE 1561

Db 1468 IMYDGLDAVGVDQQPIMNHNPMWLLYFISFLLIIVAFFVLMNFMVGVVVENFHKCRHQHEE 1527

QY 1562 EARRREKRLRRLEKKRRSKEKQMAEAOCKPYYSYDYSRFRLLVHHLCTSHYLDLFTITGI 1621

Db 1528 EARRREKRLRRLEKKRR- - - - -KAQCKPYYSYDYSRFRLLVHHLCTSHYLDLFTITGI 1580

QY 1622 GLNVVTMAMEHYQQOILDEALKICNYIFTVIFVFESVEKLVAFARFRFFQDRNQDLDA 1681

Db 1581 GLNVVTMAMEHYQQOILDEALKICNYIFTVIFVLESVEKLVAFGFRFFQDRNQDLDA 1640

QY 1682 IVLLSIMGITLLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVMQALP 1741

Db 1641 IVLLSIMGITLLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTMQUALP 1700

QY 1742 QVGNLGLLMLLFFIFAALGVLELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTG 1801

Db 1701 QVGNLGLLMLLFFIFAALGVLELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTG 1760

QY 1802 DNWNGIMKDPDRCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1861

Db 1761 DNWNGIMKDLTRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA 1820

QY 1862 KEEAELEAELEEMKTLSPQHSPLGSPFLWPVGVEGVNSTDSKPGAPHYTTAHIGAASGF 1921

Db 1821 KEEAELEAELEEMKTLSPQHSPLGSPFLWPVGVEGSDSPSKPGALHPAAHARSASHF 1880

QY 1922 SLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHGWGL 1981

Db 1881 SLEHPTMQPHPTLP- - -GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGELGHGWGL 1937

QY 1982 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRLR 2041

Db 1938 PKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWTGTPKLPPPGRSPLAQRLR 1997

QY 2042 RQAARTDSDLVQGLGSRDLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101

Db 1998 RQAARTDSDLVQGLGSRDLSEVSGPSPPLARAYFWGQSSTQAQOQHSRSHSKSKHM 2057

QY 2102 RLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDL- PSSQEEPLFPRDLKKCYSVET 2160

Db 2058 TPAPCPGPEPNWGKGPETRSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSVEA 2117

QY 2161 QSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGPSRPKKLSPPSI 2220

Db 2118 QSCORRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDPNLGGQPLGGPSRPKKLSPPSI 2177

QY 2221 SIDPPESQSRPPCSPGVCLRRRAPASDSKDPVSSPLDSTAASPPKDTLSLGLSSD 2280

Db 2178 TIDPPESQGRTPPSPGICLRRRAPSSDSKDPPLASGPPDSMAASPPKDVLSLGLSSD 2237

QY 2281 PTMDMP 2286

Db 2238 PADLDP 2243

RESULT 12

ADJ68819

ID ADJ68819 standard; protein; 2243 AA.

XX ADJ68819;

XX ADJ68819;

DT 06-MAY-2004 (first entry)

XX Human heat mitochondrial protein as a therapeutic target SeqID625.

DE Human heat mitochondrial protein as a therapeutic target SeqID625.

XX Human heat mitochondrial protein as a therapeutic target SeqID625.

KW mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI, 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 625; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 2243 AA;
Query Match 89.8%; Score 10806.5; DB 7; Length 2243;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;
QY 62 GAAGAGSTEKDPGSADSEAGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERSML 121
Db 30 GRPGSGAEKDPGSADSEAGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERSML 89
QY 122 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDDFIAFFAVEMVMVMVALGIFGKKCYLG 181
Db 90 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDDFIAFFAVEMVMVMVALGIFGKKCYLG 149
QY 182 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVTRVRLPLRAINRVPSMRILVTLLDITLP 241
Db 150 DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVTRVRLPLRAINRVPSMRILVTLLDITLP 209
QY 242 MLGNVLLLCFFVFFIGIVGVQLWAGLLRNRCFLPENFSLPLSVLEPYQOTENEDESPF 301
Db 210 MLGNVLLLCFFVFFIGIVGVQLWAGLLRNRCFLPENFSLPLSVLEPYQOTENEDESPF 269
QY 302 ICSQPRENGMRSRCSVPTLRGEGGGPPCSDIYETYNSSNTTCVNNQYTTNCSAGEHN 361

Db 270 ICSQPRENGMRSRCSVPTLRGEGGGPPCGLDYEAYNSSNTTCVNNQYTTNCSAGEHN 329
QY 362 PFKGAINFDNIGYAWIAIFQVITILEGWVDIMYFVMDAHSFYNYFIYFILLIIVGSFFMINL 421
Db 330 PFKGAINFDNIGYAWIAIFQVITILEGWVDIMYFVMDAHSFYNYFIYFILLIIVGSFFMINL 389
QY 422 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLYVILLRKAAR 481
Db 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLYVILLRKAAR 449
QY 482 RLAQVSRAIGVRAGLLSSPVARSQEQPQPSGSCSTRSHRRLSVHLLVHHHHHHHHHHLGN 541
Db 450 RLAQVSRAAGVRVGLLSSPAPLGGQETQPSSCSRSHRRLSVHLLVHHHHHHHHHHLGN 509
QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQC 601
Db 510 GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAESVHSFYHADCHLEPVRQC 569
QY 602 APPRCPSSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTLSNIPPGPF 661
Db 570 APPRSESEASGRTVGSGKVYPTVHTSPPETLKERALVEVAASSGPTLTLSNIPPGPY 629
QY 662 SSMHKLLETQSTGACHSSCKTSSPCSKADSGACGPDSCPYCARTGAGEPESADHWMPDSD 721
Db 630 SSMHKLLETQSTGACQSSCKTSSPCLKADSGACGPDSCPYCARAGAGEVELADREMPPSD 689
QY 722 SEAVYEFTQDAQHSDDLDRPHSRRRQSLGPDPAEPPSSVLAFWRLLICDTFRKIVDSKYFGRG 781
Db 690 SEAVYEFTQDAQHSDDLDRPHS-RRQSLGPDPAEPPSSVLAFWRLLICDTFRKIVDSKYFGRG 748
QY 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN 841
Db 749 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYN 808
QY 842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF 901
Db 809 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDNVATF 868
QY 902 CMLLMFIFISILGMHLFGCKFASERDGTLPDRKNFDSILLWAIIVTFQILTQEDWNKV 961
Db 869 CMLLMFIFISILGMHLFGCKFASERDGTLPDRKNFDSILLWAIIVTFQILTQEDWNKV 928
QY 962 LYNGMASSTSSWAALFYIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFFSPSVD 1021
Db 929 LYNGMASSTSSWAALFYIALMTFGNYVLFNLLVAILVEGFAEGDANKSESEPDFFSPSLD 988
QY 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSPHKSSTGTGVEALGSGSRRTS 1081
Db 989 GDGDRKKCLALVSLGEHPELRSLLPPLIIHTAATPMSLPKASTSTGLGEALGPASRRTS 1048
QY 1082 SGSAEPGAAHEMKCPPSARSSPHSPWSAASSWTSSRSNSLGRAPSLKRRSPSGRRS 1141
Db 1049 SGSAEPGAA-HEMKSPPSARSSPHSPWSAASSWTSSRSNSLGRAPSLKRRSPSGRRS 1107
QY 1142 LLSGEGQESQDEEESSEEDRASPDGSDHHRGSLEREAKSFDLPDITLQVPLHRTASGR 1201
Db 1108 LLSGEGQESQDEEESSEERASPDGSDHHRGSLEREAKSFDLPDITLQVPLHRTASGR 1167
QY 1202 SSASEHQDCNGKSASGRLARTLRITDQDGLDGGDDNDDEGNLSKGERIQAWVRSRLPACRE 1261
Db 1168 GSASEHQDCNGKSASGRLARALRPDDPLDGGDDADDEGNLSKGERVRAWIRARLPACCLE 1227
QY 1262 RDSWSAYIFPQSRFRLLCHRIITHKMPDHWVVLVIIIFLNCITIAMERPKIDPHSAERIFL 1321
Db 1228 RDSWSAYIFPQSRFRLLCHRIITHKMPDHWVVLVIIIFLNCITIAMERPKIDPHSAERIFL 1287
QY 1322 TLSNYIFTAVFLAEMTVKVVVALGWCFCGQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
Db 1288 TLSNYIFTAVFLAEMTVKVVVALGWCFCGQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1347
QY 1382 TKILGMLRVLRLTLRPLRVLISRAQGLKLVVETILMSSLKPIGNIVVICCAFFIIFGILG 1441

Db 1348 TKILMLRVLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILG 1407
QY 1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASRYRVRHKYNFDNLGOALMSLVASKDGWVD 1501
Db 1408 VQLFKGKFFVCQGEDTRNITNKSDCAEASRYRVRHKYNFDNLGOALMSLVASKDGWVD 1467
QY 1502 IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRHQEEE 1561
Db 1468 IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRHQEEE 1527
QY 1562 EARRREEKRLRLEKKRRSKEKQMAEAAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTGVI 1621
Db 1528 EARRREEKRLRLEKKRR- - - - -KAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTGVI 1580
QY 1622 GLNVVTMAEHYQQPQILDEALKICNYIFTVIFVFSVKLVAFARFRFFQDRWNQLDLA 1681
Db 1581 GLNVVTMAEHYQQPQILDEALKICNYIFTVIFVLESVKLVAFGRFFQDRWNQLDLA 1640
QY 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVMQALP 1741
Db 1641 IVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTVMQALP 1700
QY 1742 QVGNLGLLPMLLFFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTG 1801
Db 1701 QVGNLGLLPMLLFFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTG 1760
QY 1802 DNWNGIMKDPSTRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVVIAMVLMKHEESNKEA 1861
Db 1761 DNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVVIAMVLMKHEESNKEA 1820
QY 1862 KEEAELEAELEEMKTLSPQHPSPGLSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
Db 1821 KEEAELEAELEEMKTLSPQHPSPGLSPFLWPVGVEGVNSTDSPKPGALHPAAHARSASHF 1880
QY 1922 SLEHPTMVPHPPEVPVPLGPDLTVRKSGVSRTHSLPNDSYMCRNGSTAEKSLGRWGWL 1981
Db 1881 SLEHPTMQHPHTELP- - -GPDLTVRKSGVSRTHSLPNDSYMCRHGSTAEKSLGRWGWL 1937
QY 1982 PKAQSGSILSVHSQPADTSCIIQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRLR 2041
Db 1938 PKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWTGTPKLPPPGRSPLAQRLR 1997
QY 2042 RQAAIRTDSDVQGLGSRDLDLSEVSGPSCPLTRSSSFWGSSIOVQQRSGIQSKVKHI 2101
Db 1998 RQAAIRTDSDVQGLGSRDLDLAEVSGPSPPLARAYSPWQSSTQAQHSRSHSKISKHM 2057
QY 2102 RLPAPCPGLEPSWAKOPPETRSSLLELDTLSWISGDL- PSSQEEPLFPRDLKKCYSVET 2160
Db 2058 TPPAPCPGPEPNWKGPPETRSSLLELDTLSWISGDLPPGGQEEPPSPRDLKKCYVEA 2117
QY 2161 QSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSSLGQPLGGPGRPKKLSPPSI 2220
Db 2118 QSCRRRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDFSNLGGQPLGGPGRPKKLSPPSI 2177
QY 2221 SIDPPESQSRPPCSPGVCLRRRAPASDSKDPSSVSPDLSTAAASPPKKTLSLGLSSD 2280
Db 2178 TIDPPESQGRPTPPSPGICLRRRAPSSDSKQPLASGPPDSMAASPPKKTLSLGLSSD 2237
QY 2281 PTDMDP 2286
Db 2238 PADLDP 2243

RESULT 13
AAB66481
ID AAB66481 standard; protein; 2266 AA.
XX
AC AAB66481;
XX
DT 09-APR-2001 (first entry)
XX
DE Human alpha-IG T-type calcium channel protein.
XX

KW Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;
KW T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;
KW hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel.
XX Homo sapiens.
OS WO200102561-A2.
XX PN 11-JAN-2001.
XX PD 04-JUL-2000; 2000WO-CA000794.
XX PF 02-JUL-1999; 99US-00346794.
XX PR (NEUR-) NEUROMED TECHNOLOGIES INC.
XX PI Snutch TP, Baillie DL;
XX WPI; 2001-123111/13.
DR N-PSDB; AAF31684.
XX PT Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT epilepsy.
XX PS Example 3; Fig 6; 103pp; English.
XX CC The present sequence is given in a specification providing sequences and
CC partial sequences for three types of mammalian (human and rat) T-type
CC calcium channel subunits. An expression cassette has been generated which
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC subunit operably linked to control sequences to effect its expression.
CC The novel calcium channel nucleic acids and proteins are useful for
CC treating conditions characterised by undesirable levels of T-type calcium
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC hypertension, sleep disorder and epilepsy
XX SQ Sequence 2266 AA;

Query Match 87.6%; Score 10533; DB 4; Length 2266;
Best Local Similarity 91.2%; Pred. No. 0;
Matches 2050; Conservative 38; Mismatches 125; Indels 36; Gaps 6;

QY 62 GAAGAGSTEKDPGSADSEAGLPYPALAPVVFVYLSQDSRPSWCLRTVCNPFWRVSM 121
Db 30 GRPGSGSAEKDPGSADSEAGLPYPALAPVVFVYLSQDSRPSWCLRTVCNPFWRVSM 89
QY 122 VILLNCVTLMFRPCEDIACDSQRCRILQAFDDIFAFPAVEMVVMVALGIFGKKCYLG 181
Db 90 VILLNCVTLMFRPCEDIACDSQRCRILQAFDDIFAFPAVEMVVMVALGIFGKKCYLG 149
QY 182 DTNRLDFFVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPMSRILVTLTLP 241
Db 150 DTNRLDFFVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPMSRILVTLTLP 209
QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLPEYYQTENEDESPF 301
Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLPEYYQTENEDESPF 269
QY 302 ICSPRENGMRSCRSVPTLRGEGGGPPCSDLDYETYNSSNTTTCVNNQYTTNCSAGEHN 361
Db 270 ICSPRENGMRSCRSVPTLRGEGGGPPCGLDYEAYNSSKTTTCVNNQYTTNCSAGEHN 329
QY 362 PFKGAINFDNIGYAWIAFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL 421
Db 330 PFKGAINFDNIGYAWIAFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL 389
QY 422 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLYVILRKAAR 481
Db 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLYVILRKAAR 449
QY 482 FLAQVSRAGVRAGLSSPVARSGQEPQSGSCSTRSHRRLSVHHLVHHHHHHHHYHLGN 541

Db	450	RLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSRRRLSVNHLVHHNHMHNYHLGN	509
Qy	542	GTILVRPRASPEIQDRDANGSRRLMLPPPSTPTPSGPPRGAESVHSFYHADCHLEPVRQ	601
Db	510	GTILRAPRASPEIQDRDANGSRRLMLPPPSTPALSAPPGAESVHSFYHADCMLEPVRQ	569
Qy	602	APPRCPSEASGRTVGSGKYVPTVHTSPPPEILKDKALVEAPSPGPPILTSFNIPPGPF	661
Db	570	APPRSPSEASGRTVGSGKYVPTVNTSPPPETLKERALVEAASSGPPILTSNIPPGPY	629
Qy	662	SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD	721
Db	630	SSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDS	689
Qy	722	SEAVYFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDISKYFGRG	781
Db	690	SEAVYFTQDAQHSDLRDPHS-RRQRS LGPDAPSSVLAFWRLICDTFRKIVDISKYFGRG	748
Qy	782	IMIAILLVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFYIKNPYN	841
Db	749	IMIAILLVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFYIKNPYN	808
Qy	842	IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVVLMTMDNVATF	901
Db	809	IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVVLMTMDNVATF	868
Qy	902	CMLLMLEFIPISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV	961
Db	869	CMLLMLEFIPISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV	928
Qy	962	LYNGMASTSSWAALYFIALMTFGNVVLFNLLVAILVEGFQAE-----	1003
Db	929	LYNGMASTSSWAALYFIALMTFGNVVLFNLLVAILVEGFQAEISKREDASGQLSCIQLP	988
Qy	1004	-----GDATKSESEPdffpsvDGDGRKKRLALVALGEHAELRKSLLPPLIHTAATPM	1058
Db	989	VDSQGGDANKSESEPdffpslDGDGRKKCLALVSLGEHPELRKSLLPPLIHTAATPM	1048
Qy	1059	SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAHHEMKPCPSARSSPHSPWSAASWTSRR	1118
Db	1049	SLPKSTSTGLGEALGPASRTSSSGSAEPGAA-HEMKSPSARSSPHSPWSAASWTSRR	1107
Qy	1119	SSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEEDRASPAAGSDHRRHRSLERE	1178
Db	1108	SSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEERASPAAGSDHRRHRSLERE	1167
Qy	1179	AKSSFDLPDTLQVPGHLHRTASGRSSASEHQDCNGKSASGRLIARTLRTDDPQLDGGDDNDE	1238
Db	1168	AKSSFDLPDTLQVPGHLHRTASGRSSASEHQDCNGKSASGRLARALARPDPPPLDGGDDADDE	1227
Qy	1239	GNLSKGERIQAWVRSRLPACCRERDSWAYIFPPQSRFRLLCHRIITHKMFHDVVLVIF	1298
Db	1228	GNLSKGERVRAWTRARLPACYLERDSWAYIFPPQSRFRLLCHRIITNKMFHDVVLVIF	1287
Qy	1299	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEOAYLRSSWN	1358
Db	1288	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEOAYLRSSWN	1347
Qy	1359	VLDGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLRLTLRPLRVISRAOGLKLVVETILMS	1418
Db	1348	VLDGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLRLTLRPLRVISRAOGLKLVVETILMS	1407
Qy	1419	SLKPIGNIVVICCAFFIIFGILGVQLFKGKPFVCOGEDTRNITNKSDCAEASYRWRHXY	1478
Db	1408	SLKPIGNIVVICCAFFIIFGILGVQLFKGKPFVCOGEDTRNITNKSDCAEASYRWRMXY	1467
Qy	1479	NFDNLGOALMSLVLASKDGVVDIMYDGLDAVGVDQOQIMNHNPNWMLLYFISFLLIYAF	1538
Db	1468	NFDNLGOALMSLVLASKDGVVDIMYDGLDAVGVDQOQIMNHNPNWMLLYFISFLLIYAF	1527
Qy	1539	VLMNFVGVVVENFHKCRHQHEEEARRRREKRLRLEKKRRSKEQMAEAOCKPYYSDIS	1598
Db	1528	VLMNFVGVVVENFHKCRHQHEEEARRRREKRLRLEKKRR-----KAQCKPYYSDIS	1580
Qy	1599	REFLLVHHLCTSHYLDLFTITGVIGLNVVTMAMEHYQQPQILDEALKICNIFTVIFVFES	1658
Db	1581	REFLLVHHLCTSHYLDLFTITGVIGLNVVTMAMEHYQQPQILDEALKICNIFTVIFVLES	1640
Qy	1659	VEKLVAFARFRFFQDRWNQDLDAIVLLSIMGITLEBIEVNLSLPINPTIIRIMRVLRIAR	1718
Db	1641	VEKLVAFGFRFRFFQDRWNQDLDAIVLLSIMGITLEBIEVNASLPINPTIIRIMRVLRIAR	1700
Qy	1719	VLKLLKMAVGMRALHTVMQALPOVGNLGLLFFFAALGVELFGDLECDETHPCEG	1778
Db	1701	VLKLLKMAVGMRALDVTMQALPOVGNLGLLFFFAALGVELFGDLECDETHPCEG	1760
Qy	1779	LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDESRDCDQESTCYNTVISPIYFVSFVLTA	1838
Db	1761	LGRHATFRNFGMAFLTLFRVSTGDNWEGIMKDTLRDCDQESTCYFTVISPIYFVSFVLTA	1820
Qy	1839	QFVLNVVVIIVLMMKHEESNKEAEAEAELEAELMKTLSPOPHSPLGSPFLWPVEGV	1898
Db	1821	QFVLNVVVIIVLMMKHEESNKEAEAEAELEAELMKTLSPOPHSPLGSPFLNPVEGP	1880
Qy	1899	NSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLP	1958
Db	1881	DSPDSPKPGALMPAAHARSASHFSLEHPTMQPHTELP--GPDLLTVRKSGVSRTHSLP	1937
Qy	1959	NDSYMCNRNGSTAESRSLGHRGWGLPKAQSGSILSVHSOPADTSCILQLPKDVHVLQPHGA	2018
Db	1938	NDSYMCNRNGSTAEGLGHRGWGLPKAQSGSVLSVHSOPADTSYILQLPKDAPHLLQPMAS	1997
Qy	2019	PTWGAIPKLPPPPGRSPLAQRPLRRQAAIRTDSDLVQGLGSRREDLLSEVSGSPCPLTRSSS	2078
Db	1998	PTWGTIPKLPPPPGRSPLAQRPLRRQAAIRTDSDLVQGLGSRREDLLAEVSGSPPLARAYS	2057
Qy	2079	FWGGSSTQVQORSGIOQKSVSKHIRLPAPCPGLEPSWAKDPPETRRSSLELDTLSWISGDL	2138
Db	2058	FWGQSSTQAQOHSRSHSKSHHTPPAPCAGPEPNMKGPPETRRSSLELDTLSNISGDL	2117
Qy	2139	L-PSSQEEPLFPRDLKKCYSVETQSCRRRPPGFWLDEQRHRSIAVSCLDGSGQPRLCPSPS	2197
Db	2118	LPFGGQEEPPSPRDLKKCYSVQAQSCQRRRPTSWLDEQRHRSIAVSCLDGSGQPHLGTDP	2177
Qy	2198	SLGGQPLGGPSRPPKLSPPSISIDPPESQSGSRPPCPGVCLRRRAPASDSKDPSSVSP	2257
Db	2178	NLGGQPLGGPSRPPKLSPPSITIDPPESQSGPRTPSPGICLRRRAPSSDSKDPPLASGP	2237
Qy	2258	LDSTAASPPKKDTLSLSGLSSDPTDMDP	2286
Db	2238	PDSMAASPPKKDVLSLSGLSSDPAADLP	2266
RESULT 14			
ID	AAAB66476	AAB66476 standard; protein; 2359 AA.	
XX	AAAB66476;		
AC	AAAB66476;		
XX	09-APR-2001	(first entry)	
DT	09-APR-2001		
XX	Rat alpha-IH calcium channel protein.		
DE	Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;		
XX	hypotensive; cardiant; nootropic; T-type calcium channel subunit;		
KW	cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;		
KW	epilepsy; alpha-IH calcium channel.		
XX	Rattus sp.		
OS	WO200102561-A2.		
XX	11-JAN-2001.		
PN	04-JUL-2000; 2000WO-CA000794.		
XX			

QY	1680	LAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRARVLKLLKMAVGRALLHTVMQA	1739
Db	1690	LAIVLLSIMGIALEEIEENNAALPINPTIIRIMRVLRARVLKLLKMATGRALLDVTVQA	1749
QY	1740	LPQVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVS	1799
Db	1750	LPQVGNLGLLFMLFFIYAALGVLEFGRLCESDNECEGLSRHATFTNFGMAFLTLFRVS	1809
QY	1800	TGDNWNGIMKDPDRDC--DOESTCYNTVISPIYFVSFVLTAQFVLNVNVIKMLKHEE	1856
Db	1810	TGDNWNGIMKDTLRECTREDKHCLSYLPALSPVYFVTFMLVAQFVLNVNVIKMLKHEE	1869
QY	1857	SNKEAKEEALEAELEEMKILSPQPHSPLGSPFLWPCVEGVNSTDSPKPGAPHTTAHIG	1916
Db	1870	SNKEAREDAEMDAEIELEM-----AQGSTAQPPTAQES-----	1903
QY	1917	AASGFSLEHFTMVPHPEVPVLPDPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH	1976
Db	1904	-----QGTQDPTNLLVVRKVSVRMLSLPNDSYMFRPVAPAAAPHSH	1946
QY	1977	RGWGLP-----KAQSGSILSVHSQPADTSCILQLP-----KDVHYLLQPHGAPTW	2021
Db	1947	-----PLQEVEMETYTGVTSAHSPPLEPRASFQVPSAASSPARVSDPLCALSPRGTP--	1999
QY	2022	GAIPKLPPGRSPLAQRLRRQAAIRTDSLD--VOGLGSRDILLSEVSGPSCPLTRSSSF	2079
Db	2000	-----RSLSLRILCRQEAHSESLGKVDVGG--DSIPDYTEPAENMSTSQAS	2047
QY	2080	WGG-----SSIQVQORSIGIQSKVSKHRLPAPCPGLEPSPSWAKDPPETRSSLELDT	2129
Db	2048	TGAPRSPPCSPRPASVTRKHTFGQRCISSR-----PPTLGGDEAAEADP-----ADE	2095
QY	2130	ELSWISGDLPLSSQEEPLFP-----RDLKKCYSVETQSCRRRPPGFWLDE	2173
Db	2096	EVSHITSSAHPWPATEPHSPEASPTASPVKGTMGSGRDPFRPCSVDAQSFLDKPG-RPDA	2154
QY	2174	QRRHSIAV-----SCLDSGS-----QPRLCPSPSSLGGLGGPGRPKKLSPPSIS	2221
Db	2155	QRWSSVELDNGESHLESGEVGRASELEPAL-----GSRKKKMSPPCIS	2199
QY	2222	IDPP--ESQGRPPCSPG--VCLRRRAPASDS---KOPSVSSPLDSTAASP-----	2265
Db	2200	IEPPTKDEGSSRPAPAAEGGNTTLRRRTPECEAAALHRDCPEPTGPGTGGDPVAKGERWQ	2259
QY	2266	-SPKKTLSLGLSSDPTDM	2284
Db	2260	ASCRAEHLTVPNFAPEPLDM	2279

RESULT 15

AAY06299

ID AAY06299 standard; protein; 2353 AA.

AC AAY06299;

XX

DT 23-AUG-1999 (first entry)

XX

DE Human activated calcium channel alpha 1H-1 subunit.

XX

KW Calcium channel subunit 1H-1; human; neurological disorder;
KW endocrinological disorder; cardiovascular disorder; urological disorder;
KW hepatic disorder; respiratory disorder; vascular disorder.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 420..794

FT /note= "intracellular loop"

FT Region 520..528

FT /note= "poly-His region"

XX

PN WO9928342-A2.

XX
PD
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PF
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PR
PR
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PA
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PS
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CC
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CC
CC
CC
CC
CC
CC
CC
XX
SQ

10-JUN-1999.
03-DEC-1998; 98WO-US025671.
03-DEC-1997; 97US-00984709.
10-NOV-1998; 98US-00188932.
(SIBI-) SIBIA NEUROSCIENCES INC.

Williams M, Stauderman K, Harpold M, Hans M, Urrutia A;
Washburn MS;

WPI; 1999-371096/31.
N-PSDB; AAX59081.

Subunits of calcium channels.

Example 1; Page 151-161; 171pp; English.

The present sequence represents the the alpha 1H-1 subunit of a human low-voltage activated calcium channel. The sequence was deduced from cDNA (see AAX59080) isolated from a TT cell cDNA library. The invention provides calcium channel subunits, including 2 splice variants of alpha 1H-1 (see also AAY06298), and isoform alpha 1H-2 (see AAY06300). The 1H-1 splice variants were detected by RT-PCR in multiple tissues. They differ only at amino acid 2230, being either Asp or Glu. 1H-2 has a 319-amino acid deletion in the I-II intracellular loop relative to 1H-1. Cells and vectors containing nucleic acids encoding these subunits, and methods for identifying compounds that modulate the activity of calcium channels that contain the subunits are provided by the invention. Such compounds are used to treat calcium channel mediated disorders, including neurological, endocrinological, cardiovascular, urological, hepatic, respiratory and vascular disorders

Sequence 2353 AA;

Query Match 51.7%; Score 6222; DB 2; Length 2353;
Best Local Similarity 56.7%; Pred. No. 0;
Matches 1370; Conservative 208; Mismatches 529; Indels 310; Gaps 62;

QY	25	PPGRLARGWTRRRMERAPRSRDSF--VASRSSTTCPPGGAAGAGSTEKDPGSADSEAE	82
Db	19	PPGPAALVG-----ASPESGAPGREAGERSELGVSPPSPAERGAELGA--DEQR	69
QY	83	LPYPALAPVVFYLSQDSRPSRWCLRTVCNPWFERSMLVILNCVTILGMFRPCEDIACD	142
Db	70	VPYPALAAATVFCGLGQTTTPRSWCLVLCNPNWFHVSMLVIMLCVTILGMFRPCEDVECG	129
QY	143	SQCRILQAFDDFIPAFFAVEMVVMVALGIFGKKCYLGDWNLDDFFIAGMLEYSLD	202
Db	130	SERCNILEAFDAFIPAFFAVEMVIMVALGLFGQKCYLGDWNLDDFFIIVAGMMEYSLD	189
QY	203	LQNVSFSAVRTVRLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGV	262
Db	190	GHNVSLSAIRTVRLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGV	249
QY	263	QLWAGLLRNRCFLPENFSLPLSD-LEPYQTENEDESPFICSQPRENGMRSCRSVPTLR	321
Db	250	QLWAGLLRNRCFLDSAFVRNNNLTFLRPYQTETEENPFICSRDRDNGMKCSHIP---	306
QY	322	GEGGGPPCSDLYETYN-----SSSNTTCVNNQYTNCSAGHNPFKGAINFDNIGY	374
Db	307	GRRELMPCTLGWEAYTQPAEGVGAARNACINWNQYNNVCRSGDSNPHNGAINFDNIGY	366
QY	375	AWIAIFQVITLEGVNDIMVMDAHSFYNFYFILLIIVGSFFMINLCLVWIATQFSETK	434
Db	367	AWIAIFQVITLEGVNDIMVYVMDAHSFYNFYFILLIIVGSFFMINLCLVWIATQFSETK	426
QY	435	QRESQLMREQVRFLSNASTLASFSFSEPGSCVEELLYVILRKAARRLAQVSRIGVRA	494
Db	427	QRESQLMREQVRARHLSNDSTLASFSFSEPGSCVEELLYVGHIFRKVKRSLRLYARWQSRW	486

QY 495 GLLSSPVARSQBPQPSGCTSRSHR-----LSVHHLV-HHHHHHHHHYHLNGTILRV 546
Db 487 RKKVDPASVQGGP-----GHRQRRAGRHTASVHHLVYHHHHHHHHYHFSHGSPPR 538
QY 547 PRASPEIQDRDANGSRRLML--PPSPPTSPGGPRGAESVHSFYHADCHLE--PVRQQA 602
Db 539 PGPEPGACD-----TRLVRAGAPSPSPGRGPP-DAESVHSFYHADCHIEGPQERARV 591
QY 603 PPRCPSEASGR-TVGSGKV-YPTV-----HTSPPEILKDKALVEVAPSP----- 646
Db 592 AHAAATAAASURLATGLTMYPTILPSGVSGKSTSPGK-----GKWAGGPPGTG 644
QY 647 --GPPTLTSPNIPPGPFSSMHKLLETQSTGAC--HSS-----CKISSPCSKADSGACGPD 697
Db 645 GHGPLSNS-----PDPYEKIPHVVGHEGLGQAPGHLGSLVPCPLPSP--PAGTLTCELK 698
QY 698 SCPYCART-GAGEPESADHVMPPDSSEAVYEFTQDAQHSILRDP----- 740
Db 699 SCPYCTRALEDPEGELSGSESQDGRGVYEFTQDVRHGRWDPTRPPRATDTPGPGPS 758
QY 741 HSRRRQBSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQ 800
Db 759 PORRAQORAAP-GEPGWMRLWTFSGKLRIIVDSKYFSRGIMMAILVNTLSMGVEYHEQ 817
QY 801 PEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVISVWEIVGQGG 860
Db 818 PEELTNALEISNIVFTSMFALEMLLKLACGPLGIYIRNPYNIFDGIIVISVWEIVGQAD 877
QY 861 GGLSVLRTFRLMRVLKLVREFLPALQRLVLMKTMNDVNATFCMLLMFIFIFSILGMHLF 920
Db 878 GGLSVLRTFRLRLVLKLVRLPALRQLVLVLTMDNVATFCTLLMLFIFIFSILGMHLF 937
QY 921 GCKFASERD-GDTLPDRKNFDSLWAIIVTVFOILTQEDWNKVLYNGMASTSSWAALYFIA 979
Db 938 GCKFSLKTDGTVPDRKNFDSLWAIIVTVFOILTQEDWNKVLYNGMASTSSWAALYFVA 997
QY 980 LMTFGNYVLNLLVAILVEGFOAEGDATKSESEPDFSPVDGDRKKRLALVAL----- 1035
Db 998 LMTFGNYVLNLLVAILVEGFOAEGDANRSDTDEKTSVHFEEDFKLRELQTELKMS 1057
QY 1036 -----GEHAELRKSLLPLLIHTAATPM SHPKSSS-TGVEALGSGSRRTSSGSAEPGA 1089
Db 1058 LAVTPNGHLEGRGSLSPPLIMCTAATPMPTPKSSPFLDAAPSLPDSRRGSSSGDPPILG- 1116
QY 1090 AHHEMKPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRSPSGERRSLSGEQE 1149
Db 1117 --DQPPASLRSSPCAPWPGSGAWSSRRSSWSLGRAPSLKRRCQCGERESLLSGEGKG 1173
QY 1150 SQDEBSSEEDRASPA--GSDHRHRSGLEREAKSSFDLPDTL-----QVPLH-----R 1196
Db 1174 STDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPTKCRDRDQGVVALPSDFFLR 1231
QY 1197 TASGRSSASEHQDCNGKSASGRRLARTLRTDDPQLDGGDDNDDEGNLSKGERIQAWVRSRLP 1256
Db 1232 IDSHREDAELDDSDSDSCCLRLHKVLEPKPQ-----W----- 1265
QY 1257 ACCREDWSAYIFPPQSRPRLCHRITTHKMFHDHVLVLIIFLNCITIAMERP KIDPHSA 1316
Db 1266 --CRSREAWALYLFSPQNRFRVSCQKVIITHKMFHDHVLVLIIFLNCVTIALERPDIDGST 1323
QY 1317 ERIFLTSNYIFTAVFLAEMTVKVVALGWCFCGEQAVLRSSWNVLGDLVLISVIDILVSM 1376
Db 1324 ERVFLSVSNYIFTAIFVAEMVMKVVALGLLSGEHALQSSWNLLDGLVLVSLVIDIVAM 1383
QY 1377 VSDSGTKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFII 1436
Db 1384 ASAGAKILGVLRLVRLRLTLRPLRVISRAPGLKLVVETLISSLRPIGNIVLICCAFFII 1443
QY 1437 FGILGVQLFKGFFVCQGEDTRNITNKSDCAEASVWRVRRKYNFNDLGQALMSLFVLASK 1496
Db 1444 FGILGVQLFKGFYCEGPDTRNISTKAQCAAHYRWRVRRKYNFNDLGQALMSLFVLSSK 1503
QY 1497 DGWVDIMYDGLDAVGVDQOPIMNHNPMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQ 1556

Db 1504 DGWVNIMYDGLDAVGVDQOPVQNHENPMMLLYFISFLLIIVSFFVLNMFVGVVVENFHKCRQ 1563
QY 1557 HQEEEEARRREKRLRLEKKRRSKEKQMAEAQCKPYYSYSRFRLLVHHLCTSHYLDLF 1616
Db 1564 HQEAEEARRREKRLRLEKRRRRSTFPS-PEAQRPPYADYSPTRRSIHSLSCTSHYLDLF 1622
QY 1617 ITGVIGLVNVTMAMEHYQQPQILDEALKICNYIFTVIFVESVFKLVAFARFRFFQDRWN 1676
Db 1623 ITFIIICVNVITMSMEHYNQPKSLDEALKYCNVYVFTIVFEAALKLVAFGRFRFFQDRWN 1682
QY 1677 QLDLAIIVLLSIMGITLEEIEVNLSLIPINPTIIRIMRVLRIRARVLKLLKMAVGMRLHHTV 1736
Db 1683 QLDLAIIVLLSIMGITLEEIEMSAALPINPTIIRIMRVLRIRARVLKLLKMATGMRLHHTV 1742
QY 1737 MQALPQVGNLGLLMLLFFIFPAALGVLELFGDLECEDETHPCEGLGRHATFRNFGMAFLTLF 1796
Db 1743 VQALPQVGNLGLLMLLFFIYAALGVLELFGRLCESEDNPEGLSRHATFSNFGMAFLTLF 1802
QY 1797 RVSTGDNWNGIMKDPSPRDC--DQESTCYNTVISPIYFVSFVLTAQFVLNVVLAIVLMKH 1853
Db 1803 RVSTGDNWNGIMKDTLRECSREDKHLSYLPALSPVYFVFLVAQFVLNVVVAIVLMKH 1862
QY 1854 LEESNKEAKBEAEAELEAELEMKTLSPQPHSPLGSPFLWPGEVGNSTDSKPGAPHTTA 1913
Db 1863 LEESNKEAREDAELDAEIELEMA-----QPGSARRVDADRP----- 1899
QY 1914 HIGAASGFSLEHPTMVPHPEEVVPLGPDLLITVRKSGVSRTHSLPNDSYMCNNGSTA--- 1970
Db 1900 -----PLPQESPGARDAPNLVARKVSVSRMLSLPNDSYMFPRVVPASAP 1943
QY 1971 -----ERSLHRGWGLPKAQSGLSVHSQPADTSCILQLPKDVH-----YLLQP 2015
Db 1944 HPRPLQEVEMETYGAGTP---LGSVASVHSPPAESCASLQIPLAVSSPARSGEPLHALSP 2000
QY 2016 HGAPTWGAIPKLPPLPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEV-----SGPSC 2071
Db 2001 RGT-----ARSPSLRLLCRQEAHVHTDSLEGK-IDSPRDTLDPAEPEKTPVR 2047
QY 2072 PLTRSSFWGGSSIQVQORSGIQSKV--SKH-----IRLPAPCPGLEPSWAKDPPETRS 2123
Db 2048 PVTQ-----GSLQSPRSPRPASVTRKHTTFGQHCVSSRPAAPGGEAEASDP----- 2096
QY 2124 SLELDTLSWISGDLPLP--SSQEEPLFP-----RDLKKCYSVETQSCRRRPGFWLDE 2173
Db 2097 ---ADEEVSHITSSACPWQPTAEPHGPEASPVAGGERDLRRLYSVDAQGLDKPG-RADE 2152
QY 2174 QRHSIAVSLDSGSPRLCPSPSSSLGGQPLGGP--GSRPKKLSPPSISIDPP-ESQGS 2230
Db 2153 QWRPSAE---LGSGE-----PGEAKAWG-PEAEFALGARRKKMSPPCISVEPPAEDEGS 2203
QY 2231 -RPPCSPG--VCLRRRAPA-----SDSKDPSVSSPLDSTAAS-----PSPKKDTLSL 2274
Db 2204 ARPSAAEGGSTTLRRRTPSCEATPHRDSLEPTEGSGAGGDPAAKGERWGAQSCRAEHLTV 2263
QY 2275 SGLSSDPTDM-----DP 2286
Db 2264 PSFAPEPLDLGVPSGDP 2280

Search completed: November 18, 2004, 13:23:47
Job time : 201.365 secs

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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:41 ; Search time 40.6868 Seconds
(without alignments)
3727.727 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPRCVRTPLRGSAR.....KKOTLSLSGLSDPTDMDPZ 2287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	10820.5	90.0	2273	3	US-09-426-998-5
2	6221	51.7	2353	3	US-08-984-709A-50
3	5872	48.8	1207	4	US-09-398-522-52
4	5409	45.0	2175	3	US-09-404-650-2
5	5409	45.0	2175	4	US-09-935-541-2
6	5405.5	44.9	2188	3	US-09-404-650-4
7	5405.5	44.9	2188	4	US-09-935-541-4
8	5345	44.4	1835	3	US-09-404-650-5
9	5345	44.4	1835	4	US-09-935-541-5
10	1678	14.0	2343	3	US-09-268-163-4
11	1677	13.9	2337	3	US-08-713-118-2
12	1677	13.9	2337	3	US-09-452-007-2
13	1676	13.9	2339	1	US-08-455-543A-47
14	1676	13.9	2339	2	US-08-223-305C-47
15	1674	13.9	2339	3	US-09-268-163-6
16	1642.5	13.7	2237	1	US-08-455-543A-48
17	1642.5	13.7	2237	2	US-08-223-305C-48
18	1642.5	13.7	2336	3	US-09-268-163-10
19	1642	13.7	1985	4	US-09-495-714C-6
20	1640.5	13.6	2237	3	US-09-268-163-8
21	1634.5	13.6	1984	3	US-08-836-325-10
22	1634.5	13.6	1984	4	US-09-457-571-10
23	1628.5	13.5	1977	4	US-09-495-714C-4
24	1628	13.5	1873	1	US-08-435-675B-4
25	1625.5	13.5	1989	3	US-08-836-325-12
26	1625.5	13.5	1989	4	US-09-457-571-12
27	1625	13.5	2161	1	US-08-455-543A-51

28	1625	13.5	2161	2	US-08-223-305C-51	Sequence 51, Appl
29	1622	13.5	2161	1	US-07-745-206A-2	Sequence 2, Appli
30	1622	13.5	2161	1	US-08-455-543A-49	Sequence 49, Appl
31	1622	13.5	2161	2	US-08-223-305C-49	Sequence 49, Appl
32	1622	13.5	2161	2	US-08-311-363-2	Sequence 2, Appli
33	1617.5	13.4	1969	3	US-08-836-325-16	Sequence 16, Appl
34	1617.5	13.4	1969	4	US-09-457-571-16	Sequence 16, Appl
35	1616	13.4	1873	1	US-08-336-257A-7	Sequence 7, Appli
36	1614.5	13.4	1977	4	US-09-976-594-757	Sequence 757, App
37	1614.5	13.4	1977	4	US-09-919-039-367	Sequence 367, App
38	1614	13.4	1872	6	5386025-6	Patent No. 5386025
39	1595.5	13.3	1912	4	US-09-495-714C-2	Sequence 2, Appli
40	1589.5	13.2	2516	3	US-08-374-077C-2	Sequence 2, Appli
41	1589.5	13.2	2516	3	US-08-895-590-2	Sequence 2, Appli
42	1589.5	13.2	2516	4	US-09-539-879A-2	Sequence 2, Appli
43	1588.5	13.2	2016	4	US-09-514-907A-2	Sequence 2, Appli
44	1588.5	13.2	2016	4	US-09-896-994-2	Sequence 2, Appli
45	1585.5	13.2	2016	3	US-09-634-920-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-426-998-5
; Sequence 5, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
; FILE REFERENCE: CHANNEL (ALPHAIG-C)
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 5
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-426-998-5

Query Match	90.0%	Score 10820.5;	DB 3;	Length 2273;
Best Local Similarity	92.5%	Pred. No. 0;		
Matches 2080;	Conservative 35;	Mismatches 105;	Indels 29;	Gaps 5;
QY	62	GAAGAGSTEKDPGSADSEAGLPYPALAPVVFFVLSQDSRPSWCLRTVCNPFVRSML	121	
Db	30	GRPGSAEKDPGSADSEAGLPYPALAPVVFFVLSQDSRPSWCLRTVCNPFVRSML	89	
QY	122	VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG	181	
Db	90	VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG	149	
QY	182	DTWNRDLFFVIAGMLEYSLDLQNVFSFSAVTRVRLRPLRAINRVPSMRILVTLTLLDTLP	241	
Db	150	DTWNRDLFFVIAGMLEYSLDLQNVFSFSAVTRVRLRPLRAINRVPSMRILVTLTLLDTLP	209	
QY	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVLDLEPYQTENEDESPF	301	
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVLDLEPYQTENEDESPF	269	
QY	302	ICSPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSNTTCVNMNQYTTNCSAGEHN	361	
Db	270	ICSPRENGMRSCRSVPTLRGEGGGPPCGLDYEAYNSSNTTCVNMNQYTTNCSAGEHN	329	
QY	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL	421	
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL	389	

QY	422	CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLYVILRKAAR	481
Db	390	CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLYVILRKAAR	449
QY	482	RLAQVSRAGVRAGLLSSPVARSQEQEPQPSGSCSTRSHRRLSVHLLVHHHHHHHHYHLGN	541
Db	450	RLAQVSRAGVRVGLLSSPAPLGGQETQPSSCSRSRRLSVHLLVHHHHHHHHYHLGN	509
QY	542	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQC	601
Db	510	GTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPFGAESVHSFYHADCHLEPVRQC	569
QY	602	APPRCPSEASGRTVGSGKVYPTVHTSPPPPEILKALVEVAPSPGPPTLTFSNIPPGPF	661
Db	570	APPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPY	629
QY	662	SSMHKLLTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSD	721
Db	630	SSMHKLLTQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD	689
QY	722	SEAVYFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLLICDTFRKIVDSKYFGRG	781
Db	690	SEAVYFTQDAQHSDLRDPHS-RRQRSGLGPDAPSSVLAFWRLLICDTFRKIVDSKYFGRG	748
QY	782	IMIAILLVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN	841
Db	749	IMIAILLVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN	808
QY	842	IFDGVIVVISWEIVGOQGGGLSVLRTFRLMRVLKLVRLPALQRLVVLKMTMDNVATF	901
Db	809	IFDGVIVVISWEIVGOQGGGLSVLRTFRLMRVLKLVRLPALQRLVVLKMTMDNVATF	868
QY	902	CMLLMFLFIFISILGMHLFGCKFASERDGDTLPDRKNFDSLWAIIVTVFQILTQEDWNKV	961
Db	869	CMLLMFLFIFISILGMHLFGCKFASERDGDTLPDRKNFDSLWAIIVTVFQILTQEDWNKV	928
QY	962	LYNGMASTSSWAALYFIALMTFGNVYVLFNLLVAILVEGQAE-----	1003
Db	929	LYNGMASTSSWAALYFIALMTFGNVYVLFNLLVAILVEGQAEISKREDASGQLSCIQLP	988
QY	1004	-----GDATKSESEPFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPLLIHTAATPM	1058
Db	989	VDSQGGDANKSESEPFFSPSLDGDGDRKKCLALVSLGEHPELRKSLLPLLIHTAATPM	1048
QY	1059	SHPKSSSTGVGBALGSGSRRTSSSGSAEPGAAHHEMKPCPSARSSPHSPWSAASWTSRR	1118
Db	1049	SLPKSTSTGLGALGPASRRTSSSGSAEPGAA-HEMKSPPSARSSPHSPWSAASWTSRR	1107
QY	1119	SSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEEDRASPGSDHRHRSGLERE	1178
Db	1108	SSRNSLGRAPSLKRRSPSGERRSLLSGEQEQSQDEEESSEERASPGSDHRHRSGLERE	1167
QY	1179	AKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKSASGRRLARTLRTDDPQLDGGDDNDE	1238
Db	1168	AKSSFDLPDTLQVPLHRTASGRGSASEHQDCNGKSASGRRLARLPDDPPLDGGDDADDE	1227
QY	1239	GNLSKGERIQAWVRSRLPACCRERDSWASAYIFPPQSRFRLLCHRIITHKMFHDHVLVILF	1298
Db	1228	GNLSKGERVRAWIRARLPACCLERDSWASAYIFPPQSRFRLLCHRIITHKMFHDHVLVILF	1287
QY	1299	LNCITIAMERPKIDPSAERIFLTLNSYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN	1358
Db	1288	LNCITIAMERPKIDPSAERIFLTLNSYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN	1347
QY	1359	VLDGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLTLRPLRVISRAQGLKLVVETLMS	1418
Db	1348	VLDGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLTLRPLRVISRAQGLKLVVETLMS	1407
QY	1419	SUKPIGNIVWICCAFFIIFGILGVQLFKGKFVVCQGEDTRNITNKSDCAEASYRVRHKY	1478
Db	1408	SUKPIGNIVWICCAFFIIFGILGVQLFKGKFVVCQGEDTRNITNKSDCAEASYRVRHKY	1467

RESULT 2
US-08-984-709A-50
; Sequence 50, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla
; STATE: California

QY	1479	NFDNLGQALMSLFLVASKDQWVDIMYDGLDAVGVDQQPIMNHNPNWMLLYFISFLLVIAFF	1538
Db	1468	NFDNLGQALMSLFLVASKDQWVDIMYDGLDAVGVDQQPIMNHNPNWMLLYFISFLLVIAFF	1527
QY	1539	VLMNFVGVVVENFHKCRQHQQEEEEARRREEKRRLRLEKKRRSKEKQMAEAQCKPYSDYS	1598
Db	1528	VLMNFVGVVVENFHKCRQHQQEEEEARRREEKRRLRLEKKRRSKEKQMAEAQCKPYSDYS	1587
QY	1599	RERLLVHHLCTSHYLDLFTIGVIGLVNVTMAMBYHQQPQILDEALKICNYIFTVIFVLES	1658
Db	1588	RERLLVHHLCTSHYLDLFTIGVIGLVNVTMAMBYHQQPQILDEALKICNYIFTVIFVLES	1647
QY	1659	VFKLVAFARFRFFQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIAR	1718
Db	1648	VFKLVAFARFRFFQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIAR	1707
QY	1719	VLKLLKMAVGMRALHTVMQALPOVGNLGLLFFIFAALGVLEFGDLECDETHPCEG	1778
Db	1708	VLKLLKMAVGMRALHTVMQALPOVGNLGLLFFIFAALGVLEFGDLECDETHPCEG	1767
QY	1779	LGRHATFRNFGMAFLTLEFRVSTGDNWNGIMKDPDRDCCQESTCYNTVISPIYFVSFVLTA	1838
Db	1768	LGRHATFRNFGMAFLTLEFRVSTGDNWNGIMKDTLRDCCQESTCYNTVISPIYFVSFVLTA	1827
QY	1839	QFVLNVVIVAVLMKHLEESKEAEAEAELEEMKTLSPQHPSPGLSPFELWPGVEGV	1898
Db	1828	QFVLNVVIVAVLMKHLEESKEAEAEAELEEMKTLSPQHPSPGLSPFELWPGVEGP	1887
QY	1899	NSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLP	1958
Db	1888	DSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTLP---GPDLLTVRKSGVSRTHSLP	1944
QY	1959	NDSYMCNCSGTAERSLGHARGWGLPKAQSGSILSVHSPADTSCILQLPKDVHYLLQPHGA	2018
Db	1945	NDSYMCNCSGTAEGPLGHARGWGLPKAQSGSVLSVHSPADTSYILQLPKDAPHLLQPHSA	2004
QY	2019	PTWGAIPKLPPPPGRSPPLAQRPLRQAARTDSDLVDQGLSREDLLSEVSGPSCPLTRSSS	2078
Db	2005	PTWGTIPKLPPPPGRSPPLAQRPLRQAARTDSDLVDQGLSREDLLAEVSGPSPPLARAYS	2064
QY	2079	FWGSSSIQVQQRSGIQSKVSKHRIPLPAPCPGLEPSPWAKDPPETRRSSLELDTLSWISGDL	2138
Db	2065	FWGQSSTQAQHSRSHSKISKHMTTPPAPCPGPEPNWGKBPETRRSSLELDTLSWISGDL	2124
QY	2139	L-PSSQEEPLFPRDLKKCYSVETQSCRRRRPGFWLDEQRHRSIAVSCLDGSGQPLCPSPS	2197
Db	2125	LPFGGQEEPPSPRDLKKCYSVEAQSCRRRPTSWLDEQRHRSIAVSCLDGSGQPHLGTDP	2184
QY	2198	SLGGQPLGGPSRPPKKLSPPSISIDPPESQSGSRPPCSPGVCLRRRAPASDKDPSVSSP	2257
Db	2185	NLGGQPLGGPSRPPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDKDPLASGP	2244
QY	2258	LDSTAASPSPKDTLSLSGLSSDPTDMDP	2286
Db	2245	PDSMAASPSPKDVLSSLGLSSDPADLDP	2273

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; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,709A
; FILING DATE: 02-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 587-5360
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-984-709A-50

Query Match 51.7%; Score 6221; DB 3; Length 2353;
Best Local Similarity 56.6%; Pred. No. 0;
Matches 1368; Conservative 209; Mismatches 530; Indels 310; Gaps 62;

QY 25 PGPRLARGWTRRRMERAPRRDSP--VASRSSTTCPGPGAAGAGSTKDPGSADSEAE 82
Db 19 PPGPAALVG-----ASPESGAPGREAEERGSELGVSPESPAERGAELGA--DEEQR 69
QY 83 LPYPALAPVVFYLSQDSRPRSCLRTVCNPNWFERVSMVLVILLNCVTLGMFRPCEDIACD 142
Db 70 VPYPALAAATVFVCLGQTTRPRSWCLRLVCNPNWFEHVSMVLVIMLNCVTLGMFRPCDECG 129
QY 143 SQRCRIQAFDDFIAPFAFVAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLD 202
Db 130 SERCNILEAFDAFIAPFAFVAVEMVIMVALGLFGQKCYLGDTWNRLDFFIVVAGWMEYSLD 189
QY 203 LQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGV 262
Db 190 GHNVSLSAIRTVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGV 249
QY 263 QLWAGLLNRNCFLPENFSLPLSVD-LEPYVQTENEDESPFICSPRENGMRSCRSVPTLR 321
Db 250 QLWAGLLNRNCFLDSAFVRNNLTFLRPYYQYQTEEGEENPFICSSRRDNGMKCSHIP--- 306
QY 322 GEGGGGPPCSLDYETYN-----SSSNTTCVNNQYNTNCSEAGEHNPFKGAINFDNIGY 374
Db 307 GRRELNPCTLGWEAYTQPAQEGVGAARNACINWNQYINVCRSGDSNPHNGAINFDNIGY 366
QY 375 AWIAIFQVITLEGWVDIMYFVMDAHSFYNFYFILLIIVGSFFMINCLVVIATQFSETK 434
Db 367 AWIAIFQVITLEGWVDIMYVYMDAHSFYNFYFILLIIVGSFFMINCLVVIATQFSETK 426
QY 435 QRESQLMREQVRFLSNASTLASFSEPGSCYCEELLKYLVIILKAARRLAQVSRAGVRA 494
Db 427 QRESQLMREQVRARHLSNDSTLASFSEPGSCYCEELLKYVGCHIFRKVKRRSLRLYARWQSRW 486
QY 495 GLLSSPVARSQEQPPSGSCSTRSHRR-----LSVHHLV-HHHHHHHHHYHLNGTTLRV 546
Db 487 RKKVDFSAVQGGP-----GHRQRAGRHTASVHHLVYHHHHHHHHHHYHFSHGSPRR 538
QY 547 PRASPEIQDRDANGSRRLML--PPPTPTPSGGPPRGAESVHSFYHADCHLE--PVRCQA 602

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QY 1082 SGSAEPGAHHEMKCPPSARSSPHSPWSAASSWTSSRRSSNSLGRAPSLKRRSPSGERRS 1141
Db 1049 SGSAEPGAA-HEMKSPPSARSSPHSPWSAASSWTSSRRSSNSLGRAPSLKRRSPSGERRS 1107
QY 1142 LLSGEGQESQDEBESSEEDRASPGSDHHRGSLEREAKSSFDLPDTLQVPLHRTASGR 1201
Db 1108 LLSGEGQESQDEBESSEERASPGSDHHRGSLEREAKSSFDLPDTLQVPLHRTASGR 1167
QY 1202 SSASEHQDCNGKSASGRRLARTLRTDDPQLDGGDDDDNDEGNL 1241
Db 1168 GSASEHQDCNGKSASGRRLARALRPDDPPLDGGDDADDEGNL 1207

RESULT 4
US-09-404-650-2
; Sequence 2, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Joseph G.
; APPLICANT: McGivern, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-650-2

Query Match 45.0%; Score 5409; DB 3; Length 2175;
Best Local Similarity 50.5%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 513; Indels 450; Gaps 64;

QY 51 ASRSSTTCGPGAAGAGSTEKDPG--SADSEAEGL-----PYPALAPVVFYLS 97
Db 5 ASPSSSAAAP-AAEPGVTTQPGPRSPSPSGPGLBPDGADPHVPHDLAPIAFFCLR 63

QY 98 QDSRPRSWCLRTVCNPFERVSMVLVILLNCVTLGMFRPCEDIAQDSQRCRILQAFDDFIF 157
Db 64 QTTSPRNWCIKWCVNPFECVSMVLVILLNCVTLGMVQPCDDMDCLSDRCKILQVDFDIF 123

QY 158 AFFAVEMVVKMVALGIFGKCYLGDTWNRLDFFIVAGLMLEYSLDLQNVSFAVTRVRL 217
Db 124 IFFAMENVLKMVALGIFGKCYLGDTWNRLDFFIVAGMVEYSLLDLQNINLSAIRTVRL 183

QY 218 RPLRAINRVPSMRILVILLDTLPMNLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLE 277
Db 184 RPLKAINRVPSMRILVLLDTLPMNLGNVLLLCFFVFFIFGIIIGVQLWAGLLNRNCFLEE 243

QY 278 NFSPLSVLDLEPYQOTENEDESPFCISQPRENGMRSCRSVPTLRGEGGGPPCSL----- 332
Db 244 NFTIQGDVALPPYYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDV 300

QY 333 -DYETYNSSNTT--CVNWNQYVYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWV 389
Db 301 YDFGAGRDNLNASGLCVNWRNYNVCRTGSANPHKGAINFDNIGYAWIVFQVITLEGWV 360

QY 390 DIMYFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFL 449
Db 361 EIMYVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYL 420

QY 450 SNASTLASFEPGSCYEBELLKYLVIYILRKAARLAQVSRAGVRAGLSSPVARSGQEPQ 509
Db 421 S-SSTVASAEPGDCYEBIFQYVCHILRAKR-----RALGLYQALQS----- 462

QY 510 PSGSCTRSHRRRLSVHLLVHHHHHHHHYHLGNGLRVPRASPEIQDRDANGSRRLMLPPP 569
Db 463 -----RRQAL-----GPE-----APAP 474

QY 570 STPTPSGGPPRGAESVHSFYHADCHLEBPVRCQAPPPRCPSSEASGRTVSGKVYPTVHTSP 629
Db 475 AKGP-----HAK-----EPRHYQLCPQHSPLDA-----TPHT-- 502

QY 630 PPEILKOKALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLLETOSTGAC-HSSCKISSPCSK 688
Db 503 -----LVQ-----PIPATLAS-----DPASCPCCQHEGRRPSGLGS 534

QY 689 ADGACGPDSCPYCARTGAGEPESADHVPDSDSEAVYEFTQDAQHSDDLDPHSHRRQRS 748
Db 535 TDSGQEGSGS-----GSSAGGEDEA-----DGDGA-----RSSEDCASSELGKEEEEQ-- 579

QY 749 LGPDAEPSSVLA--FWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTN 806
Db 580 -----ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMAILVNTVSMGIEHHEQPELTN 635

QY 807 ALEISNIVTSLFALEMLLKVYGPFGYIKPNYPNIFDGVIVVISVWEIVGQGGGLSVL 866
Db 636 ILEICNVVFTSMFALEMILKLAAGLFDYLRNPYNIFDSIIVISIWEIVGQADGGLSVL 695

QY 867 RTFRLMRVLKVRFLPALORQLVVLMTMDNVATFCMLLMFIFIFSILGMLHFGCKFAS 926
Db 696 RTFRLRLVLRFPALRQLVVLMTMDNVATFCMLLMFIFIFSILGMLHFGCKFSL 755

QY 927 ERD-GDTLPDRKNFDSLLWAVTVFQILTQEDWNKVLNGMASTSSWAALFYIALMTFGN 985
Db 756 RTDTGDTVPDRKNFDSLLWAVTVFQILTQEDWNVVLNGMASTSPWASLYFVALMTFGN 815

QY 986 YVLFNLLVAILVEGFOAEGDATKSESEPDFFPSV-----DGDGDRKRLALVAL 1035
Db 816 YVLFNLLVAILVEGFOAEGDANRSYDEDOSSSNIIEFCLKQEGLDSSGDPK--LCPIPM 873

QY 1036 GEHAELRKSLLPPLIHT----AATPMHPKSSSTGVGEALGSGRRRTSSSGSAEPGAH 1091
Db 874 TPNGHLDPSL--PLGGHLGPAGAAAGPA--PRLSLQDPLMLVALGSRKSSVMSL---GRMS 926

QY 1092 HEMKPPSARSPHSPWSAASSWTSSRRSSNSLGRAPSLKRRSPSGERRSLLSGE-QGES 1150
Db 927 YDQRLSSSRSSYYGPWGRSAAWASRRSSWN-----SLKHKPPSAEHESLLSAERGGGA 980

QY 1151 QDEBESSEE--DRASPAAGSDH-----RHRGSLEREAKSSFDLPDTLQVPG 1193
Db 981 RVCEVAADGPPRAAPLHTPHAHHHGPHLAHRHRHRTLSLDRDSVDLAELVPAVG 1040

QY 1194 LHRTASGRSS--ASEHQDCNGKSASGRRLARTLRTD-DPQLDGGDDNDNDEGNLSKGERIQAW 1250
Db 1041 AHPRAAWRAAGPAPGHEDCNGRMPS--IAKDVTMGDRGDRGEDEEIDYTLCFRVRKM 1098

QY 1251 VRSRLPACCRERDSWYIFPPQSRFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERP 1310
Db 1099 IDVYKPDWCEVREDWSVLFSPENRFRVLCQITIAHKLFDYVVLAFIFLNCITIALERPQ 1158

QY 1311 IDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVI 1370
Db 1159 IEAGSTERIFLTVSNYIFTAIFVGENTLKVVSIGLYFGEQAYLRSSWNVLDGFLVFSII 1218

QY 1371 DILVSMVSDSGTKILGMLRVLRLTLRLPLRVISRAQGLKLVVETLMSSLKPIGNIVIC 1430
Db 1219 DIWVSLASAGAKILGVLRLVRLTLRLPLRVISRAPGLKLVVETLISSLKPIGNIVLIC 1278

QY 1431 CAFFIIFGILGVQLFKGKFFVCOGEDTRNITNKSDCAEASYRVRHKNYFNFDNLGOALMSL 1490
Db 1279 CAFFIIFGILGVQLFKGKFYHCLGVDTRNITNRSDCMAANYRVRHKNYFNFDNLGOALMSL 1338

QY 1491 FVLASKDGVTDIMYDGLDAVGDDQQPTMNNHNPWMLLYFISFLLVAFVFLNMFVGVVVEN 1550
Db 1339 FVLASKDGVWNIMYNGLDVAVDQQPVTHNPNWMLLYFISFLLVSPFVFLNMFVGVVVEN 1398

QY 1551 FHKCRQHQQEERREKRLRLEKKRRSKEKQMAEAQCKPYSDYSRFRLLVHHLCTS 1610
Db 1399 FHKCRQHQAEEARREKRLRLEKKRR-----KAQRLPYATYCHTRLLIHSMCTS 1451

QY	986	YVLFNLLVAILVEGFOAEGDATKSESEPDFFSV-----DGDGDRKKRLALVAL	1033
Db	816	YVLFNLLVAILVEGFOAEGDANRSYDEQSSNIEEFDKLEGLDSSGDPK--LCPIM	873
QY	1036	GEHAELKSLPLLIHT---AATPMShPKSSSTGVGEALGSGSRRTSSSGSAEPGAH	1091
Db	874	TPNGHLDPSL--PLGGHLGPAGAA--PRLSLQDPMVLVALGSRKSSVMSL---GRMS	926
QY	1092	HEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGF-QGES	1150
Db	927	YDQSLSSSRSSYYGPWGRSAAWASRRSSWN-----SLKHKPPSAEHESLLSAERGGGA	980
QY	1151	QDEEESSE--DRASPAAGSDH-----RHRGSLEREAKSSFDPDLTLQVPG	1193
Db	981	RVCEVAADGPPRAAPLHTPHAHHIHHGPHLAHRHRHRRTLSLDNRDSVDLAELVPAVG	1040
QY	1194	LHRTASGRSS--ASEHQDCNGKSASGLARTLRTD-DPQLDGGDDNDEGNLSKGERIQAW	1250
Db	1041	AHPRAAWRAAGPAPGHEDCNGRMPS--IAKDVFTKMGDRGDRGEDEEIDYTLCFVRKX	1098
QY	1251	VRSLPACCRERDSWAYIFPPQSRFRLCHRITTHKMFHDVVVLVIIFLNCITIAMERP	1310
Db	1099	IDVYKPDWCEVRDWSVYLFSPENRFRVLCQTIIAHKLFDDYVVLAFIFLNCITIALERP	1158
QY	1311	IDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFFGEQAYLRSSWNVDGLVLSVI	1370
Db	1159	IEAGSTERIFLTVSNYIFTAIFVGMTLKVVSLGLYFGEQAYLRSSWNVDGLVFSVI	1218
QY	1371	DILVMSVDSGKILGMLRVLRLRLTLRPLRVLSRAQGLKVETLMSLKPIGNIVVIC	1430
Db	1219	DIVVSLASAGGAKILGVLRLRLTLRPLRVLSRAPGLKVETLISLKPIGNIVLIC	1278
QY	1431	CAFFIIFGILGVLFKGFVFCQGEDTRNITNKSDCAEASYRWRHXYKNFNDLGOALMSL	1490
Db	1279	CAFFIIFGILGVLFKGFYHCLGVDTRNITNRSDCMAANYRWHVHXYKNFNDLGOALMSL	1338
QY	1491	FVLASKDGVNDIMYDGLDAVGVDQOQIMNHNPMWLLYFISFLLIVAFVLMFVGUVVEN	1550
Db	1339	FVLASKDGVNIMYNGLDVAVDQOQVTHNHPMWLLYFISFLLIVSFVLMFVGUVVEN	1398
QY	1551	FHKCRHQHEEABRRREKRLRLEKRRSKEQMAEAQCKPYYSYDSRFRLLVHHLCTS	1610
Db	1399	FHKCRHQHEEABRRREKRLRLEKRR-----KAQRLPYVATYCHTRLLIHSMTCS	1451
QY	1611	HYLDLFTITVGLNVVTMAMEHYQQOQILDEALKICNYIFTVIFVESVFKLVAFARFR	1670
Db	1452	HYLDIFITICLVNVVTSLEHYNQPTSLTALKYCNYMFTTVFVLEAVLKVAFGLRRF	1511
QY	1671	FQDRWNQLDAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIARVLKLLKMAVGMR	1730
Db	1512	FKDRWNQLDAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIARVLKLLKMATGMR	1571
QY	1731	ALLHTVMQALPQVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCGLGRHATFRNFGM	1790
Db	1572	ALLDITVQALPQVGNLGLLFMLFFIYAALGVLEFGKLVNDENPCEGMSRHATFENFGM	1631
QY	1791	AFLTFRVSTGDNWNGIMKDPDRDC-DQESTCYNTV--ISPIYVVSFVLTAQFVLNVVVI	1847
Db	1632	AFLTFRVSTGDNWNGIMKOTLRDCTHRSCLSSQLQFVSPLYFVSFVLTAQFVLNVVV	1691
QY	1848	AVLMKHLEESNKEAEAELEAELEEM-KTSLSPQSPHSLGSPFLWP-----	1894
Db	1692	AVLMKHLDNSKEAQEDAEMDAELEMAHGLGPGPRLPTGSPGA-PGRPGGAGGGGDT	1750
QY	1895	-----VEG-VNSTDSPKPGAPHTTAHIGAASG-----	1920
Db	1751	EGGLCRRCYSPAQDSLEGELTIIDNLSGSIFH--HYSSPAGCKKHDKQEVQLAETEA	1807
QY	1921	-----FSLEHPTMVP-----HPEEVPV-PLGPDLLTVRKSGVS	1952
Db	1808	FSLNSDRSSILLGDDLSLEDPTACPPGRKDKSGELDPPEPMRVGDLGECFFPLSSTA	1867

RESULT 6

US-09-404-650-4

; Sequence 4, Application US/09404650

; Patent No. 6309858

GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/404,650

; CURRENT FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

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; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 4

LENGTH: 2188

THE : PART :
: : OBJECTS :

; ORGANISM: Homo sapiens
 ITS-09-404-650-4

FD-0000-0000-0000-0000-0000

Query Match 44.9%; Score 5405.5; DB 3; Length 2188;
Best Local Similarity 50.3%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;

[illegible]

Db 961 HESLLSGEGGSCVRACEGAREEAPTRTAPLHAPHAAHGHGPHLAHRHRRHRTLSLDT 1020

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Db 1021 RDSVDLGELVPVGAHRAAWRGAGQAPGHEDCNGRMPN--IAKDVTMKMDRRDRGEDE 1078

QY 1237 DEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVI 1296

Db 1079 EEIDYTLCFVRKMDIDVYKPDWCEVREDWSYVLFSPENKFRILCQIIAHKLFDYVVLAF 1138

QY 1297 IFLNCITIAMERPKIDPHSAERIFLTLNSYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSS 1356

Db 1139 IFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSGLYFGEQAYLRSS 1198

QY 1357 WNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLRLTLRLRVLVISRAQGLKLVVETL 1416

Db 1199 WNVLDGFLVFSIIDIVSVASAGGAKILGVRLVRLRLTLRLRVLVISRAPGLKLVVETL 1258

QY 1417 MSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRH 1476

Db 1259 ISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTNRNITNRSDCVAANYRWVHH 1318

QY 1477 KYNFDNLGQALMSLFVLASKDGMVIMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLIIVA 1536

Db 1319 KYNFDNLGQALMSLFVLASKDGMVIMYNGLDAVAVDQQPVTHNPNWMLLYFISFLIIVS 1378

QY 1537 FVLNMFVGVVVENFHKCRQHQBEEARRREEKRLRLEKRRSKEKQMAEAQCKPYISD 1596

Db 1379 FVLNMFVGVVVENFHKCRQHQBEEARRREEKRLRLEKRR-----KAQRLPYIAT 1431

QY 1597 YSRFRLLVHLLCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQILDEALKICNYIFTVIFVF 1656

Db 1432 YCPTRLLIHSMCTSHYLDIFITFICLVNVTMSLEHVNQPTSLETALKYCNYMFTTVFVL 1491

QY 1657 ESVEKLVAFAFRFFQDRWNQDLAIVLLSIMGITLBEIEVNLSLPINPTIIRIMRVLRI 1716

Db 1492 EAVLKLVAFLRLRFFKDRWNQDLAIVLLSVMGITLBEIEINAALPINPTIIRIMRVLRI 1551

QY 1717 ARVLKLLKMAVGMRAHLLHVMQALPQVGNLGLLFFMLFFFAALGVLEFGDLECDETHPC 1776

Db 1552 ARVLKLLKMATGMRALDVTVQALPQVGNLGLLFFMLFFFIYAALGVLEFGKLVCDENPC 1611

QY 1777 EGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPSSDC-DQESTCYNTV--ISPIYFVS 1833

Db 1612 EGWSRHATFENFGMAFLTFRVSTGDNWNGIMKDTLRDCTHRTCLSSLOFVSPLYFVS 1671

QY 1834 FVLTAQFVLNVVIAVLMKHEESNKEAKEAELEAELEEMKTLSPQPHSPLGSPFLWP 1893

Db 1672 FVLTAQFVLINVVAVLMKHLDDSNKEAQEDAEMDAEIELEM----- 1713

QY 1894 GVEGVNSTDSPKPGAPHTTAHIGAASGFSLHPTVMVPHPEVPVP-LGPDLLTV----- 1946

Db 1714 -AHGLGPCPGPCG-----PCPCPCPCACAPRLPTSSPGAPG 1750

QY 1947 RKSGVSRTHSLPNDSYMCRN-GSTAERSLGRGWGLPKAQSGSILSVHSQPADTSCILQL 2005

Db 1751 RSGGAGAGG-DTSHLCRHCYSPAQETL-----W-----LDSVSLIKDSLEGELTIIDNL 1801

QY 2006 PKDV-HYLLQPHG 2017

Db 1802 SGSVFHHYASPDG 1814

RESULT 9

US-09-935-541-5

; Sequence 5, Application US/09935541

; Patent No. 6589787

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/935,541

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 1835

; TYPE: PRT

; ORGANISM: Rattus sp.

US-09-935-541-5

Query Match 44.4%; Score 5345; DB 4; Length 1835;

Best Local Similarity 55.4%; Pred. No. 0;

Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

QY 43 PRSRDSPVASRSSTTCGPGAAGAGAGSTEKDPGSADSEAE-----LPYPALAPVVFFYLSQ 98

Db 8 PSSAAAPAPPEPGITEQGP-----RSPPPSPGLEEPLGTNPDPVPHDLPAPVAFCLRQ 62

QY 99 DSRPRSWCLRTVCNPFERVSMLVILLNCVTLMFRPCEDSQRCLIQAFDDFIFA 158

Db 63 TTSPRNWCIMKVCNPFECVSMVLILLNCVTLMGYQPCDDMECLSDRCKILQVDDFIFI 122

QY 159 FFAVEMVVMVALGIFGKKCYLGTWNRLDFFIVIAGLEYSLDLQNVSFSAVTRVLR 218

Db 123 FFAMEMVLKMWALGIFGKKCYLGTWNRLDFFIVMAGVVEYSLDLQINLSAIRTVRVLR 182

QY 219 PLRAINRVPSMRILVTLLDLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRRCFLPEN 278

Db 183 PLKAINRVPSMRILVNLDDLPLMGNVLLLCFFVFFIFGIIQVQLWAGLLRRCFLEEN 242

QY 279 FSLPLSVLDLEPYQOTENEDESPFCISQPRENGMRSRCSVPTLRGEGGGPPCSL----- 332

Db 243 FTIQGDVALPPYQPEEDDEMPFICSLTGDNGIMGCHEIPPLKEQ---GRECCLSKDDVY 299

QY 333 DYETYNSSNTT--CVWNQYTYNCASGEHNPFGAINFDNIGYAWIAIFQVITLEGWVD 390

Db 300 DFAGARQDLNASGLCVWNRYNVCRTGNANPHKGAINFDNIGYAGIVFQVITLEGWVE 359

QY 391 IMYFVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLS 450

Db 360 IMYVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQYLS 419

QY 451 NASTLASFSEPGSCVEELLKYLVIILKAAARLAQVRAIGVRAGLLSSPVARSGEQPQ 510

Db 420 -SSTVASAEPGDCYEIEFYQVCHILRKAKR-----RALGLYQAL----- 458

QY 511 SGCSCTRSHRRLSVHHLVHHHHHHHHYHLNGNLTLRVPRASPEIQDRDANGSRRLMLPPPS 570

Db 459 -----QNRROA-----MGPGT-----PAPA 473

QY 571 TPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRVTGSGKVYPTVHTSPP 630

Db 474 KPGP-----HAK---EPHCKLCPRHSPLD-----PTPHT--- 500

QY 631 PEILLKDKALVEVAPSPGPPTLTSTFNIPGPFSSMHKLLLETQSTGACHSSCKISSPCSAD 690

Db 501 -----LVQ-----PISAIL----- 509

QY 691 SGACGPDSCPYC-----ARTGAGEPESADHVMPSDSEAVYEFTQDAQH 734

Db 510 --ASDPSSCPHCQHEAGRRPSGLSTDSGQEGSGSGSAE---AEANGDGL-QSSEDEVGS 563

QY 735 SDLRDPHSRRRQSLGPDAPSSVLA-----FWRLICDTFRKIVDSKYFGRGIMAILVN 789

Db 564 SD-----LGKEEQEDGAARLCGDVWRETRKKLRGIVDSKYFNRGIMMAILVN 611

QY 790 TLSMGIEVHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGFYIKNPNYIFDGVIVV 849

Db 612 TVSMGIEHHEQPEELTNILEICNVVFTSMFALEMILKLAAGFLFDYLRNPNYIFDSIIVI 671

QY 850 ISVWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVVLMTMDNVATFCMLLMLEFI 909

Db	1714	-AHGLGPCPCPG-	1750
QY	1947	RKSGVSRTHSLPNDSYMCRN-GSTAERSLHRGWGLPKAQSGSILSVHSQPADTSCILQL	2005
Db	1751	RGSGGAGAGG-DTESHLCRHCYSPAQETL-----W-----LDSVSLIIKDSLEGELTIIDNL	1801
QY	2006	PKDV-HYLLQPHG	2017
Db	1802	SGSVFHHYASPDG	1814
RESULT 10			
US-09-268-163-4			
: Sequence 4, Application US/09268163B			
: Patent No. 6353091			
: GENERAL INFORMATION:			
: APPLICANT: Lipscombe, Diane			
: APPLICANT: Schorge, Stephanie			
: TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF			
: FILE REFERENCE: B1055/7000			
: CURRENT APPLICATION NUMBER: US/09/268,163B			
: CURRENT FILING DATE: 1999-03-12			
: EARLIER APPLICATION NUMBER: US 60/077,901			
: EARLIER FILING DATE: 1998-03-13			
: NUMBER OF SEQ ID NOS: 28			
: SOFTWARE: FastSeq for Windows Version 3.0			
: SEQ ID NO 4			
: LENGTH: 2343			
: TYPE: PRT			
: ORGANISM: Homo sapiens			
US-09-268-163-4			
Query Match 14.0%; Score 1678; DB 3; Length 2343;			
Best Local Similarity 23.3%; Pred. No. 4.5e-126;			
Matches 625; Conservative 354; Mismatches 828; Indels 872; Gaps 81;			
QY	59	PGPGAAGASTEKDPGSADSEAEGLPYPALAPV-----VFFYLSQDSRRPSWCLRT	109
Db	32	PGPGGLQPGQRLVYKQSIQAQARTMALYNPIPVKQNCFTVNRSLFVSEDNVVRKYAKRI	91
QY	110	VCPNPFERVSMLVILLNCVILGWERPCEDIACDSQRCLILQAFDD--FIFAFFAVEMVW	166
Db	92	TEWPPFEYMLATIIANCIVLAL-----EQHLPDGDKTPMSERLDDTEPYFIFIGCFEAGI	147
QY	167	KMVALG-IPGKKCYLGDWNRDLDPFIVIAQMLEYS---LDLQNVFSFSAVRTVRVLRPLRA	222
Db	148	KIIALGFVFKGSYLRNGWNVDVAVVLTGILATAGTDFDLR-----TLRAVRVLRPLKL	202
QY	223	INRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNCFLPENFSLP	282
Db	203	VSGIPSLQVVLKSIMKAMVPLLQIGLLFFAILMFAIIGLEFYMKGFKHACF-----P	255
QY	283	LSVDLEPYQTENEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSN	342
Db	256	NSTDAPV-----GDFPCGKEAPARLCEGD	280
QY	343	TTCVWNQYYTNCISAGEHNPFKGAINFEDNIGYAWJAFQVITLEGWVDIMYFVMD-AHSF	401
Db	281	TEC---REYWP-----GPNFGITNFDNLFALITVFQCIWEGWTDILYNTNDAAGNT	330
QY	402	YNFIYFILLIIVGSFFMINCLVVIATQFSETKQES-----QLMREQVRFLSNASTL	455
Db	331	WNWLYFIPLIIGSFFMLNLVLGVLGSFEFAKERERVENRRAFLKLRQQQIE-----	382
QY	456	ASFSEPGSCYEELLYVILRKAARRLAQVSRAGLVAGLLSSPVARSGOEPQSGSCT	515
Db	383	-----RELNGYLEWIFKAEVMLEAED-----RNAEKSPLDVLK	417
QY	516	RSRRRLSVHLLVHHHHHHHHHHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPPS	575
Db	418	RAATKKSRLDLIH-----AEEGEDRFAD-----	440
QY	576	GGPPRGAESVHSFYHADCHLEPVRCPAPPVRCVSGKVPYFVHTSPPEILK	635

; Sequence 2, Application US/08713118
; Patent No. 6040436
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,118
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-713-118-2

Query Match 13.9%; Score 1677; DB 3; Length 2337;
Best Local Similarity 23.4%; Pred. No. 5.4e-126;
Matches 627; Conservative 350; Mismatches 829; Indels 868; Gaps 82;
QY 59 PGPGAAGAGSTEKDPGSADSEAEGLPYPALAPV-----VFFYLSQDSRPRSWCLRT 109
Db 32 PGPGGLQPGQVLYKQSIQAQRARTMALYNPIPVKQNCFTVNRSLFVFSNEDNVVRKYAKRI 91
QY 110 VCNPFERVSMLVLLNCVTGLMFRPCEDIAQSCRCRILQAFDD---FIFAFFAVEMVV 166
Db 92 TEWPPFEYMILATIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIGIFCFEAGI 147
QY 167 KMAVAG-IFGKKCVIGDVTNRLDFFIVIAQMLEYS---LDLQNVSPSAVRTVRVLRPLEA 222
Db 148 KIIALGFVFKHGSYLRNGWVMDFVVVLGTILATAGTDFDLR-----TLRAVRVLRPLKL 202
QY 223 INRVPSMRILVTLILDLPMLGNVLLLCFFVFFIFGIQVGVQLWAGLLRNRCFLPENFSLP 282
Db 203 VSGIPSLQVVLKSIKMAVPLLLQIGLLLFALLMFAIIGLEFFYMGKFHKACF-----P 255
QY 283 LSVLDLEPYQOTENEDESPFCISQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSN 342
Db 256 NSTDAEPV-----GDFPCGKEAPARLCEGD 280
QY 343 TTCVNNWQYNTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMD-AHSF 401
Db 281 TEC---REYWP-----GPNFGITNFDNILFALTQVFCITMEGWTDILYNTNDAAGNT 330
QY 402 YNPIYFILLIIVGSFFMINCLVVIATQFSETKQRES-----QLMREQVRVFLSNASTL 455
Db 331 WNWLYFIPLIIGSFFMLNLVLGVLGSEFAKERERVENRRAFLKLRQOOIE----- 382
QY 456 ASFSEPGSCYEELLKYLVTILRKAARRLAQVSRIGVRAGLLSSPVARSGQEPQPSGSCT 515

Db 383 -----RELNGYLEWIFKAEVVMLAED-----RNAEKSPLDVLK 417
QY 516 RSHRRLSVHLLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTPS 575
Db 418 RAATKKSRLDIH-----AEEGEDRFAD----- 440
QY 576 GGPPRGAESVHSFYHADCHLEPVRCQAPPPCPSEASGRTVGSGKVYPTVHTSPPEILK 635
Db 441 ----- 440
QY 636 DKALVEVAPSPGPPTLTSFNIPPGPFSSMHKILLETQSTGACHSSCKISSPCSKADSGACG 695
Db 441 -----LCAVGSPPFARAS----- 452
QY 696 PDSCPYCARTGAGEPESADHVMPDSDSEAVYFTQDAQHSDLRDPHSRRRQSRSLGPDAP 755
Db 453 -----LKSGKTESSESYF-----RRKEK----- 469
QY 756 SSVLAFWRLLICDTRFKIVDSKYFGRGIMIALVNTLSMGIEYHEQPEELTNALEISNIVF 815
Db 470 --MREFF-----IRRMVKAQSFYVVVLCVVALNTLCVAMVHYNQPRRLTTTLYFAEFV 521
QY 816 TSLFALEMLLLKLLVYGPFGYIKNPYNIFDGVIVIVSWEIVGQ-----QGGLSVLRTFR 870
Db 522 LGLELTEMSLKMYGLGPRSYFRSSFCDFGVIVGSVFVWAAIKPGSSFGISVLRAIR 581
QY 871 LMRVLKLVRLPALQRLVVLVMTMDNVATFCMLLMFLIFIFSIILGMLHFGCKFASERDG 930
Db 582 LLRIPKVTKYWSSLRNLVSVLLNSMKSIISLLFLFLFVIVFALLGMQLFGGQNFQDET 641
QY 931 DTLPRKDNFDSLLWAIVTVFQILTQEDWNKVLVNGM-----ASTSSWAALYFIALMTFGN 985
Db 642 PT---TNFDTFPAAILTVFQILTGEDWNAVMYHGIFSGGVSXKMPSSFFIVLTFLGN 697
QY 986 YVLFNLLVAILVEGFAEGDAFKSESEPDFSPVSDGDRKKRLALVALGHAELRKSL 1045
Db 698 YTLNVLFLAIVDNLANAQELTKDEEEMEEAA-----NQLALQKAKEVAEV--SP 746
QY 1046 LPPLIIHTAATPMSHPKSSSTGVGEA----- 1071
Db 747 MSAANISIAARQONSAKARSVMQASQLRLQNLRASCEALYSEMDPEERLRFATRRHR 806
QY 1072 -----LGSGSRRTSSSGSAEPGAA-----HH---EMKCP----- 1097
Db 807 PDMKTHLDRPLVVELGRDARGPVGCKARPEAAEAPGVDPDRHHHRDKDKTPAAGDQ 866
QY 1098 -----PSARSS---PHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERSL 1142
Db 867 DRAEAPKAESGEPGAREPRPHRSKSEAA--GPPEARSEGRGP-----GPEGGRHH 919
QY 1143 LSGEGESQDEE-----ESSEDRASPAGSDHHRGSLE---REAKSSFDLEDTL 1189
Db 920 RRGSPEEAEREPRRHRHRHQDPKSKCAGAKGERRARHGGPRAGPREAESG----- 972
QY 1190 QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA-----RTLRTDDPQLDGGDDNDE 1238
Db 973 EEPARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS 1032
QY 1239 GNLSKGERIQAVVRSRLPACCRER-----DSW----- 1265
Db 1033 GTVTVGP-----MHTLPSTCLQKVEEQPEDADNQNVNTRMGSDPPDPTNIVHIPVMLTG 1086
QY 1266 -----SAXIFPPQSRFRLLCHRI 1283
Db 1087 PLGEATVPSGNVDLESQAEGKKEVEADVMRSGRPIVPYSSMFCLSPTNLLRRFCHYI 1146
QY 1284 ITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLNSYIFTAVFLAEMTVKVVAL 1343
Db 1147 VTMRYFEVILVVIALLSSIALAEDP-VRTDSPRNALKYLDYIFTGVFTFEMVIKMDL 1205
QY 1344 GWCFGQAYLRSSWNVLDGLLVLSVIDILYSMV-SDSGTKILGMLRVLLRLTLRLPRV 1402

Db 1206 GULLHPGAYFRDLWNILD---FIVVSGALVAFSGSKGKDINTIKSLRVLRLPLKT 1261

QY 1403 ISRAQGLKLVETIMSSSLKPIGNIVVICAPFIIFGILGVQLFKGKFFVCQGE-----D 1456

Db 1262 IKRLPKLKAVFDCVVNSLKNVLNILIVYMLPMFIFAVIAVQLFKGKFFYCTDESKELERD 1321

QY 1457 TRN---ITNKSDCAEASR-WVRHKYNFDNLGQALMSLVLASDKGWVDIMYDGLDAVGVD 1513

Db 1322 CRQYLDYEKEEVEAQAQPRQWKYDFHYDNVLMWALLTLFTVSTGEGPMVKHSDVATYEE 1381

QY 1514 QQPIMNHNPMWLLYFISFLLIIVAFFVLNMFVGVVNFHFKCRQHQBEEAARRRREKRLRR 1573

Db 1382 QGSPGYRMELSIFVYVVFVFPFFVFVNFIFVALIITF-----QEQGDKVMSE-----CS 1431

QY 1574 LEKRRSKEKQMAEAQCKPYYSYSR--FRLLVHLLCTSHYLDLFTIGVIGLNVVTNAME 1631

Db 1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKWTFTFVSPPPBYFIMAMIALNTVVLMMK 1491

QY 1632 HYQOQILDEALKICNYIFTVIFVFESVFKLVAPAFRRFFQDRWNQOLDLAIVLLSIMGIT 1691

Db 1492 FYDAPYEYELMKCLNIVFTSMFMECVLKIIFAGVLNFRDAWNVDFVTVLGSITDIL 1551

QY 1692 LEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVMQALPQVGNLGLFM 1751

Db 1552 VTEIANNF---IN---LSFLRLFRARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIA 1605

QY 1752 LFFFIYALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTGDNNWNGIMKD- 1810

Db 1606 MLFFFIYALIGMQVFGNIALDDD---TSINRHNFRFTFLOALMLLRSATGEAWHEIMLSC 1662

QY 1811 -PSRDCQOE--STCYNTVISPIYVVSFVLTAQFVLNVVIAVLM-----K 1852

Db 1663 LSNQACDEQANATECGSDFAYFVFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPH 1722

QY 1853 HLEE-----1856

Db 1723 HLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPGLGKCKPARVAYKRLVRMNMPISN 1782

QY 1857 -----SNKEAKEAELEAEL-----ELEMKTLS--PQPH 1883

Db 1783 EDTVHTSTLMALIRTALEIKLAPAGTKHQCDALKEISVVWANLPQKTLDLLVPPH 1842

QY 1884 SP----LGSPF---LWPGVEGVNSTDSPKPGAPHTTAHGAAGSFLEHPTMVPHPPEEV 1935

Db 1843 KPDEMTVGKVAALMIFDFYKQNKTRDQMOPGGLSQMGVSLF---HPLKATLEQTQ 1899

QY 1936 PVPL-GPDLTLVRKSGVSRTHSLPNDSYMCRNGSTAERSLHGRGWGLPKAQSGSILSVHS 1994

Db 1900 PAVLRGARVFLRQKST---SLNGGAIQNESGIKESV---SWGTRQTDQ-----1945

QY 1995 QPADTSCILQLPKDVHLLQPHGAPTGWAIPLPPPGRSPLAQRLRQAAIRTD-----2049

Db 1946 -----PHEA-----APPLERGHSTEIPVGRSGALAVDVQMOS 1977

QY 2050 -----SLDVQGLSREDLLSEVSGPSCPLTRSSSFVGGSSIQVQQRSGIQSKV 2097

Db 1978 ITRRGPDGEPQPGLESQG---RAASMPRLAETQPVTDASPMKRSISTLAQRPRG-----2029

QY 2098 SKHIRLPAPCPGLEPSWAKDPPETRS-----SLELDTELSWISGDLPL 2140

Db 2030 -THLCSTTP-----DRPPPSQASSHHHRRCHRRDRKQSRLEKGPSLS-ADMDGAP 2079

QY 2141 SSQEEPLFP-----RDLKKCYSVETQSCRRRPGFWLDEQRHRSIAVSCLDGSGQPR 2191

Db 2080 SSAVGPGLPPGEGPTGCRERRRQRRSRQRRRQPSSSSSKQRF---YSCDRFGGREG 2136

QY 2192 LCPSPS-----SLGQPL-----GGGSRPKKLSLSP- 2217

Db 2137 PKPKPSLSSHPTSPTAGQEPGPHQPGSGSVNGSPLLSTSGASTPGRGRRQLPQTPLTPR 2196

QY 2218 PSISIDPPES-----QGSRRPPCSPG-----VCLRRRAPASD-----SKDP 2252

Db 2197 PSITYKTANSSPIHFAGAQTSLPAPSPGRLSRGLSEHNALLQRPDPLSQPLAPGSRIGSDP 2256

QY 2253 SVSSPLDSTAASPSPKKDTLSL-----SGLSS 2279

Db 2257 YLGQRLDSEASVHALPEDTLTTFEEAVATNSGRSS 2290

RESULT 12

US-09-452-007-2

; Sequence 2, Application US/09452007

; Patent No. 6140485

; GENERAL INFORMATION:

; APPLICANT: Franco, Rodrigo

; APPLICANT: Sun Chen, Ai Ru

; APPLICANT: Suey, David J.

; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL

; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: USA

; ZIP: 02173-4799

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/452,007

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/713,118

; FILING DATE: 16-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Mata, Elizabeth W.

; REGISTRATION NUMBER: 38,236

; REFERENCE/DOCKET NUMBER: ACC96-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2337 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-452-007-2

Query Match 13.9%; Score 1677; DB 3; Length 2337;

Best Local Similarity 23.4%; Pred. No. 5.4e-126;

Matches 627; Conservative 350; Mismatches 829; Indels 868; Gaps 82;

QY 59 PGPGAAGAGSTEKDPGSADSEAEGLPYPALAPV-----VFFYLSQDSRPRSWCLRT 109

Db 32 PGPGGLQPGQVRVLYKQSIARARTMALYNPIPVKQNCFTVNRSLFVFSEDNVVRKYAKRI 91

QY 110 VCNPFWEFVSMVLVLLNCVTILGMFPCEDACDSQRCRILQAFDD---FIFAFFAVEMVV 166

Db 92 TEWPPFEYMLATIANCIVLAL-----EQHLPDGDKTPMSERLDDTEPYFIFGCFEAGI 147

QY 167 KMVALG-IFGKKCYLGDTWNRLDFFIVIAMLEYS---LDLQNVFSASVTRVRLRLRA 222

Db 148 KIIALGFVFKGSLYLRNGWNVDFVVLVTGILATAGTDFDLR-----TLRAVRVLRPLKL 202

QY 223 INRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENSLP 282

Db 203 VSGIPSLQVVLKSIKAMVPLQLIGLLFFAILMFAIIGLEFYMGKFHACF-----P 255

QY 283 LSVLDLEPYVQTENEDESPFICSPQPRENGMRSCRSVPTLRGEGGGPPCSLDYETNSSN 342

Db 256 NSTDAEPV-----GDFPCGKEAPARLCBGD 280

QY 343 TTCVNWNOYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMD-AHSF 401

Db 281 TEC---REYWP-----GPNFGITNFDNILFALLTVFQCITMEGWDILYNTNDAAGNT 330

QY 402 YNFIYFILLIIVGSPFMINCLVVIATQFSETKQRES-----QIMREQVRFLSNASTL 455

Db 331 WNWLFIPLIIGSPFMINLVGLVSGEFAKERERVENRRAFLKURQOQIE-----382

QY 456 ASFSEPGSCYEELKVLVILRKAARRLAQVSRRAIGVRAGLLSSPVARSQGEPPQPSGSC 515

Db 383 -----RELNGYLEWIFKAEVWLAEBD-----RNAEKSPLDVLK 417

QY 516 RSHRRLSVHLLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPS 575

Db 418 RAATKKSRLDIH-----AEEGEDREAD-----440

QY 576 GGPGRGAESVHSFYHADCHLEPVRCAQPPPCPSEASGRTVGSKVYPTVHTSPPEILK 635

Db 441 -----440

QY 636 DKALVEVAPSPGPTLTSTENIPPPGFSSMHKLELTQSTGACHSSCKISSPCSKADSGACG 695

Db 441 -----LCAVGSPFARAS-----452

QY 696 PDSCPYCARTGAGEPEASADHWMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQORSGLGPAEP 755

Db 453 -----LKSGETESSYF-----RRKEK-----469

QY 756 SSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALIEISNIVF 815

Db 470 --MERFF-----IRRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLYFAEFVF 521

QY 816 TSLFALEMLIKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QGGGLSVLRFTF 870

Db 522 LGLFLEMSLKMVGLGPRSYFRSSFCDFGVIVGVSFVFWAAIKPGSSFGISVLRALR 581

QY 871 LMRVLKLVRLPALORQLVVLMTMDNVATFCMLLMLEFIFISILGMHLFGCKFASERDG 930

Db 582 LLRIKVTYKWSLRLNLVSLNSMKSIIISLLFLFLFVIVFALLGMQLFGGQFNQDET 641

QY 931 DTLPRKKNFDSLLWAIIVTVFOILTQEDWNKVLYNGM-----ASTSSWAALFYFIALMTFEGN 985

Db 642 PT---TNFDTFPAAILTVFOILTGEDWNAVYHGIESQGGVSKGMFESSFYFIVLTLEGN 697

QY 986 YVLFNLVAILVEGFAEGDATKSESEDDFFSPSVDGDGRKKRLALVALGEHAELRKS 1045

Db 698 YTLLNVFLAIVDNLANAQELTKDEEEMEEAA-----NOKLALQAKEVAEV--SP 746

QY 1046 LPPLIHTAATPMSPHKSSSTGVGEA-----1071

Db 747 MSAANISIAARQONSAKARSVWEQASQLRLQNLRASCEALYSEMPEERLRFATTHRR 806

QY 1072 -----LGSGSRRTSSSGSABPGAA-----HH-----EMKCP-----1097

Db 807 PDMKTHLDRPLVVELGRDGARGPVGKARPEAAEAPEGVDPPIRRHRRDKDKTPAAGDQ 866

QY 1098 -----PSARSS---PHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSL 1142

Db 867 DRAEAPKAESGEPGAREERPRPHRSKSKEAA--GPPEARSERGRGP-----GPEGGRRH 919

QY 1143 LSGEQESQDEE-----ESSEEDRASPGSDHRRHRSLE--REAKSSFDLPDTL 1189

Db 920 RRGSPAEAAREPRRRAHRHQDPSKECAGAKGERARRHRRGGPRAGPREAESG-----972

QY 1190 QVPG-LHRTASGRSSASE--HQDCNGKSASGLA-----RTLRTDDPQLDGGDDNDE 1238

Db 973 BEPARRRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNEQPREPHCDLETS 1032

QY 1239 GNLSKGERIQAWVRSLRPACCRER-----DSW-----1265

Db 1033 GTVTVGP-----MHTLPSTCLQKVEQPEDADQNVRMVGSPPPDNTIVHIPVMTG 1086

QY 1266 -----SAYIFPPQSRFRLLCHRI 1283

Db 1087 PLGEATVVPSENVNDESAQEGKKEVEADVMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI 1146

QY 1284 ITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNXYFTAVFLAEMTVKVVAL 1343

Db 1147 VTMRYFEVVLVIALSSIALAAEDP-VRTDSPRNNAKYLDYFTGVTTFEMVIKMDL 1205

QY 1344 GWCFGEOAYLRSSWNVDGLLLVISIDILVSMV-SDSGTKILGMLRVLRLRLTLRPLRV 1402

Db 1206 GLLHPGAYFRDLWNILD---FIVVSGALVAFAPSGSKGKDINTIKSLRVLRLPLKT 1261

QY 1403 ISRAQGLKLVVETLMSSLKPIGNIVVICAPFIIIFGILGVQLFKGKFFVCQGE-----D 1456

Db 1262 IKRLPKLKAVFDCVVVNSLKNVLNIIIVVMLEMEIFAVIAVQLFKGKFFYCTDESKELERD 1321

QY 1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFLVASKDGWVDIMYDGLDAVGD 1513

Db 1322 CRGQYLDYEKEEVEAQRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE 1381

QY 1514 QOPIMNHPWMLLYFISFLLIIVAFVFLNMFVGVVVENFHKRQHQHEEEARRREKRLRR 1573

Db 1382 QGSPGYRMELSIFVYVYVFWVFPFFVFNIFVALIITF-----QEQGDKVMSE---CS 1431

QY 1574 LEKRRSKEKQMAEAQCKPYYSYSR--FRLLVHHLCTSHYLDLDFITGVIGLNVVTMAME 1631

Db 1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKWTFTVVSPPFEYFIMAMIALNTVWLMMK 1491

QY 1632 HYQOPQILDALKICNYIPTVIVFVESVFKLVAFAPRRFFQDRWNQLDLAIVLLSIMGIT 1691

Db 1492 FYDAPYEYELMLKCLNIVTSMFMECVLKIIAFGVNLNFRDAWNVDFVTVLGSITDIL 1551

QY 1692 LEEIEVNLSLPINPTIIRMRVLRIARVLKLLKMAVGMRALHTVMQALPOVGNLGLLFM 1751

Db 1552 VTEANNF---IN---LSFLRLFAARLIKLLRQGYTIRILLTWVQSFKAIPYVCLLIA 1605

QY 1752 LLEFFIPAALGVLEFGDECETHPCCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKD- 1810

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QY 1811 -PSRDCQDE--STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLM-----K 1852

Db 1663 LSNQACDEQANATECGSDFAFYFVFSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPH 1722

QY 1853 HLEE-----1856

Db 1723 HLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPGLGKKCPARVAYKRLVRNMNPISN 1782

QY 1857 -----SNKEAKEEALEAEAL-----ELEMKTLS--PQPH 1883

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QY 1884 SP-----LGSPF---LWPGVEGVNSTDSPKPGAPHTTAHIGAAAGFSLEHPTMVPHPEEV 1935

Db 1843 KPDEMTVGKYAALMIFDFYKQNKTRDQMQQAPGGLSQMGVPSLF---HPLKATLEQTQ 1899

QY 1936 PVPL-GPDLTLVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHGWLPKAQSGSILSVHS 1994

Db 1900 PAVLRGARVFLRQKSST---SLSNGGAIQNESGIKESV---SWGTRTQDA-----1945

QY 1995 QPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRLRRQAIRTD-----2049

Db 1946 -----PHEA-----RPPLERGHSTHPIVGRSGALAVDVQMOS 1977

QY 2050 -----SLDVQGLSREDLLSEVSGPCPLTRSSSFWGSSIQVQQRSGIQSKV 2097

Db 1978 ITRGPDGEPQPGLESQG---RAASMPRIAAETQVTDASEMKRSISTLAQRPRG-----2029

QY 2098 SKHIRLPAPCPGLEPSWAKDPPETRS-----SLELDTLSWISGDLPL 2140

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QY	871	LMRVLKLVRFALQRLVLMKTMNDNVATFCMLLMFLIFISILGMHLFGCKFASERDG	930	1747	GLLEMLLFFFAALGVELFGDLECDETHPCBGLGRHATERNFGMAFLTTLFRVSTGDNMNG	1806
Db	582	LIRIFKVTYKWSLRLNVSLNMSKSIISLLFLFLFVVFALLGMQLFGGQFNQDET	641	1603	CLLIAMLFFIYALIGMQVFGNIALDDD---TSINRHNFRFTLQALMLLRSATGEAMHE	1659
QY	931	DTLPDRKNFDSLWAVTVFQILTQEDMKNKVLNGM-----ASTSSWAALYFIALMTFGN	985	1807	IMKD--PSRDCDQB--STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLM-----	1851
Db	642	PT-----TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGVSKGMFSSFYFIVLTLFGN	697	1660	IMLSCLSNQACDEQANATECGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS	1719
QY	986	YVLFNLLVAILVEGQABGDATKSESEPDPFFSPVDGDGRKKRLALVALGEHAELRKS	1045	1852	-----KHLEE-----	1856
Db	698	YTLNVLFLAIVDNLANAQELTKDEEEMEEAA-----NOKLALQKAKEVAEV--SP	746	1720	ILGPHHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPGLGKKCPARVAYKRLVRMN	1779
QY	1046	LPPLIIHTAATPMShPKSSSTGVGEA-----	1071	1857	-----SNKEAKEAELEAEL-----ELEMKTLS--	1879
Db	747	MSAANISIAARQOQSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATRHLR	806	1780	MPISNEDMTVHFTSTLMALIRTALIKLAPAGTKHQCDALRKEISVVMWANLPQKTLDL	1839
QY	1072	-----LGSGSRTSSSGSAEPGAA-----HH-----EMKCP-----	1097	1880	-PQHPSP-----LGSPF-----LWPGVEGVNSTDSPKPGAPHTTAHIGAAAGFSLEHPTMVP	1930
Db	807	PMKTHLDRPLVVELGRDARGVPVGKARPEAAEPGVDPPIRRHHHRDKDKTPAAGDQ	866	1840	LVPHPKPDGMTVGKYYAALMIFDFYKQNKTRDQMOPGGLSQMGPSVSLF---HPLKAT	1896
QY	1098	-----PSARSS---PHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSL	1142	1931	HPEEVPVPL-GPDLITVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHHRGWLKPAQSGSI	1989
Db	867	DRAAPKAESGEPGAREERPRPHRSKKEA--GPPEARSERGRGP-----GPEGRRHH	919	1897	LEOTQPAVLRGARVFLRQKST---SLNNGGAIQNESGIKESV---SWGTRTQDA--	1947
QY	1143	LSGEGQESQDEE-----ESSEEDRASPGSDHHRGSLF---REAKSSFDLPDTL	1189	1990	LSVHSQPADTSCILQLPKDVHLLQPHGAPTWGALPKLPPGGRSPLAQRPLRRQAIRTD	2049
Db	920	RRGSPEEAAERPRRHRAHRHQDP\$KECAGAKGERARHRRGGPRAGPREAESG-----	972	1948	-----PHEA-----RPPLERGHSTEIFVGRSGALAVD	1974
QY	1190	QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA-----RTLRTDDPQLDGDNDDE	1238	2050	-----SLDVQGLGSRREDLLSEVGPSCPLTRSSSFWGGSSSIQVQORSG	2092
Db	973	EEPARRHARHKAQPAHEAVEKETEKETEKEAEIIVEADKEKELRNHQPREHCDLETS	1032	1975	VQMOSITRRRGPDGEPQPGLESQG---RAASMPRLAAETQPVTDASPMKRSISTLAORPRG	2031
QY	1239	GNLSKGERIQAWVRSLPACCRR-----DSW-----	1265	2093	IQSKVSKHIRLPAPCPGLEPSWAKDPPETRS-----SLELDTELSWIS	2135
Db	1033	GTVTVGP-----MHTLPSTCLQKVEEQPEDADNQNRNVRMGSQPPDNTIIVHPVMTG	1086	2032	-----THLCSTTP-----DRPPPSQASSHHHHHRRRRDRKQSRLEKGP\$LS-AD	2076
QY	1266	-----SAYIFPPQSRFRLLCHRI	1283	2136	GDLPSQEEPLFP-----RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDS	2186
Db	1087	PLGEATVPSGNVDLESQAEGKKEVEADDVMRSGPRPIVYSSMFCLSPTNLLRRFCHYI	1146	2077	MDGAPSSAVGPGLPPEGEGPTGRRERRRQGRSQRERRQPS\$SSSEKQRF---YSCDRF	2133
QY	1284	ITHKMFHDHVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL	1343	2187	GSQRLCPSPS-----SLGGQPL-----GGPGSRPKK	2213
Db	1147	VTMRYPFVVILVVIALSSIALAAEDP-VRTDSPRNNAKLYLDYIFTGVFTFEMVIKMDL	1205	2134	GREPPKPKPSLSSHPTSPTAGQEPGPHPOQSGSVNGSFPLLSTSGASTPGRGRRQLPQT	2193
QY	1344	GWCFGEQAYLRSSWNVDLGLLVLSVIDILVSMV-SDSGTKILGMLRVLRLLRTRPLRV	1402	2214	KLSP-PSISIDPPES-----QGSRRPPCSPG-----VCLRRRAPASD-----	2248
Db	1206	LLLLHPGAYFRDLWNILD---FIVVSGALVAFAFSGSKGKDINTIKSLRVLRVLRPLKT	1261	2194	PLTPRPSITYKTANS\$PIHFAGQTSLPAPSPGRLSRGLSEHNALLQRDPLSQPLAPGSR	2253
QY	1403	ISRAQGLKLVETILMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGE-----D	1456	2249	-SKDPSVSSPLDSTAASPSPKDITLSL-----SGLSS	2279
Db	1262	IKRLPKLKAVFDCVNVSLKNVLNILIVMLFMFIFAVIAVQLFKGKFFCYCTDESKELERD	1321	2254	IGSDPYLGQRLDSEASVHALPEDTLTFEEAVATNSGRSS	2292
QY	1457	TRN--ITNKSDCAEASYSR-WVRHKYNFDNLGQALMSLFLVLSKDGWVDIMYDGLDAVGVD	1513			
Db	1322	CRGQYLDYEKEEVEAQRQWKYDFHYDNVLMWALLTLFTVSTGEGWPMVLKHSVDATYEE	1381			
QY	1514	QQPIMNHNPMMLLYFISFLLIIVAFVFLNMVGVVVENFHKCRQHQEEEEARRREEKRLRR	1573			
Db	1382	QGPSPGYRMEL\$IFYVVYFWFPFFFFVNFVALIITF-----QEQGDKVMSE-----CS	1431			
QY	1574	LEKKRRSKEQMAEAQCKPYSDYSR--FRLLVHHLCTSHYLDLFTGVIGLNVVTMAME	1631			
Db	1432	LEKNERACIDFAISAKPLTRYMPQNRQSFQYKWTWTFVWSPPFYFIMAMIALNTVVLMMK	1491			
QY	1632	HYQQPQILDEALKICNVIFTVFVFESVFKLVAPAFRRFFQDRWNQLDLAIVLLSIMGIT	1691			
Db	1492	PYDAPYEYELMLKCLNIVFTSMFSMECVLKIIAFGVNLNFRDAWNFDVTVLGSITDIL	1551			
QY	1692	LEBIE-----VNLSLPINFTIIRIMRVLRIARVLKLLKMAVGMRALIHTVMQALPQVGNL	1746			
Db	1552	VT\$IAETNNFINLS-----FLRLFRARLLIKLRQGYTIRILLWTFVQ\$KALPYV	1602			

RESULT 14
US-08-223-305C-47
; Sequence 47, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA

QY 576 GPPRGAESVHSFYHADCHLEPVRQCAPPRCBPSEASGRITVSGKVYPTVHTSPPEILK 635
Db 441 -----
QY 636 DKALVEVAPSGPPTLTSTFNIPPGPFSSMHKLETSQSTGACHSSCKTSSPCSKADSGACG 695
Db 441 -----
QY 696 PDSCPYCARTGAGEPESADHVPDSDSEAVVEFTQDAQHSDLRDPHSRRRQORSLGPDAP 755
Db 453 -----
QY 756 SSVLAEWRLICDTRKIVDSKYFGRGIMTALVNTLSMGIEYHEQPEELTNALEISNIVF 815
Db 470 --MERFF-----IRRMVKAQSFYVVVLCVVALNTLCVAMVHYNQPRRLTTTLTYFAEFVF 521
QY 816 TSLFALEMLLKVGPFGYIKNPYNIPTDGVIVWISVWEIVGQ-----QGGGLSVLRTFR 870
Db 522 LGLFLTEMSLKMVGLGPRSYFRSSFCDFGVIVGSVFVWAAIKPGSSFGISVLRALR 581
QY 871 LMRVLKLVRLPALQRLVLMKTMNDNVATFCMLLMFLFIFISILGMHLFGCKFASERDG 930
Db 582 LLRIFKVTYWSLRLNVVLSLNSMKSILSLFLFLFVIVFALLGMQLFGGQNFQDET 641
QY 931 DTLPRKDNFDSLWAVTVFQILTOQDNKVLNGM-----ASTSSWAALFYFIALMTFGN 985
Db 642 PT-----TNPDTPPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIVLTLFGN 697
QY 986 YVLFNLVAILVEGFAEGDATKSESEPDPFFSPSVDGDRKKRLALVALGEHAELRKSL 1045
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QY 1046 LPPLIHTAATPMSHPKSSSTGVGEA-----
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QY 1072 -----LGSGSRSTSSGSAEPGAA-----HH-----EMKCP----- 1097
Db 807 PDMKTHLDRPLVVELGRDARGVPVGGKARPEAAEPGVDPPPRRHRRDKDKTPAAGDQ 866
QY 1098 -----PSARSS---PHSPWSAASSWTSSRNSLGRAPSLKRRSPSGERRSL 1142
Db 867 DRAEAPKAESGEPGAREPRPHRSHSKEAA--GPPEARSERGRG-----GPEGGRHH 919
QY 1143 LSGEQESQDEE-----ESSEEDRASPCGSDHRRHGSLE---REAKSSFDLPDTL 1189
Db 920 RRGSPPEAAERPRRHRHRHQDPSPKECAGAKERRARHGGPRAGPREAESG----- 972
QY 1190 QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA-----RTLRTDDPQLDGGDDNDE 1238
Db 973 BEPARRHARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS 1032
QY 1239 GNLSKGERIQAWVRSRLPACCRER-----DSW-----
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QY 1266 -----
Db 1087 PLGEATVVPNGVNDLESQAEGKKEVEADDVMRSGPRPIVPYSSMFCLSPTNLLRRFCHYI 1146
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Db 1147 VTMRYFEVVLVIALSSIALAAEDP-VRTDSPRNALKYLDYIFTGVFTFEMVIKMIDL 1205
QY 1344 GWCGEQAYLRSSWNVLDGLLVLSVIDILVSMV-SDSGTKILGMLRVLRLRLRLRPLRV 1402
Db 1206 GLLLHPGAYFRDLWNILD----FIVVSGALVAFAFSGSKGKDINTIKSLRVLRLRPLKT 1261
QY 1403 ISRAQGLKLVVETLMSSLKPIGNIVVICAPFIIFGILGVQLFKGKFFVCQGE-----D 1456
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QY 1457 TRN--ITNKSDCAEASR-WVRHKYNFDNLGQALMSLFLVASKDGWVDIMYDGLDVGVD 1513
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QY 1514 QOPIMHNPNMMLLYPISFLLIIVAFFVLNMVGVVVENFHKCRHQHEEEARRRREKRLRR 1573
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QY 1632 HYQQPQILDEALKICNYIFTVIFVFESEVFKLVAFARFRFFQDRWNQOLDLAIIVLLSIMGIT 1691
Db 1492 FYDAPYEYELMLKCLNIVFTSMFMECVLKIIAFGVNLNYFRDANVVEFVTVLGSIITDIL 1551
QY 1692 LEEIE-----VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVMQALPQVGNL 1746
Db 1552 VTEIAETNNFINLS-----FLRLFRAARLIKLLRQGYTIRILLWTFTVQSFKALPYV 1602
QY 1747 GLLFMLLFFFAALGVELFGDLECDETHPCCEGLGRHATFENFGMAFLTLLFRVSTGDNWNG 1806
Db 1603 CLLIAMLFFIYAIIGMQVFGNIALDDD---TSINRRHNFRFTLQALMLLFRSATGEAWHE 1659
QY 1807 IMKD--PSRDCDQE--STCYNTVISPIYFVSFVLTAQFVLNVVVIIVLM----- 1851
Db 1660 IMLSCLSNQACDEQANATECGSDPAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS 1719
QY 1852 ----KHLEE-----
Db 1720 ILGPHLHDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPLGLGKCPARVAYKRLVRMN 1779
QY 1857 -----SNKEAKEBAEAEAL-----ELEMKTLS- 1879
Db 1780 MPISNEDMTVHTSTLTMALIRTALAIKAPAGTKHQHQAELKEISVVWANLPQKTLDL 1839
QY 1880 -POHSP----LGSPF----LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMPV 1930
Db 1840 LVPPHKPDEMVTGVVVAALMIFDFYKQNKTTTQDMQAPGGLSQMGVPSLFI---HPLKAT 1896
QY 1931 HPEEVPVPL-GPDLTLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRCWGLPKAQSGSI 1989
Db 1897 LEQTPAVLRGARVFLRQKSST---SLSNGGAIQNESGIKESV---SWGRTQDA-- 1947
QY 1990 LSVHSQPADTSCILQLPKDWHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPRLRQAIRTD 2049
Db 1948 -----PHEA-----RPPLERCHSTEIPVGRSGALAVD 1974
QY 2050 -----SLDVQGLSREDLLSEVSGPSCPLTRSSSFWGSSIQVQORSG 2092
Db 1975 VQMOSITRRGPDGEPQPLESQG---RAASMPRLAAETQPVTDASPMKRSISTLAQRPRG 2031
QY 2093 IQSKVSKHIRLPAPCPGLEPSWAKDPPETRS-----SLELDTLSWIS 2135
Db 2032 -----THLCSTTP-----DRPPPSQASSHHHHHRRHRRDRKQRSLEKGPSSL-AD 2076
QY 2136 GDLLPSSQEEPLFP-----RDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLD 2186
Db 2077 MDGAPSSAVGCLPPGEGPTGCRRERRRQERGRSQERRQSPSSSEKQRF---YSCDRF 2133
QY 2187 GSQPRLCPSPS-----SLGGQPL-----GGGSRPKK 2213
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QY 2214 KLSP-PSISIDPPES-----QGSRRPPCSPG-----VCLRRRAPASD----- 2248
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Mon Nov 22 06:47:52 2004

Search completed: November 18, 2004, 13:35:56
Job time : 78.6868 secs

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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:32:41 ; Search time 180.328 Seconds
(without alignments)
4491.206 Million cell updates/sec

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Perfect score: 12028
Sequence: 1 MLPHRVRCVTPPLRGSAR.....KKDTLSLSGLSDPTDMDPZ 2287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	11532	95.9	2374	10	US-09-383-894-2
3	10806.5	89.8	2243	16	US-10-408-765A-625
4	10732.5	89.2	2377	17	US-10-757-262-16
5	6222	51.7	2353	16	US-10-408-765A-1128
6	5409	45.0	2175	9	US-09-935-541-2
7	5409	45.0	2175	14	US-10-425-800-2
8	5405.5	44.9	2188	9	US-09-935-541-4
9	5405.5	44.9	2188	14	US-10-425-800-4
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					Sequence 2, Appli
					Sequence 625, App
					Sequence 16, Appl
					Sequence 1128, Ap
					Sequence 2, Appli
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 19, Appl
					Sequence 6836, Ap

14	1680.5	14.0	2264	15	US-10-627-370-2	Sequence 2, Appli
15	1678	14.0	2327	17	US-10-736-883-38	Sequence 38, Appl
16	1678	14.0	2343	13	US-10-033-026-4	Sequence 4, Appli
17	1676	13.9	2339	15	US-10-375-253-12	Sequence 12, Appl
18	1674	13.9	2339	13	US-10-736-883-32	Sequence 6, Appli
19	1674	13.9	2339	17	US-10-736-883-44	Sequence 32, Appl
20	1673	13.9	2331	17	US-10-736-883-40	Sequence 44, Appl
21	1662.5	13.8	2288	17	US-10-736-883-28	Sequence 40, Appl
22	1661	13.8	2333	17	US-10-736-883-28	Sequence 28, Appl
23	1647.5	13.7	2313	16	US-10-322-696-178	Sequence 178, App
24	1642.5	13.7	2337	15	US-10-375-253-14	Sequence 14, Appl
25	1642.5	13.7	2336	13	US-10-033-026-10	Sequence 10, Appl
26	1642.5	13.7	2336	17	US-10-736-883-30	Sequence 30, Appl
27	1640.5	13.6	2237	13	US-10-033-026-8	Sequence 8, Appli
28	1640.5	13.6	2237	17	US-10-736-883-34	Sequence 34, Appl
29	1638	13.6	2251	15	US-10-375-253-38	Sequence 38, Appl
30	1637.5	13.6	2270	15	US-10-375-253-40	Sequence 40, Appl
31	1636	13.6	2251	16	US-10-322-696-84	Sequence 84, Appl
32	1635.5	13.6	2270	16	US-10-322-696-176	Sequence 176, App
33	1634.5	13.6	1984	10	US-09-457-571-10	Sequence 10, Appl
34	1631	13.6	2181	13	US-10-029-413A-18	Sequence 18, Appl
35	1631	13.6	2181	13	US-10-029-413A-20	Sequence 20, Appl
36	1631	13.6	2181	14	US-10-205-823-50	Sequence 50, Appl
37	1631	13.6	2181	14	US-10-411-010-29	Sequence 29, Appl
38	1631	13.6	2181	16	US-10-322-696-54	Sequence 54, Appl
39	1631	13.6	2339	17	US-10-736-883-42	Sequence 42, Appl
40	1630.5	13.6	2166	13	US-10-029-413A-4	Sequence 4, Appli
41	1628	13.5	1873	13	US-10-029-413A-22	Sequence 22, Appl
42	1625.5	13.5	1989	10	US-09-457-571-12	Sequence 12, Appl
43	1617.5	13.4	1969	10	US-09-457-571-16	Sequence 16, Appl
44	1617	13.4	2161	15	US-10-375-253-2	Sequence 2, Appli
45	1614.5	13.4	1977	10	US-09-919-039-367	Sequence 367, App

ALIGNMENTS

RESULT 1
US-09-383-894-4
; Sequence 4, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2425
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-383-894-4

Query Match	96.0%;	Score 11542.5;	DB 10;	Length 2425;
Best Local Similarity	95.4%;	Pred. No. 0;		
Matches 2219;	Conservative	3;	Mismatches 54;	Indels 51; Gaps 4;
QY	3	PHRVRCVTRTPPLRGSARPSDDPGPRLARGWTTRRRMERAPRSRDSPPVASRS-----	54	
Db	21	PTGVPRLRDTSSEGLRSLFLGPPCAPAG-----QRMDEEDGAGAESGQPRSFQ	72	
QY	55	-STTCPGGAAGAGAGSTEKDPGSAADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNP	113	
Db	73	LNDLGAGGRQGGSTKDPGSAADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNP	132	
QY	114	WFERVSMVLVLLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIFAFFAFAVMMVAVLGI	173	

Db	133	WFERVSMVLILNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGI	192
QY	174	FGKKCYLGDITWNRLDFFIIVIAGMLEYSLDLQNVSFSAVRTVRURPLRAINRVPSMRILV	233
Db	193	FGKKCYLGDITWNRLDFFIIVIAGMLEYSLDLQNVSFSAVRTVRURPLRAINRVPSMRILV	252
QY	234	TLLLDITLPMLGNVLLLCFFVFFIFIGIVGVLWAGLLRNRCLFENFSLPLSDVLEPYQT	293
Db	253	TLLLDITLPMLGNVLLLCFFVFFIFIGIVGVLWAGLLRNRCLFENFSLPLSDVLEPYQT	312
QY	294	ENEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSSNTTCVNWNQYXT	353
Db	313	ENEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSSNTTCVNWNQYXT	372
QY	354	NCSAGEHNPFKGAINFNIGYAWIAIFQVITILEGWVDIMYFVMDAHSFYNFIFYILLIIV	413
Db	373	NCSAGEHNPFKGAINFNIGYAWIAIFQVITILEGWVDIMYFVMDAHSFYNFIFYILLIIV	432
QY	414	GSFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYL	473
Db	433	GSFFMINLCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYL	492
QY	474	YILRKAARRLAQVSRAIGVRAGLLSSPVARSQBEPQSGSCSTRSHRRLSVHHLVHHHHH	533
Db	493	YILRKAARRLAQVSRAIGVRAGLLSSPVARSQBEPQSGSCSTRSHRRLSVHHLVHHHHH	552
QY	534	HHVHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTSPGGPPRGAESVHSFYHAD	593
Db	553	HHVHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPTSPGGPPRGAESVHSFYHAD	612
QY	594	HLEPVRQAPPPRCPPSEASGRITVSGKVYPTVHTSPPPEILKDXALVEVAPSPGPTLTS	653
Db	613	HLEPVRQAPPPRCPPSEASGRITVSGKVYPTVHTSPPPEILKDXALVEVAPSPGPTLTS	672
QY	654	FNIPPGPFSSMHKLLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESA	713
Db	673	FNIPPGPFSSMHKLLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESA	732
QY	714	DHVMPSDSSEAVYEFTQDAQHSDLRDPHSRRRQRLGPDAPSSVLAFWRLLICDTERKIV	773
Db	733	DHVMPSDSSEAVYEFTQDAQHSDLRDPHSRRRQRLGPDAPSSVLAFWRLLICDTERKIV	792
QY	774	DSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGP	833
Db	793	DSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLIVYGP	852
QY	834	GIYKNPYNIFDGVTVVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVVLMK	893
Db	853	GIYKNPYNIFDGVTVVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVVLMK	912
QY	894	TMDNVATFCMLMLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQIL	953
Db	913	TMDNVATFCMLMLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQIL	972
QY	954	TQEDWNKVLNGMASTSSWAALYFIALMTFGNVVLFNLVAILVEGFGQAE-----	1003
Db	973	TQEDWNKVLNGMASTSSWAALYFIALMTFGNVVLFNLVAILVEGFGQAEIGKREDASG	1032
QY	1004	-----GDATKSESEPDPFFSPVDGDGRKRLALVALGHAELRKSLLPPLI	1050
Db	1033	QLSCIQLPVNSQGGDATKSESEPDPFFSPVDGDGRKRLALVALGHAELRKSLLPPLI	1092
QY	1051	IHTAATPM SHPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHMKCPFSARSSPHSPWSA	1110
Db	1093	IHTAATPM SLPKSSSTGVGEALGSGSRRTSSSGSAEPGAAHHMKCPFSARSSPHSPWSA	1152
QY	1111	ASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHR	1170
Db	1153	ASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHR	1212
QY	1171	HRSGLEREAKSSFDLPDITLQVPLHRTASGRSSASEHQDCNGKSASGRLARTLRDTPQL	1230
Db	1213	HRSGLEREAKSSFDLPDITLQVPLHRTASGRSSASEHQDCNGKSASGRLARTLRDTPQL	1272
QY	1231	DGDDNDNEGNSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMF	1290
Db	1273	DGDDNDNEGNSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMF	1332
QY	1291	HVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLNSYIIFTAVFLAEMTVKVVALGWCFCGEQ	1350
Db	1333	HVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLNSYIIFTAVFLAEMTVKVVALGWCFCGEQ	1392
QY	1351	AYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRPLRPLRVISRAQGLK	1410
Db	1393	AYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRPLRPLRVISRAQGLK	1452
QY	1411	LVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEAS	1470
Db	1453	LVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEAS	1512
QY	1471	YRWVRHKYNFNDLGOALMSLFLVASKDGWVDIMYDGLDAVGVDQOQIMNHNPMWLLLYFIS	1530
Db	1513	YRWVRHKYNFNDLGOALMSLFLVASKDGWVDIMYDGLDAVGVDQOQIMNHNPMWLLLYFIS	1572
QY	1531	FLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREKRLRLEKKRR-----	1579
Db	1573	FLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREKRLRLEKKRRNMLDDVIAAG	1632
QY	1580	SKEKQMAEAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTIGVIGLVVVTNAMEHYQQPQIL	1639
Db	1633	SSASAASEAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTIGVIGLVVVTNAMEHYQQPQIL	1692
QY	1640	DEALKICNYIFTVIFVPESVPKLVAFAFRFFQDRWNQDLDAIVLLSIMGITLEEIEVNL	1699
Db	1693	DEALKICNYIFTVIFVPESVPKLVAFAFRFFQDRWNQDLDAIVLLSIMGITLEEIEVNA	1752
QY	1700	SLPINPTIIRIMRVLRIRVULKLMVAGMRALLHTVMQALPQVGNLGLLFFFAA	1759
Db	1753	SLPINPTIIRIMRVLRIRVULKLMVAGMRALLHTVMQALPQVGNLGLLFFFAA	1812
QY	1760	LGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMKDPDRDCDOES	1819
Db	1813	LGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMKDLTRDCDOES	1872
QY	1820	TCYNTVISPIYFVSFVLTAQFVLVNVVIVAVLMKHLEESNKEAKEAELEAELEMKTILS	1879
Db	1873	TCYNTVISPIYFVSFVLTAQFVLVNVVIVAVLMKHLEESNKEAKEAELEAELEMKTILS	1932
QY	1880	PQPHSPLGSPFLWPGEVGNSTSPKPGAPHTTAHIGAASGFSLEHPTMVPHPPEEVPVL	1939
Db	1933	PQPHSPLGSPFLWPGEVGNSTSPKPGAPHTTAHIGAASGFSLEHPTMVPHPPEEVPVL	1992
QY	1940	GPDLLTVRKSGVSRTHSLPNDSYMCNPGSTAERSLHGRGWGLPKAQSGSILSVHSQPADT	1999
Db	1993	GPDLLTVRKSGVSRTHSLPNDSYMCNPGSTAERSLHGRGWGLPKAQSGSILSVHSQPADT	2052
QY	2000	SCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQORPLRQAARTDSDLVQGLGSR	2059
Db	2053	SCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQORPLRQAARTDSDLVQGLGSR	2112
QY	2060	EDLLSEVSGPSCPLTRSSSFWGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPP	2119
Db	2113	EDLLSEVSGPSCPLTRSSSFWGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPP	2172
QY	2120	ETRSSLDELDTLSWISGDLLPSSQEEPLFRDLKKCYSVETQSCRRRPFGLDEQRRHSI	2179
Db	2173	ETRSSLDELDTLSWISGDLLPSSQEEPLFRDLKKCYSVETQSCRRRPFGLDEQRRHSI	2232
QY	2180	AVSCLDSGSQPRLCPSPSLGGQPLGGPGSRPKKLSPPSISIDPPESQGSRRPPCSPGVC	2239
Db	2233	AVSCLDSGSQPRLCPSPSLGGQPLGGPGSRPKKLSPPSISIDPPESQGSRRPPCSPGVC	2292
QY	2240	LRRRAPASDSKDPSSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP	2286
Db	2293	LRRRAPASDSKDPSSVSSPLDSTAASPSPKKDTLSLSGLSSDPTDMDP	2339

QY	1828	PIYFVSFLTAQFVLVNVVIAVLMKHLEESNKEAEAELEAELEEMKTLSPQPHSLG	1887
Db	1830	PIYFVSFLTAQFVLVNVVIAVLMKHLEESNKEAEAELEAELEEMKTLSPQPHSLG	1889
QY	1888	SPFLWPGEVNSTDSPKGPAPHTTAHGAAGFSLEHPTMVPHPEEVVPLGPDLLTVR	1947
Db	1890	SPFLWPGEVNSTDSPKGPAPHTTAHGAAGFSLEHPTMVPHPEEVVPLGPDLLTVR	1949
QY	1948	KSGVSRTHSLPNDSYMCRNGSTAERSLHRCWGCLPKAQSGSILSVHSQPADTSCILQLPK	2007
Db	1950	KSGVSRTHSLPNDSYMCRNGSTAERSLHRCWGCLPKAQSGSILSVHSQPADTSCILQLPK	2009
QY	2008	DVHYLLQPHGAPTWGAIPKLPPLPPGRSPLAQRPLRRQAAIRTDSDVQGLGSREDLLSEVS	2067
Db	2010	DVHYLLQPHGAPTWGAIPKLPPLPPGRSPLAQRPLRRQAAIRTDSDVQGLGSREDLLSEVS	2069
QY	2068	GPSCPLTRSSSFVGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSL	2127
Db	2070	GPSCPLTRSSSFVGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSL	2129
QY	2128	DTELSWISGDLPLSSQEEPLPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLD	2187
Db	2130	DTELSWISGDLPLSSQEEPLPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLD	2189
QY	2188	SQPRLCPSPSSSLGGQPLGGPSRPPKKLSPPSISIDPPESQSGRRPPCSGVCLLRRAPAS	2247
Db	2190	SQPRLCPSPSSSLGGQPLGGPSRPPKKLSPPSISIDPPESQSGRRPPCSGVCLLRRAPAS	2249
QY	2248	DSKDPSSVSSPLDSTAASPPKXDTLSLGLSSDPTDMDP	2286
Db	2250	DSKDPSSVSSPLDSTAASPPKXDTLSLGLSSDPTDMDP	2288
RESULT 3			
US-10-408-765A-625			
; Sequence 625, Application US/10408765A			
; Publication No. US20040101874A1			
; GENERAL INFORMATION:			
; APPLICANT: Ghosh, Soumitra S.			
; APPLICANT: Fahy, Eoin D.			
; APPLICANT: Zhang, Bing			
; APPLICANT: Gibson, Bradford W.			
; APPLICANT: Taylor, Steven W.			
; APPLICANT: Glenn, Gary M.			
; APPLICANT: Warnock, Dale E.			
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION			
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME			
; FILE REFERENCE: 660088.465			
; CURRENT APPLICATION NUMBER: US/10/408,765A			
; CURRENT FILING DATE: 2003-04-04			
; NUMBER OF SEQ ID NOS: 3077			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 625			
; LENGTH: 2243			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-408-765A-625			
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Best Local Similarity 93.3%; Pred. No. 0;			
Matches 2076; Conservative 33; Mismatches 104; Indels 13; Gaps 5;			
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Db	30	GRPGGSAEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERISML	89
QY	122	VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFAFVEMVVKMVALGIFGKKCYLG	181
Db	90	VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFAFVEMVVKMVALGIFGKKCYLG	149
QY	182	DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLD	241
Db	209	DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLD	241
Db	209	DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLD	209
QY	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSDVLEPYQYQ TENED	301
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSDVLEPYQYQ TENED	269
QY	302	ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSNTTCVWNQYITNC	361
Db	270	ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSNTTCVWNQYITNC	329
QY	362	PEKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGS	421
Db	330	PEKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGS	389
QY	422	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYBELLKYLVYL	481
Db	390	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYBELLKYLVYL	449
QY	482	RLAQVSRAGVRAGLLSSPVARSQEPQPSGSCSTRSHRRLSVHHLVHHHHHHH	541
Db	450	RLAQVSRAGVRAGLLSSPVARSQEPQPSGSCSTRSHRRLSVHHLVHHHHHHH	509
QY	542	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTSPGGPPRGAESVHSFYHADCH	601
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTSPGGPPRGAESVHSFYHADCH	569
QY	602	APPPRCPEASGRTVSGKVPYVHTSPPPPEIKDKALVEVAPSPGPPILTSENIP	661
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QY	662	SSMHKLLTQSTGACHSSCKISSPCSKADSGACGDDSCPYCARTGAGEPESAD	721
Db	630	SSMHKLLTQSTGACHSSCKISSPCSKADSGACGDDSCPYCARTGAGEPESAD	689
QY	722	SEAVYFTQDAQHSDLRDPHSRRQRSLGDAEPSVLAFWRLICDTRFKIVDSKY	781
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QY	782	IMAILVNTLSMGIEYHEQPELTNALEISNIVFTSIFALEMLLKLIVGPGYIK	841
Db	749	IMAILVNTLSMGIEYHEQPELTNALEISNIVFTSIFALEMLLKLIVGPGYIK	808
QY	842	IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTM	901
Db	809	IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTM	868
QY	902	CMLLMFIFIFSILGMHLFGCKFASERDGTLPDRKNEDSLLWAIIVTFQILT	961
Db	869	CMLLMFIFIFSILGMHLFGCKFASERDGTLPDRKNEDSLLWAIIVTFQILT	928
QY	962	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPD	1021
Db	929	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPD	988
QY	1022	GDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPMHPKSSSTGVGEALGS	1081
Db	989	GDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPMHPKSSSTGVGEALGS	1048
QY	1082	SGSAEPGAAHEMKCPPSARSSPHSPWSAASSWTSSRRSSRNLSI GRAPSLK	1141
Db	1049	SGSAEPGAAHEMKCPPSARSSPHSPWSAASSWTSSRRSSRNLSI GRAPSLK	1107
QY	1142	LLSGEGQESQDEEESSEEDRASPGSDHHRGSLEREAKSSFDLPDTLQVPL	1201
Db	1108	LLSGEGQESQDEEESSEEDRASPGSDHHRGSLEREAKSSFDLPDTLQVPL	1167
QY	1202	SSASEHQDCNGKSASGRRLARTLRTDDPQLDGGDDNDDEGNLSKGERIQAW	1261
Db	1168	SSASEHQDCNGKSASGRRLARTLRTDDPQLDGGDDNDDEGNLSKGERIQAW	1227
QY	1262	RDSWSAYIFPPQSRFRLLCHRIITHKMFHVVLVIIIFLNCITIAMERPKID	1321
Db	1228	RDSWSAYIFPPQSRFRLLCHRIITHKMFHVVLVIIIFLNCITIAMERPKID	1287

QY	1322	TLSNYIFTAVFLAEMTVKVV	ALGWCFGEQAYLRSSWN	VLDGLVLIVSIDILVSMVSDSG	1389
Db	1288	TLSNYIFTAVFLAEMTVKVV	ALGWCFGEQAYLRSSWN	VLDGLVLIVSIDILVSMVSDSG	1347
QY	1382	TKILGMLRVLRLLRTLPLR	VISRAQGLKLVETLMSSLK	PIGNIVVICCAFFIIFGILG	1441
Db	1348	TKILGMLRVLRLLRTLPLR	VISRAQGLKLVETLMSSLK	PIGNIVVICCAFFIIFGILG	1407
QY	1442	VQLFKGFFVCQGEDTRNIT	NKSDCAEASRWRVHRKYN	FDNLGQALMSFLVASKDGWVD	1501
Db	1408	VQLFKGFFVCQGEDTRNIT	NKSDCAEASRWRVHRKYN	FDNLGQALMSFLVASKDGWVD	1467
QY	1502	IMYDGLDAVGVDQOQIMNH	NPWMLLYFISFLLIVAF	FLNMFGVVVENFHKCRHQEEE	1561
Db	1468	IMYDGLDAVGVDQOQIMNH	NPWMLLYFISFLLIVAF	FLNMFGVVVENFHKCRHQEEE	1527
QY	1562	EARRREEKRLRLEKKRRS	KEKQMAEAQCKPYYS	DYSRFRLLVHHLCTSHYLDL	FITGVI 1621
Db	1528	EARRREEKRLRLEKKRR	-----KAQCKPYYS	DYSRFRLLVHHLCTSHYLDL	FITGVI 1580
QY	1622	GLNVVTMAMEHYQQPQIL	DEALKICNYIFTVIFV	ESVPKLVAFRRFFQDRWNQDLA	1681
Db	1581	GLNVVTMAMEHYQQPQIL	DEALKICNYIFTVIFV	ESVPKLVAFRRFFQDRWNQDLA	1640
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Db	1641	IVLLSIMGITLEEIEVNL	SLPINPTIIRIMRVLR	IARVLKLLKMAVGMRAL	LHTVMQALP 1700
QY	1742	QVGNLGLLFMLLFFIFA	ALGVELFGDLECDETH	PCCEGLGRHATFRNFGMA	FLTLFRVSTG 1801
Db	1701	QVGNLGLLFMLLFFIFA	ALGVELFGDLECDETH	PCCEGLGRHATFRNFGMA	FLTLFRVSTG 1760
QY	1802	DNWNGIMKDPDRCDQEST	CYNTVISPIYFVS	FVLTAQFVLNVVIAVLMK	HLEESNKEA 1861
Db	1761	DNWNGIMKDTLRDCQEST	CYNTVISPIYFVS	FVLTAQFVLNVVIAVLMK	HLEESNKEA 1820
QY	1862	KEAELEAELELENKTLSP	QPHSPLGSPFLNPGVE	GVNSTDSPKPGAPHTTAH	IGAASGF 1921
Db	1821	KEAELEAELELENKTLSP	QPHSPLGSPFLNPGVE	GVNSTDSPKPGALHPAAH	ARSASHF 1880
QY	1922	SLEHPTMVPHPPEVPVL	GPDLTLTVRKSGVSR	THSLPNDSYMCRNGSTA	ERSLHRCWGL 1981
Db	1881	SLEHPTMQHPPELP--	-GPDLTLTVRKSGVSR	THSLPNDSYMCRHGSTA	EGLHRCWGL 1937
QY	1982	PKAQSGSILSVHSQPAD	TSCILQLPKDVHLLQ	PHGAPTWGAIPKLPPGR	SPLAQRPLR 2041
Db	1938	PKAQSGSVLSVHSQPAD	TSYILQLPKDAPHLL	QPHSAPTWTGTIPKLPP	GRSPLAQRPLR 1997
QY	2042	RQAAIRTDSDVQGLS	REDLLSEVSGPSCPL	TRSSSFWGSSITVQQR	SGIQSKVSHI 2101
Db	1998	RQAAIRTDSDVQGLS	REDLLAEVSGFPPLA	RYSFWGQSSTAQAQHS	RSRSHSKISKHM 2057
QY	2102	RLPAPCPGLEPSPWAK	PPETRSSLELDTLS	WISGDLL- PSSQEE	PLFPRDLKKCYSVET 2160
Db	2058	TPPAPCPGPEPNWKG	PPETRSSLELDTLS	WISGDLLPPGQEE	PPSPRDLKKCYVEA 2117
QY	2161	QSCRRRPGFWLDEOR	RHSIAVSCLD	SGQPRLCPSPSSLG	QPLGGPGRPKKLSPPSI 2220
Db	2118	QSCORRPTISWLEOR	RHSIAVSCLD	SGSQPHLGTDP	SNLGGQPLGGPGRPKKLSPPSI 2177
QY	2221	SIDPPESQGSRRPPC	SPGVCLRRRAPAS	DSKDPSSVSSPLD	STAASPPKKTLSLSGSSD 2280
Db	2178	TIDPPESQGPRTPP	SPGICLRRRAPSS	DSKDPLASGPPD	SMAASPPKKTLSLSGSSD 2237
QY	2281	PTDMDP	2286		
Db	2238	PADLDP	2243		

RESULT 4

US-10-757-262-16

; Sequence 16, Application US/10757262

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; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPI03-007P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-16

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Query Match 89.2%; Score 10732.5; DB 17; Length 2377;
Best Local Similarity 88.3%; Pred. No. 0;
Matches 2078; Conservative 33; Mismatches 109; Indels 133; Gaps 7;

QY	62	GAAGAGST	EKDPGSAD	SEAEGLP	YPALAPV	VVFFYL	SQDSRPR	SWCLRT	VCNPNW	FERVSM	121
DB	30	GRPGPSA	EKDPGSAD	SEAEGLP	YPALAPV	VVFFYL	SQDSRPR	SWCLRT	VCNPNW	FERISML	89
QY	122	VILLNCVT	LGMFPCED	IACDSQRC	RILOAFDD	FIFAFFA	VEVMVVM	ALGIFG	KKCYLG		181
DB	90	VILLNCVT	LGMFPCED	IACDSQRC	RILOAFDD	FIFAFFA	VEVMVVM	ALGIFG	KKCYLG		149
QY	182	DTWNRLD	FFIVIA	AGMLEY	SIDLQNV	SFSAVRT	VRVLRPL	RAINRVP	SMRILVT	LLD	241
DB	150	DTWNRLD	FFIVIA	AGMLEY	SIDLQNV	SFSAVRT	VRVLRPL	RAINRVP	SMRILVT	LLD	209
QY	242	MLGNVLL	LCFFVFF	IFGIVG	VQLWAGLL	LRNRCFL	PNFSLPL	SVLDLE	PPYQ	TENEDE	301
DB	210	MLGNVLL	LCFFVFF	IFGIVG	VQLWAGLL	LRNRCFL	PNFSLPL	SVLDLE	PPYQ	TENEDE	269
QY	302	ICSQPRE	NGMRC	SVPTLR	GEGGGP	PCSLDY	ETYNSS	NTTCV	WNQYYT	NCSAGE	361
DB	270	ICSQPRE	NGMRC	SVPTLR	GEGGGP	PCGLDYE	AYNSS	NTTCV	WNQYYT	NCSAGE	329
QY	362	PFKGAIN	FDNIGY	AWIAIF	QVITLEG	WVDIMY	FVMDA	HSFYNF	IYFILLI	IVGSSFF	421
DB	330	PFKGAIN	FDNIGY	AWIAIF	QVITLEG	WVDIMY	FVMDA	HSFYNF	IYFILLI	IVGSSFF	389

QY 422 CLVVIATQFSETKQESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 481
Db 390 CLVVIATQFSETKQESQLMREQVRFLSNASTLASFSEPGSCYEBELLKYLVIILRKAAR 449
QY 482 RLAQVSRAGVRAGLSSPVARSGQEPQSGSCSTRSHRRLSVHHLVHHHHHHHHVHLGN 541
Db 450 RLAQVSRAGVRVGLSSPAPLGGQETQSSSCSRSHRRLSVHHLVHHHHHHHHVHLGN 509
QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPSPSTPSPGPPRGAESVHSFYHADCHLEPVRQ 601
Db 510 GTLRAPRASPEIQDRDANGSRRLMLPPSPSTPSPALSGAPPGAESVHSFYHADCHLEPVRQ 569
QY 602 APPPRCPSEASGRTVSGKVYPTVHTSPPPPEILKDKALVEVAPSPGPTLTSLNIPPGPF 661
Db 570 APPPRSPSEASGRTVSGKVYPTVHTSPPPPETLKEKALVEVAASSGPTLTSLNIPPGPY 629
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADGACGPDSCPYCARTGAGEPESADHVMPSD 721
Db 630 SSMHKLLETQSTGACQSSCKISSPCLKADGACGPDSCPYCARAGAGEVELADREMPDSD 689
QY 722 SEAVYEFTQAOHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTERKIVDSKYFGRG 781
Db 690 SEAVYEFTQAOHSDLRDHS - RRQSLGPDAPSSVLAFWRLICDTERKIVDSKYFGRG 748
QY 782 IMTAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLVYGPFGYIKNPYN 841
Db 749 IMTAILVNTLSMGIEYHEQPELTNALEISNIVFTSLFALEMLLKLVYGPFGYIKNPYN 808
QY 842 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDNVATF 901
Db 809 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDNVATF 868
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Db 869 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTFQILTQEDWNKV 928
QY 962 LYNGMASTSSWAALYFIALMTFGNVVLFNLLVAILVEGFQAE - - - - - 1003
Db 929 LYNGMASTSSWAALYFIALMTFGNVVLFNLLVAILVEGFQAEIISKREDASGQLSCIQLP 988
QY 1004 - - - - -GDATKSESEPDFSPSVGDBGDRKKRLALVALGHAELRKSLLPLIHTAATPM 1058
Db 989 VDSQGGDANKSESEPDFSPSLDGDGDRKKCLALVSLGHPBLRKSLLPLIHTAATPM 1048
QY 1059 SHPKSSSTGVGEALGSGRRRTSSSGSAEPGAHHEMKPPSARSSPHSPWSAASWTSRR 1118
Db 1049 SLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA - HEMKSPSARSSPHSPWSAASWTSRR 1107
QY 1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEEDRASPAAGSDHRRHRSLERE 1178
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QY 1179 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKASGRRLAPTILRTDDPOLDGGDDNDE 1238
Db 1168 AKSSFDLPDTLQVPGLHRTASGRSSASEHQDCNGKASGRRLAPALRPDDPPLDGGDDADDE 1227
QY 1239 GNLSKGERIQAWVSRLPACCRERDSWSAYIFPPQSRFRLCHRIITHKMFHDVVLVILF 1298
Db 1228 GNLSKGERVRAWIRARLPACCLERDSWSAYIFPPQSRFRLCHRIITHKMFHDVVLVILF 1287
QY 1299 LNCITIAMERPKIDHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1358
Db 1288 LNCITIAMERPKIDHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1347
QY 1359 VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTLRLRVLVSRAGQLKLVVETLMS 1418
Db 1348 VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTLRLRVLVSRAGQLKLVVETLMS 1407
QY 1419 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVQCGEDTRNITNKSDCAEASRYWRHKY 1478
Db 1408 SLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVQCGEDTRNITNKSDCAEASRYWRHKY 1467

QY 1479 NFDNLQALMSLFLVASKDGVVDIMYDGLDAVGVDQQQIPMHNHPWMLLYFISFLLIVAFF 1538
Db 1468 NFDNLQALMSLFLVASKDGVVDIMYDGLDAVGVDQQQIPMHNHPWMLLYFISFLLIVAFF 1527
QY 1539 VLNMFVGVVVENFHKCRHQHEEEARRREKRLRLEKKRR - - - - -SKEKQMAE 1587
Db 1528 VLNMFVGVVVENFHKCRHQHEEEARRREKRLRLEKKRRNMLDDVIASSSSASAASE 1587
QY 1588 AQCKPYYSYSRFRLLVHHLCTSHYLDLFTSHYLDLFTVIGLVNVTMAMEHYQQOQILDEALKICN 1647
Db 1588 AQCKPYYSYSRFRLLVHHLCTSHYLDLFTVIGLVNVTMAMEHYQQOQILDEALKICN 1647
QY 1648 YIFTVIFVFESEVKLVAFARFRFFQDRWNQDLAIIVLLSIMGITLEEIEVNLSPINPTI 1707
Db 1648 YIFTVIFVLESEVKLVAFGRFRFFQDRWNQDLAIIVLLSIMGITLEEIEVNLSPINPTI 1707
QY 1708 IRIMRVLRIARVLKLLKMAVGMRALHTVMQALPQVGNLGLLFFIFAALGVLEFGD 1767
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QY 1828 PIYFVSFVLTAQFVLNVVVIIVLMMKHEESKEAEEAELELEMKTLSPQPHSPLG 1887
Db 1828 PIYFVSFVLTAQFVLNVVVIIVLMMKHEESKEAEEAELELEMKTLSPQPHSPLG 1887
QY 1888 SPFLWPGEVGNSTDSKPGAPHTTAHIGAASGFSLEHPT - - - - - 1927
Db 1888 SPFLWPGEVGNSTDSKPGALHPAAHARSASHFSLEHPTDRQLFTISLLIQGSLEWEL 1947
QY 1928 - - - - - 1927
Db 1948 KLMDLAGPGGQPSAFPSAPSLGGSDPQIPLAEMEALSLTSEIVSEPSCSLALTDLSLPD 2007
QY 1928 - - - - -MVPHPEVVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCNNGSTAERSL 1974
Db 2008 DMHTLLLSALESNMQPHTELP - - -GPDLLTVRKSGVSRTHSLPNDSYMCNNGHSTAEGPL 2064
QY 1975 GHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHVLQPHGAPTWGAIPKLPPGRSP 2034
Db 2065 GHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWTGTIPKLPPGRSP 2124
QY 2035 LAQRPLRQAAIRTDSDLVQGLGSRDRLLESEVSGPSCPLTRSSSFVGGSSIQVQORSIQ 2094
Db 2125 LAQRPLRQAAIRTDSDLVQGLGSRDRLLEAEVSGPSPPLARAYSFWGQSSTQAOQHSRSH 2184
QY 2095 SKVSKHIRLPAPCPGLEPSWAKDPPETRRSSLELDTLSWISGDL - PSSQEEPLEFRDLK 2153
Db 2185 SKISKHMTTPAPCPGPEPNWKGPPETRRSSLELDTLSWISGDL - PPGQEEPPSPRDLK 2244
QY 2154 KCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPLCPSPSSSLGGQPLGGGSRPKK 2213
Db 2245 KCYSVEAQSCQRRRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDPNLTGQPLGGGSRPKK 2304
QY 2214 KLSPPSISIDPPESQSRPPCSPGVCLRRRAPASDSKOPSVSSPLDSTAASPSPKKDTLS 2273
Db 2305 KLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKDVLS 2364
QY 2274 LSGLSSDPTMDP 2286
Db 2365 LSGLSSDPPADLP 2377

RESULT 5
US-10-408-765A-1128
; Sequence 1128, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing

; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1128
; LENGTH: 2353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1128

Query Match 51.7%; Score 6222; DB 16; Length 2353;
Best Local Similarity 56.7%; Pred. No. 0;
Matches 1370; Conservative 208; Mismatches 529; Indels 310; Gaps 62;
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QY 83 LPYPALAPVVFYLSQDSRPRSCWCLRTVCNPFERVSMLVLLNCVTLGMFRPCEDIACD 142
Db 70 VPYPALAAATVFFCLGQTTTPRSWCLRLVCNPFWEHVSMVIMLNCVTLGMFRPCEDVECG 129
QY 143 SQRCRILOAFDDIFAFEAFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLD 202
Db 130 SERCNILEAFDAFIFAFFAVEMVIMVALGLFGQKCYLGDTWNRLDFFIVVAGMMEYSLD 189
QY 203 LQNVSPSAVRTVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFIFGIVGV 262
Db 190 GHNVSLSAIRTVRVLRLPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFIFGIVGV 249
QY 263 QLWAGLLNRCLFLENFSLPLSD-LEPYQOTENEDSPFICSQPRENGMRSCRSVPTLR 321
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QY 322 GEGGGPPCSLDYETYN-----SSNTTCVNMNOYVTCNSAGEHNPFGAINFDNIGY 374
Db 307 GRRELMPCTLGWEAYTQPAEGVGAARNACINNQYVNCVSGDSNPHNGAINFDNIGY 366
QY 375 AWIAIFQVITLEGWVDIMYVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETK 434
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QY 1036 -----GEHAELKSLPLPLIHTAATPMSPHPKSSS-TGVEALGSGSRRTSSSGSAEPGA 1089
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QY 1090 AHHEMKCPSPARSPPHSPWASSWTSRRSSRNLSGRAPSLKRRSPSGERRSLISGEGQE 1149
Db 1117 ---DQKPPASLRSSPCAPWGSPGAWSSRRSSWSLGRAPSLKRRGQCGERESLSGEGKG 1173
QY 1150 SQDEESSEEDRASPA--GSDHRHRGSLEREAKSSFDLPDL-----QVPGHL-----R 1196
Db 1174 STDDE--AEDGRAAPGPRATPLRAESLDPRPLRPAALPPTKCRDRDGVVVALPSDFFLR 1231
QY 1197 TASGRSSASEHQDCNGKSGASGLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSRLP 1256
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Db 1266 --CRSREAWALYLFSPQNRFRVSCQKVITHKMFEDHVVLVIFLNCVTIALERPDIPEGST 1323
QY 1317 ERIFLTLSNYIFTAVFLAEMTVKVALGWCFCGQAYLRSSWNVDGLLVLSVIDILVSM 1376
Db 1324 ERVFLSVSNYIFTAIFVAEMMVKVVALGSLGSHAYLQSSWNLLDGLLVLSLVDIVAM 1383
QY 1377 VDSGKTKILGMLRVLLRLTLRPLRVISRAQGLKLVWETLMSLKPIGNIVVICCAFFII 1436
Db 1384 ASAGGAKILGVLRLRLTLRPLRVISRAPGLKVWETLISLRPIGNIVVICCAFFII 1443
QY 1437 FGILGVQLFKGKFFVQCGEDTRNITNKSDCAEASRYRVRHKYNFEDNLGOALMSLVASK 1496
Db 1444 FGILGVQLFKGFYFCGPDTRNISTKAQCAAHYRVRVRKYNFEDNLGOALMSLVSSK 1503
QY 1497 DGWVDIMYDGLDAGVDQOPIMNHNPMWLLYFISFLLIVAFVLMFVGVVVENFHKCRQ 1556
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QY 1557 HQEEEEARRRREKRLRLEKKRRSKEKQMAEAOCKPYYSYRFRLLVHHLCTSHYLDLF 1616
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QY 1617 ITGVIGLVNVTNAMEHYQQOILDEALKICNYIFTVIFVFSVFKLVAFARRFFQDRWN 1676
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QY 1737 MQALPQVGNLGLLMLLFFIFALGVLEFGDLECEDETHPCGLGRHATFRNFGMAFLTFL 1796
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QY 1797 RVSTGDNWNGIMKDP SRDC-----DQESTCYNTVISPIYVFSVFLTAQFVLNVVIAVLMKH 1853

Db 1803 RVSTGDNWNGMKDTLRECSREDKHCLSYLPALSPVYFVFLVAQFVLNVVAVLMKH 1862

QY 1854 LEESNKEAEAELEAELEEMKTLSPQPHSPGLSPFLWPVGVNSTDSKPGAPHTTA 1913

Db 1863 LEESNKEAREDAELDAIELEMA-----QGPGSARRVDADR----- 1899

QY 1914 HIGAASGFSLEHPTMVPHPPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA--- 1970

Db 1900 -----PLPQESPGARDAPNLVARKVSVSRMLSLPNDSYMFRPVVPASAP 1943

QY 1971 -----ERSLGRGWGLPKAQSGSILSVHSQPADTSCILQPKDVH-----YLLQP 2015

Db 1944 HPRPLQEVEMETYGATP---LGSVASVHSPAESCASLQIPLAVSSPARSGEPLHALSP 2000

QY 2016 HGAPTWGAIPKLPPPGSRPLAQRPLRRQAAIRTDLSLVQGLGSRDILLSEV---SGPSC 2071

Db 2001 RGT-----ARSPSLRLLCRQEAHVHTDSLEGK-IDSPRDTLDPABEGEKTVPV 2047

QY 2072 PLTRSSFWGGSSIQVQQRSGIQSKV--SKH-----IRLPAPCPGLEPSWAKDPPETRS 2123

Db 2048 PVTQ-----GSLQSPRSPRPASVTRKHTFGQHCVSSRPAAPGGEAEASDP----- 2096

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Db 2097 ---ADEEVSHITSSACFWQTAEPHGPEASPVAGGERDLRLYSVDAQGLDKPG-RADE 2152

QY 2174 QRRHIAVCLDSGSPRLCPSPSSLGQPLGGP--GSRPKKLSPPSISIDPP-ESQGS 2230

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QY 2231 -RPPCSPG--VCLRRRAPA-----SDSKDPSVSSPLDSTAAS-----PSPKDTLSL 2274

Db 2204 ARPSAABGSGTTLRRRTPSCEATPHRDSLEPTEGSAGGDPAAKGERWGQASCRAEHLTV 2263

QY 2275 SGLSSDPTDM-----DP 2286

Db 2264 PSFAFEPLDLGVPSGDP 2280

RESULT 6

US-09-935-541-2

; Sequence 2, Application US/09935541

; Patent No. US20020150911A1

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/935,541

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 2175

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-935-541-2

Query Match 45.0%; Score 5409; DB 9; Length 2175;

Best Local Similarity 50.5%; Pred. No. 0;

Matches 1225; Conservative 236; Mismatches 513; Indels 450; Gaps 64;

QY 51 ASRSSTTCPGGAAGAGSTKDPG--SADSEAGL-----PYPALAPVVFYLS 97

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QY 98 QDSRPRSWCLRTVCNPNWFERVSMVLILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIF 157

Db 64 QTTSPRNWCIKMCNPNWFECVSMVLILLNCVTLMGYQPCDDMDCLSDRCKILQVDFDDFIF 123

QY 158 AFFAVEMVVKMVALGIFGKKCYLGDWTNRDLDFIVIAIGMLEYSLDLQNVSPSAVRTVRVL 217

Db 124 IFFAMEMVLKMVALGIFGKKCYLGDWTNRDLDFIVMAGMVEYSLDLQNLNSAIRTVRVL 183

QY 218 RPLRAINRVFSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLDE 277

Db 184 RPLKAINRVFSMRILVNLDDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLEE 243

QY 278 NFSPLSLVDLEPYQ TENEDESPFCISQPRENGMRSCRSVPTLRGEGGGPPCSL----- 332

Db 244 NFTIQGDVALPPYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDV 300

QY 333 -DYETYNSSSNTT--CVNWNQYTYTNCAGEHNPFGKAINFDNIGYAWIAIFQVITLEGW 389

Db 301 YDFGAGRQDLNASGLCVNWNRYNVCRGTSANPHKGAINFNIGYAWIVIFQVITLEGW 360

QY 390 DIMYFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFL 449

Db 361 EIMYVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYL 420

QY 450 SNAATLASFSEPGSCYBELLKYLVIILKRAARLAQVSRAGLRLSSPVARSQGEPO 509

Db 421 S-SSTVASAEPGDCYEEIFQYVCHILRKAKR-----RALGLYQALQS----- 462

QY 510 PSGSCTRSHRRLSVHLVHHHHHHHHVHLGNGTLRVPRASPEIQDRDANGSRRLMLPPP 569

Db 463 -----RRQAL-----GPE-----APAP 474

QY 570 STPTSPGGPPRGAEVSHSFYHADCHLEPVRCQAPPPPCPSEASGRTVSGKVVPTVHTSP 629

Db 475 AKPGP-----HAK---EPRHYQLCPQHSPLDA-----TPHT-- 502

QY 630 PPEILKDKALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLELTQSTGAC-HSSCKISSPCSK 688

Db 503 -----LVQ-----PIPATLAS-----DPASCPCQCHEDGRPSGLGS 534

QY 689 ADGACGPDSCPYCARTAGGEPESADHVPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRS 748

Db 535 TDGQEGSGS-----GSSAGGEDEA-----DGGA---RSSEGDGASSELGKEEEEEEQ-- 579

QY 749 LGPDAEPSSVLA--FWRLICDTPRKIVDSKYFGRGIMAILVNTLSMGIEYHEQEPELTN 806

Db 580 ----ADGAVMLCGDVWRETRAKLRGIVDSKYFNRMGIMAILVNTVSMGIEHHEQEPELTN 635

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QY 867 RTFRLMRVLKVRFLPALQRLVLMKTMNDVATFCMLMLFIFISILGMHLFGCKPAS 926

Db 696 RTFRLRLVLKVRFPALRRQLVLMKTMNDVATFCMLMLFIFISILGMHLFGCKFSL 755

QY 927 ERD-GDTLPDRKNFDSLWAIIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGN 985

Db 756 RTDTGDTVPDRKNFDSLWAIIVTVFQILTQEDWNKVLYNGMASTSPWASLYFVALMTFGN 815

QY 986 YVLFNLLVAILVEGFQAEGDATKSESEDFPSPSV-----DGDGDRKKRLALVAL 1035

Db 816 YVLFNLLVAILVEGFQAEGDANRSYDEQSSNIEEFDKLQEGLDSSGDPK--LCPIPM 873

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QY 1092 HEMKCPPSARSSPHSPWSAASSWTSSRRSNLSGRAPSLKRRSPSGERRSLLSGE-GQES 1150

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QY 1151 QDEEESSEE--DRASAGSDH-----RHRGSLEREAKSSFDLPTLQVPG 1193

Db 981 RVCEVAADGPPRAAPLHTPHAHIIHGHPLAHRHRHRRRTLSLDRDSVDLAELVPVAVG 1040

QY 570 STPTSGGPRGAEVSHFYHADCHLEPPVRCQAPPRCPSEASGRVTGSGKVYPTVHTSP 629
Db 475 AKGP-----HAK---EPRHYQLCPQHSPLDA-----TPHT-- 502
QY 630 PPEILKDKALVEVAPSGPPTLTSTFNIPGPPFSSMHKLLTETQSTGAC-HSSCKISSPCSK 688
Db 503 -----LVQ-----PIPATLAS-----DPASCPCQHQEDGRRPSGLGS 534
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Db 535 TDGQEGSGS-----GSSAGGEDEA-----DGDGA---RSSEDDGASSELGKEEEEEEQ-- 579
QY 749 LGPDAEPSSVLA--FWRLICDTFRKIVDSKYFGRGIMIAILVNLSMGIEYHEQPEELTN 806
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QY 807 ALBISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWBEIVGQGGGLSVL 866
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QY 1151 QDEEESSEE--DRASPAAGSDH-----RHRGSLEREAKSSFDPDLTQVPG 1193
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QY 1194 LHRTASGRSS--ASEHQDCNGKASGRILARTLD-DPQLDGDNDNDEGNLSKGERIQAW 1250
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QY 1251 VRSRLPACCREDSWSAYIFPPQSRFLLCHRIITHKMFHDVVLVIFLNCITIAMERPK 1310
Db 1099 IDVYKPDWCVEKEDWSVYLFSPENRFRVLCQIIAHKLFVYVLAFLFNCITIALERPQ 1158
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QY 1431 CAFFIIFGILGVQLFKGFFVCQGEDTRNTNKSDCAEASRWRVHKYNFDNLGOALMSL 1490
Db 1279 CAFFIIFGILGVQLFKGFYHCLGVDTRNTNRSDCMAANYRWVHHKYNFDNLGOALMSL 1338
QY 1491 FVLASKDGVDMYDGLDAVGDVQDQOPIMNHNPMWMLLYFISFLLIIVAFVLMFVGVVVEN 1550
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QY 1551 FHKCRQHOOEAEARRREKRLRLEKKRRSKEQMAEAQCKPYYSYDYSRFRLLVHHLCTS 1610
Db 1399 FHKCRQHOOEAEARRREKRLRLEKKRR-----KAQRLPYATYCHTRLLIHSMTCS 1451

QY 1611 HYLDLFTITGVLNVVTMAMEHYQQOILDEALKICNYIFTVIFVFESVFKLVAFARRF 1670
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QY 1671 FQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1730
Db 1512 FKDRWNQDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIARVLKLLKMATGMR 1571
QY 1731 ALLHTVMQALPOVGNLGLLMLLFFIFAALGVELFGDLECDTHPECEGLGRHATFRNFGM 1790
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QY 1791 AFLTLFRVSTGDNWNGIMKDPDRDC-DQBSTCYNTV--ISPIYFVSFVLTAQFVLNVVI 1847
Db 1632 AFLTLFOVSTGDNWNGIMKDTLRDCTHDSRSLSSQLQFVSPLYFVSFVLTAQFVLNVV 1691
QY 1848 AVLKMLEESNKEAEAELEAELELEM-KTILSPQPHSPLGSPFLWPG----- 1894
Db 1692 AVLKHLDDSNKEAQEDAEMDAELEMAHGLGPGPRLPTGSPGA-PGRPGGAGGGDT 1750
QY 1895 -----VEG-VNSTDSPKPGAPHTTAHIGAASG----- 1920
Db 1751 EGGLECRRCYSPAQDSLEGELTIIDNLSSIFH---HYSSPAGCKKCHDKQEVQLAETEA 1807
QY 1921 -----FSLEHPTMVP-----HPEEVPV-PLGPDLLTVRKSGVS 1952
Db 1808 FSLNSDRSSILLGDDLSLEDPTACPPGRKDSKGELDPPEPMRVGDLGECFFPLSSTAVS 1867
QY 1953 RTHSLPN-DSYMCNRNGSTAERSLHGRWGLPKAQSGSILSVHSQPADTSCILQLPKDVHY 2011
Db 1868 -----PDPENFLCEMEEIPFNPV--RSW--LXHDSSQAPPSFSPDASSPLLPMPAEFFH 1918
QY 2012 -----LLQPHGAPTWGAIPKLPPLPG-----RSLAQRLRRQAIRTDLSLDVQGLGRE 2060
Db 1919 PAVSASQKPEKGTGTGLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLDAS----- 1972
QY 2061 DLLSEVSGPSCPLTRSSSFWGSSSIQVQORSIGIQSVSKVSKHIRLPAPCPGLEPSPSWAKDPPE 2120
Db 1973 -----PSSSAGSLQTTLEDLSLTLSDSPPRALGPPAPAG----- 2006
QY 2121 TRSLELDTLSWISGDLPLSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDBQRRHSIA 2180
Db 2007 -----PRAGLSPAARRRL-----SLRGRGLFSLRGLRAHQRS 2038
QY 2181 VSCLDSGSPRLCPSPSSL-----GQPLGPGSPPKKLSPPSIS---IDPPESQG 2229
Db 2039 HS--SGGSTSPGCTHDSMDPSDEEGRGAGGGAGGAGSEHSETLSLSLTSLFCPPP--- 2092
QY 2230 SRPPCSPGVCLRR-----RAP---ASDSKDPSSVSSPLDSTA 2262
Db 2093 --PPAPGLTPARKFSSTSLAAPGRPHAAALAHGLARSPSWAADRSKDPGGRAPLPMGL 2150
QY 2263 ASPSPKKTLSLSGLSDPTMDP 2286
Db 2151 GPLAPPPQPL-----PGELEP 2166

RESULT 8

US-09-935-541-4
; Sequence 4, Application US/09935541
; Patent No. US2002015091A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4																									
; LENGTH: 2188																									
; TYPE: PRT																									
; ORGANISM: Homo sapiens																									
US-09-935-541-4																									
Query Match 44.9%; Score 5405.5; DB 9; Length 2188;																									
Best Local Similarity 50.3%; Pred. No. 0;																									
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;																									
QY	51	ASRSST	CPGPGAAGAGSTEKDPG--SADSAEGL-----	----	PYPALAPVVFYLS	97	986	YVLENL	LVAILVEGFOAEGDATKSESEPDFFSPSV-----	-----	DGDGRKKRLALVAL	1035													
Db	5	ASPPSS	AAAAAP-AAEPGVTTTEQPGPRSPSPSGPGL	EEPLDGDADPHVPHDLAPIAFFCLR	63		816	YVLENL	LVAILVEGFOAEGDANRSYDEDEQSSSNI	EEFDKLEGLDSSGDPK--LCPIPM	873														
QY	98	QDSRPR	SWCLRTVCNPFERVSMLVILLNCVTLGMFRPC	EDIACDSQRCRILQAFDDFI	157		1036	GEHAEL	RKSLPLLIHT-----	AATPMSPKSSSTGVGEALGSGGRR	TSSSGSAEPGAH	1091													
Db	64	QTTSRPN	WCIMVCNPFECVSMVLVILLNCVTLGMYPQ	PCDDMCLSDRCKILQVFFDFI	123		874	TPNGHL	DPSSL--PLGGHLGPAGA	GPA--PRLSQDPDMLVALGRKSSVMSL--	--GRMS	926													
QY	158	AFFAVEM	VVMVALGIFGKCYLGD	TWNRLLDFFIV	IAGMLEYSLDLQNVSFSAVRTVRVL	217		1092	HEMKCPP	SARSPHSPWSAASWT	SRSSRNSLGRAPSLKRRSPSGERRSLLSGE	-GQES	1150												
Db	124	IFFAME	MVLKMWALGIFGKCYLGD	TWNRLLDFFIV	MAGMVEYSLDLQNVINLSAIRTVRVL	183		927	YDQSL	SSSRSSYGPWGRSA	AWASRRSSWN-----	SLKHKPPSAEHESLLSAERGGA	980												
QY	218	RPLRAIN	RVPMSRILVTL	LLDTPLMLGNVLL	LCFFVFFIFGIVGVQLWAGLLRNRCLPE	277		1151	QDEESSEE	--DRASPA	GSDH-----	RHRGSLEREAKSSFDL	PDTLQVPG	1193											
Db	184	RPLKAIN	RVPMSRILVTL	LLDTPLMLGNVLL	LCFFVFFIFGIVGVQLWAGLLRNRCLPE	243		981	RVCEVA	ADGPPRAAPLHT	PHAHHIHGPHLAHRRHRRRTLSL	DNRDSVDLAELVPAVG	1040												
QY	278	NFSLPL	SVLDLEPPYQ	TENEDESPFICSQPREN	GMRSRCSVPTLRGEGGGPPCSL-----	332		1194	LHRTAS	GRSS--ASEHQD	CNGKSASGR	LARTLD--DPQLDGD	DDNDEGNLSKGERIQAW	1250											
Db	244	NFTIQD	VALPPYQPEED	DEMPFICSLSGDNGIM	GCHIEPPLKEQ--GRECCLSKDDV	300		1041	AHPRAA	WRAAGPAPGH	EDCNGRMPS--IAKDVFT	KMGDRGRGEDEE	IDYTLCFRVRKM	1098											
QY	333	-DYETN	SSSNTT--CVNNQ	YVNTCSAGEHNP	FKGAINFDNIGYAWIAIFQVITLEGWV	389		1251	VRSLPA	CCRERDSW	SAYIFPPQSR	FRLLCHRIITHK	MEPHVVLVIIFLNCITIAMERPK	1310											
Db	301	YDFG	AGRODLNASGLCVN	WRNYNVCRTGSAN	PHKGAINFDNIGYAWIVIFQVITLEGWV	360		1099	IDVYK	PDWCEVRED	WSVYLFSP	ENRFRVLCQTII	AHKLFDYVVLAFIFLNCITIALERPQ	1158											
QY	390	DIMYF	MDAHSFYNFY	FILLIIVGSFFMIN	CLVVIATQFSETKQRESQLMREQRVRL	449		1311	IDPHSA	ERIFLTL	SNYIIFTAV	FLAEMTVKVVAL	GWCFGEQAYLRSSWN	VLDGLLVLSVI	1370										
Db	361	EIMYV	MDAHSFYNFY	FILLIIVGSFFMIN	CLVVIATQFSETKQREHRLMLEQRQYL	420		1159	IEAGST	ERIFLTV	SNYIIFTA	IVGEMTLKV	VSLGLYFG	EQAYLRSSWN	VLDGFLVFSII	1218									
QY	450	SNAST	LASFSEPGSCYEEL	LKVLVYLK	KAARLQAQVSR	AIQVRAGLLSPVARSGQEPQ	509		1371	DILVSM	VSDSGTKIL	GMRLVRL	LRLLRPLR	LVISRAQGLK	LVWETLMS	SLKPIGNIVVIC	1430								
Db	421	S-SST	VASYAEP	GCYEEIFQYV	CHILRKAKR-----	RALGLYQALQS-----	462		1219	DIVVSL	ASAGGAKIL	GVLRVLR	LLRPLR	LVISRAPGLK	VWETLIS	SLKPIGNIVLIC	1278								
QY	510	PSGCT	SRHRRLSVHL	VHHHHHHHH	HYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPP	569		1431	CAPFI	IFGILGV	QLFKGK	FPVCGED	TRNITN	KSDCAE	ASYRVR	WHKYNF	DNIGQALMSL	1490							
Db	463	-----	RRQAL	-----	-----	GPE-----	APAP	474	1279	CAPFI	IFGILGV	QLFKGK	FPVCGED	TRNITN	RSDCMA	ANYRWH	VHKKYNF	DNIGQALMSL	1338						
QY	570	STPTP	SGPPRGAESVHS	FYHADCHLEPV	RCQAPPRCPSEASGR	TGSGKVYPTVHTSP	629		1491	FVLASK	DGWDIMYD	GLD	AVGV	DQOPI	MNHN	PNWMLLYFIS	FLLI	VAFVLM	FVGVVVEN	1550					
Db	475	AKGP	-----	-----	-----	-----	TPHT--	502	1339	FVLASK	DGWDIMYD	GLD	AVGV	DQOPI	MNHN	PNWMLLYFIS	FLLI	VAFVLM	FVGVVVEN	1550					
QY	630	PPEIL	KD	KALVEAPSPGP	PTLT	SFNIPGCPSSMHKLL	ETQSTGAC-HSSCKISSP	CSK	1551	FKCRQ	HQEEEE	ARRR	EEKRLR	LEKKRR	SKB	QMAE	AQCKPY	YSYR	FRLLVH	HLCTS	1610				
Db	503	-----	LVQ	-----	-----	-----	-----	-----	1399	FKCRQ	HQEEEE	ARRR	EEKRLR	LEKKRR	SKB	QMAE	AQCKPY	YSYR	FRLLVH	HLCTS	1610				
QY	689	ADSGA	CPDSCPYCART	GAGEPESADH	VPDSDSEAVYEFTQ	DACHSDLRDPHSRRRORS	748		1611	HYLD	FIT	IGLVN	VVTMA	EHYQ	QOIL	DE	ALKIC	NYIFT	VI	FV	FESV	EKLVAFAFRF	1670		
Db	535	TDSG	QEGSGS	-----	GSSAGGE	DEA-----	DGDGA--	RSSE	1452	HYLD	FIT	IGLVN	VVTMA	EHYQ	QOIL	DE	ALKIC	NYIFT	VI	FV	FESV	EKLVAFAFRF	1670		
QY	749	LGPDA	ERPSSVLA--FWRL	ICD	TFRKIVDSKYFGR	GIMIAILVNTLSM	GIEYHEQ	PEELTN	1671	QDRW	NQ	LDLAI	VLLSIM	GITLEE	IEVNL	SLP	INPTII	RIMR	VLRI	ARVLKLL	KMAVGM	1730			
Db	580	----	ADGAV	WLCGDVWRE	TRAKLRGIVDSKYFNR	GIMMAILVNTVSM	GIEHHEQ	PEELTN	1512	FKDR	WNQ	LDLAI	VLLSIM	GITLEE	IEVNL	SLP	INPTII	RIMR	VLRI	ARVLKLL	KMAVGM	1730			
QY	807	ALEIS	NIVTSLPALEML	LKLLVYG	PFYKPNYPNIF	DGVI	VVISVWEIV	GOQGGLSVL	1731	ALLH	TMQ	ALPQV	GNLGLL	FMLFFI	PAAL	GV	ELFG	LECD	ETHP	CEGL	GRHAT	FRNFGM	1790		
Db	636	ILEIC	NVVTSMFALEM	ILKLA	AFGLFDYLRN	PNYIFDSII	VIISWEIV	GOQGGLSVL	1572	ALLD	TVQ	ALPQV	GNLGLL	FMLFFI	PAAL	GV	ELFG	LECD	ETHP	CEGL	GRHAT	FRNFGM	1790		
QY	867	RTFRL	MRVLKLV	RF	LPALQRLV	LMKTDNVAT	FCMLLM	LFI	FISIL	GMHL	FGCK	PAS	926												
Db	696	RTFRL	LRVLKLV	RF	MPALRRQLV	LMKTDNVAT	FCMLLM	LFI	FISIL	GMHL	FGCK	PAS	926												
QY	927	ERD	-GDT	LPDR	KNFDSL	LWAI	VT	V	FQIL	TQED	WNK	VLYNG	MAS	TSSW	AALY	F	I	A	L	M	T	F	G	N	
Db	756	RTD	TG	DTVP	DR	KNFDSL	LWAI	VT	V	FQIL	TQED	WNK	VLYNG	MAS	TSSW	AALY	F	I	A	L	M	T	F	G	N

QY 1941 PDLTVRKSGVSRTHSLPN-DSYMCNNGSTAERSLCHRGWGLPKAQSGSILSVHSQPADT 1999
Db 1869 ECFFPLSSTAVS-----PDPENFLCEMBEIPFNPV--RSW--LKHDSSQAPSPSPFDAS 1919
QY 2000 SCILQLPKDVHY-----LLQPHGAPTGAIPKLPPPG-----RSPLAQRPLRRQAIRT 2048
Db 1920 SPLLEMPAEFFHFAVSASQKGEKGTGTGLPKIALQGSWASLRSPRVNCTLLRQATGSD 1979
QY 2049 DSLDVQGLGSRDILLSEVSGPCPLTRSSFWGSSIQVQQRSGIQSKVSKHIRLPAPCP 2108
Db 1980 TSLDAS-----PSSAGSLQTTLEDLSLTSDSPRRALGPPAPAP 2018
QY 2109 GLEPSWAKOPPETRSSLLELDTLSWISGDLPLSSQEEPLFPRLDKKCYSVETQSCRRRPG 2168
Db 2019 G-----PRAGLSPAARRL-----SLRGRGL 2039
QY 2169 FWLDEQRHRSIAVCLDSGSPRLCPSPSSL-----GGQPLGGGSRPKKLSPPSI 2220
Db 2040 FSLRGLRAHORSHS--SGGSTSPGCTHHDSMDPSDEEGRGGAGGGAGSEHSETLSLSL 2097
QY 2221 S-----IDPPESQGRPPCPGVCVCLRR-----RAP---ASDSK 2250
Db 2098 TSLFCPPP-----PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAADRSK 2151
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Db 2152 DPPGRAPLPMGLGPLAPPQPL-----PGELEP 2179
RESULT 9
US-10-425-800-4
; Sequence 4, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-425-800-4
Query Match 44.9%; Score 5405.5; DB 14; Length 2188;
Best Local Similarity 50.3%; Pred. No. 0;
Matches 1225; Conservative 236; Mismatches 514; Indels 461; Gaps 64;
QY 51 ASRSSTTCPGGAGAGSTKDPG--SADSAEGL-----PYPALAPVFFYLS 97
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QY 98 QDSRPRSWCLRTVCNPFERVSMLVILNCVTLMGFRPCEDIACDSCRILQAFDDFIF 157
Db 64 QTTSPRNWCIXMVCNPFECVSMVLVILNCVTLMGWQPCDDMDCLSDRCKILQVFFDDFIF 123
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Db 124 IFFAMEMVLKVALGIFGKKCYLGDWTNRLDFFIWMAGMVEYSLDLQNLNSAIRTVRVL 183
QY 218 RPLRAINVPMSRILNLTLLDTPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNCFLPE 277
Db 184 RPLKAINRVPMSRILNLTLLDTPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNCFLPE 243
QY 278 NFSLPLSVDLPEPYQOTENEDESFPICSPRENEMSCRSVPTLRGEGGGPPCSL----- 332

Db 244 NFTIQGDVALPPYYQPEEDDEMPFICSLSGDNGIMGCHEIPLPLKEQ---GRECCLSKDDV 300
QY 333 -DYETYNSSNTT--CVWNQYITNCSAGEHNPEKGAINFDNIGYAWIAIFQVITLEGWV 389
Db 301 YDFGAGRQDLNASGLCVWNRYNVNCRGTSANPHKGAINFDNIGYAWIVIFQVITLEGWV 360
QY 390 DIMYFVMDAHSPYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFL 449
Db 361 EIMYYVMDAHSPYFIYFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYL 420
QY 450 SNASTLASFSEPGSCYEELLYLVYILRKAARRLAQVSRAGIVRAGLLSSPVARSQGEPO 509
Db 421 S-SSTVASAEPGDCYEELIYQYVCHILRKAAR-----RALGLYQALQS----- 462
QY 510 PSGSCTRSHRRLSVHHLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRLMLPPP 569
Db 463 -----RRQAL-----GPE-----APAP 474
QY 570 STPTPSGGPPRGAEVSHSFYHADCHLEPVRQCAPPVRCPCSEASGRTVSGGKVPTVHTSP 629
Db 475 AKPGP-----HAK---EPRHYQLCPQHSPLDA-----TPHT-- 502
QY 630 PBEILKDKALVEAPSPGPTLTLSFNIPPGPFSSMHKLLETQSTGAC-HSSCKISSPCSK 688
Db 503 -----LVQ-----PIPATLAS-----DPASCPCQCHEDGRRPSGLGS 534
QY 689 ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRS 748
Db 535 TDSGQEGSGS---GSSAGGEDEA-----DGGA---RSSEGDGASSELGKEEEEEQ-- 579
QY 749 LGPDAEPSSVLA--FWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTN 806
Db 580 ----ADGAVWLCDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTN 635
QY 807 ALEISNIVFTSLFALEMLLKLIVYGPFGYIKXNPYNIPDGVIVVISVWEIVGQGGGLSVL 866
Db 636 ILEICNVVFTSMFALEMILKLAFAFLDYLRNPYNIPFDSIIVISIWEIVGQADGGLSVL 695
QY 867 RTFRLMRVLKVRFLPALQRLVVLTKMTMDNVATFCMLLMFIFIFISILGMHLFCCKFAS 926
Db 696 RTFRLLRVLKVRFPALRRQLVVLTKMTMDNVATFCMLLMFIFIFISILGMHIFGCKFSL 755
QY 927 ERD-GDTLPDRKNFDSLLWAIIVTFQILTQEDWNKVLNMGMASTSSWAALYFIALMTFGN 985
Db 756 RTDTGDTVPDRKNFDSLLWAIIVTFQILTQEDWNVVLNMGMASTSPWASLYFVALMTFGN 815
QY 986 YVLFNLLVAILVEGFOAEGDATKSESEPDFFSPSV-----DGDGDKRKLALVAL 1035
Db 816 YVLFNLLVAILVEGFOAEGDANRSYDEDDQSSNIEBDFLQEGLDSSGDPK--LCPIPM 873
QY 1036 GEHAELRKSLLPPLIHT---AATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGAH 1091
Db 874 TPNGLHLDPSL--PLGGHLGPAGAAGA--PRLSLQDPMLVALGSRKSSVMSL---GRMS 926
QY 1092 HEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGE-GQES 1150
Db 927 YDQRLSSSRSSSYGPGWGRSAAWASRRSSWN-----SLXHKPPEAEHESLLSAERGGA 980
QY 1151 QDEEESSEE--DRASPAAGSDH-----RHRGSLREBAKSSFDLPDTLQVPG 1193
Db 981 RVCEVAADGPPRAAPLHTPHAHIIHHGPHLAHRHRHRRRTLSLDRDSVDLAELVPVAVG 1040
QY 1194 LHRTASGRSS--ASEHQDCNGKSASGRRLARTLTD-DPQLDGGDDNDDEGNLSKGERIQAW 1250
Db 1041 AHPRAAWRAAGAPAGHEDCNGRMP--IAKDVFTKMGDRGDEDEEIDYTLCFRVRKM 1098
QY 1251 VRSRLPACCRERDSWYIFPPQSRFRLLCHRIITHKMFHVVLVIIFLNCITIAMERP 1310
Db 1099 IDVYKPDWCEVREDWSVLFSPENRFRVLCTIIAHKLFYVVLAFIPLNCITIALERPQ 1158
QY 1311 IDPHSAERIFLTLSNYITFTAVFLAEMTVKVALGWCFCGEQAYLRSSWNVLDGLLVLSVI 1370
Db 1159 IEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSGLYFGEQAYLRSSWNVLDGFLVFSII 1218

Db 510 --ASDPSSCPHCQHEAGRRPSGLGSTDGSGSGGSABE--AEANGDGL-QSSEDDGVS 563

Qy 735 SLDLDPHRRRQRSLGPDAPSSVLA-----FWRLICDTFRKIYVDSKYFGRGIMAILVN 789

Db 564 SD-----LGKEEQEDGAARLCGDVWRETRKKLRLGLVDSKYFNRGIMAILVN 611

Qy 790 TLSMGIEYHEQPELTNALEISNIVFTSLPALEMLLKLTVGPPGYIKPNYINIFDGVIV 849

Db 612 TVSMGIEHHEQPELTNILEICNVVFTSMFALEMILKLAAGLFDYLRNPYNIFDSIIVI 671

Qy 850 ISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALORQLVLMKMTMDNVATFCMLLMLEFI 909

Db 672 ISIWEIVGQADGGLSVLRTFRLRLVRLKLVRLPALRRQLVLMKMTMDNVATFCMLLMLEFI 731

Qy 910 FIFSILGMHLFGCKFASERD-GDTLPDRKNFDSLLWAIIVTVFOILTQEDWNKVLXNGMAS 968

Db 732 FIFSILGMHIFGCKFSLRTDGTVPDRKNFDSLLWAIIVTVFOILTQEDWNVLYNGMAS 791

Qy 969 TSSWAALYFIALMTFCNVVLENLLVAILVEGFQAEAGDATKSESEPDFSPSVDG----- 1022

Db 792 TTPWASLYFVALMTFCNVVLENLLVAILVEGFQAEAGDANRSCDEQSSNLEEFDKLPE 851

Qy 1023 --DGRKKRLALVALGHAELRKSLLPLLIH--TAATPMSHPKSSSTGVEALGSGRR 1078

Db 852 GLDNRDLKLCPIPMTPNGHLDPSL--PLGAHLGPAGMTGTAPRLSLQDPVVLVALDSRK 909

Qy 1079 TSSSGSAEPGAHAHEMKCPSPARSSPHSPWSAASSWTSRRSSNSLGRAPSLKRRSPSGE 1138

Db 910 SSVMSL--GRMSYDQRLSSSSSYGPGWGRSGTWSARRSSWN-----SLXHKPPSAE 960

Qy 1139 RRSLLSSEGEQES--QDEEESSE--DRASPAGSDH-----RHRGSLEREA 1179

Db 961 HESLLSSEGGGSCVRACEGAREEAPTPTAPLHAPHAAHHAHGHPLAHRHRRHRTLSLDT 1020

Qy 1180 KSSFDLPDTLQVPLHRTAS--GRSSASEHQDCNGKSASGRLARTLTD-DPQLDGDDDN 1236

Db 1021 RDSVDLGLVFPVGAHSRAAWRGAGQAPGHEDCNGRMPN--IAKDVFTKMDRRDRGEDE 1078

Qy 1237 DEGNLSKGERIQAWVRSLRPACCRERDSWSAYIFPPQSRPRLIICHRITTHKMPDHVVLVI 1296

Db 1079 EEIDYTLCEFRVRKMDIVYKPDWCCEVPREDWSVYLFSPENKFRILCQITIAHKLFDYVVLAF 1138

Qy 1297 IFLNCITIAMERPDKIDPHSAERIFLTLSNVIPTAVFLAEMTVKVVALGWCFFGEQAYLRSS 1356

Db 1139 IFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMLTKVSLGLYFGEQAYLRSS 1198

Qy 1357 WNVLDGLLVLSVIDILVMSVSDSGTKILGMLRVLLRLRLPLRVISRAQGLKLVVETL 1416

Db 1199 WNVLDGLVLFVSIIDIVSVASAGGAKILGVLRLRLRLRLPLRVISRAPGLKLVVETL 1258

Qy 1417 MSSLKPIGNIVVICAPFIIFGILGVOLFPGKFFVCQGEDTRNITNKSDCAEASRWVRH 1476

Db 1259 ISSLKPIGNIVLICAPFIIFGILGVOLFPGKFFYHCLGVDTRNITNRSDCVAANYRWVHH 1318

Qy 1477 KYNFDNLGQALMSFLVASKDGWVDIMYDGLDAVGVDQOQIMNHNPMWMLLYFISFLLIYA 1536

Db 1319 KYNFDNLGQALMSFLVASKDGWVNIWYNGLDVAVDQOQVPTNHNPMWMLLYFISFLLIYS 1378

Qy 1537 FVVLNMFVGVVVENFHKCRHQHEEEARRREKRLRLLEKKRRSKBKQMAEAOCKPYYS 1596

Db 1379 FVVLNMFVGVVVENFHKCRHQHEEARRREKRLRLLEKKRR-----KAQRLPYVAT 1431

Qy 1597 YSRFRLLVHHLCTSHYLDLFTIGVIGLVNVTMMEHYQOQIILDEALKICNYIFTVIFVF 1656

Db 1432 YCPTRLLIHSMCTSHYLDLFTITFIICLVNVTMSLEHYNQPTSLETALKYCNMYMTTVFVL 1491

Qy 1657 ESVFKLVAFAPRRFFQDRWNQDLAIVLSIMGITLEEIEVNLSLPINPTIIRIMRVLRI 1716

Db 1492 EAVLKLVAFLGLRRFFKDRWNQDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRI 1551

Qy 1717 ARVLKLLKMAVGMRRALLHTVMQALPQVGNLGLLFMLFFIFI AALGVLEFGLCEDETHPC 1776

Db 1552 ARVLKLLKMATGMRRALLDTVVQALPQVGNLGLLFMLFFIFIYAALGVLEFGLKLVNDENPC 1611

Qy 1777 EGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPDRDC-DQESTCYNTV--ISPIYFVS 1833

Db 1612 EGMSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLDRCTHDERTCLSSLOFVSPLYFVS 1671

Qy 1834 FVLTAQFVLNVVIAVLMKHLEESNKEAKEAEAELEEMKTLSPQPHSPGLSPFLWP 1893

Db 1672 FVLTAQFVLINVVAVLMKHLDSDNKEAQEDAEMDAEIELEM----- 1713

Qy 1894 GVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTVMPPHEEVVPV-LGPDLLTV----- 1946

Db 1714 -AHGLGPCPCPG-----PCPCPCPCPCAGPRLPTSSPGAPG 1750

Qy 1947 RKSQVSRTHSLPNDSYMCRN-GSTAERSLHGRGWGLPKAQSGSILSVHSQPADTSCILQL 2005

Db 1751 RSGSGAGAGG-DTESHLCRHCYSPAQETL-----W-----LDSVSLIKDSLEGELTIIDNL 1801

Qy 2006 PKDV-HYLLQPHG 2017

Db 1802 SGSVFHHYASPDG 1814

RESULT 11

US-10-425-800-5

; Sequence 5, Application US/10425800

; Publication No. US20030180886A1

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/10/425,800

; CURRENT FILING DATE: 2003-04-29

; PRIOR APPLICATION NUMBER: US/09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 5

; LENGTH: 1835

; TYPE: PRT

; ORGANISM: Rattus sp.

; US-10-425-800-5

Query Match 44.4%; Score 5345; DB 14; Length 1835;

Best Local Similarity 55.4%; Pred. No. 0;

Matches 1138; Conservative 216; Mismatches 375; Indels 324; Gaps 45;

Qy 43 PRSRDSPVASRSSTCTCPGGAAGAGSTKDPGSADSEAG---LPYPALAPVVFYLSQ 98

Db 8 PSSAAAPAPEPGITEQGP-----RSPPPSPGLEELEGINPDVPHDPLAPVAFCLRQ 62

Qy 99 DSRPRSWCLRTVCNPPWFERVSMVLVLLNCVTLGMFPCEDIACDSQRCRILQAFDDFIFA 158

Db 63 TTSPRNWCIMVCNPPWFEVCVSMVLVLLNCVTLGMYPQDDMECLSDRCKILQVDFDFIFI 122

Qy 159 FFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVAGMLEYSLDLQNVSFSAVRTVRVLR 218

Db 123 FFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNLINLSAIRTVRVLR 182

Qy 219 PLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLMAGLLNRNRCFLPEN 278

Db 183 PLKAINRVPSMRILVNLDDTLPLMGNVLLLCFFVFFIFGIVGVQLMAGLLNRNRCFLEEN 242

Qy 279 FSLPLSVLEPYQOTENEDESFFICSQPRENGMRSCRSVPTLRGEGGGPPCSL----- 332

Db 243 FTIQGDVALPPYQBEDDEMPFFICSLTGNMGIMGCHEIPLPKEQ--GRECCLSKDDVY 299

Qy 333 DYETYNSSSNTT--CVNWNQYTNCSAGEHNPFGAINFDNIGYAMTAFQVITLEGWVD 390

Db 300 DFGAGRQDLNASGLCVNWNRYNVCRTGNANPHKGAINFNDNIGYAGIVIFQVITLEGWVE 359

Qy 391 IMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQIMREQRVFLS 450

QY 111 CNPWFERSMLVILLNCVTGLMFRPCEDIACDSQRCRILOAFEDDIFAFFAVEMVVMVA 170
Dd 124 CT-WFECVSMVLVILLNCVTGLMYQPCDDMDCLSDRCKILQVDFDIFIFFAMEMVLKMA 182
QY 171 LGIFGKKCYLGDWNRDLDFIVIAAGMLEYSLDLQNVFSFSAVRTVRLRPLRAINRVPSMR 230
Dd 183 LGIFGKKCYLGDWNRDLDFIVMAG-----NINLSAIRTVRLRPLKAINRVPSMR 233
QY 231 ILVTLLLDTPMLGNVLLLCFFVFFIFIGVQVLWAGLLRNRCFLPENFSPLSVDLEPY 290
Dd 234 ILVNLLLDTPMLGNVLLLCFFVFFIFIGVQVLWAGLLRNRCFLEENFTIQGDVALPPY 293
QY 291 YQTENEDESPFICSPRENGMRSRCSVPTLRGEGGGPPCSL-----DYETYNSSSNTT 344
Dd 294 YQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECCLSKDDVYDFGAGRQDLNAS 350
QY 345 --CVWNQYNTNCSAGHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFY 402
Dd 351 GLCVWNRYNVNCRGTSANPHKGAINFNDNIGYAWIVIFQVITLEGWVEIMYVMDAHSFY 410
QY 403 NFIFYFILLII----- 412
Dd 411 NFIFYFILLIIISELIHLVMPDCSFSTAQSPKCGQDGLPGVAESLLLRDSSSVITDEAAA 470
QY 413 ----- 412
Dd 471 MENLLAGTSKDESILLRLAGSQVHSAQAQMLGRGLGPESLETGETEHPHWSPRATRRWDP 530
QY 413 -----VGSFFMINCLVVIATQFSETKQRESQLMRQVRFLSNASTLA 456
Dd 531 QCQPGQPLPLHFMQAQVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVA 589
QY 457 SFSEPGSCYEELLKYLVIYILRKAARRLAQVSRAGVIRAGLLSSPVARSQEPQPSGSCTR 516
Dd 590 SYAEPGDCYEEIFQYVCHILRKAQR-----RALGLYQALQSRRLQALGPEAPAPA----- 638
QY 517 SHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPTPTPSG 576
Dd 639 -----KPGPHAKEPRH 649
QY 577 GPPRGAESVHSFYHADCHLEPVRCQAPPPRCPEASGRIVSGKVYPTVHTSPPPPIKLD 636
Dd 650 YPLTVWESILGRQAECTL---RAAAHP-----SSGASHPGVGSSEAEPLCPQ 694
QY 637 KALVEVAP---SPGPPTLTFSNIPPGFSSMHKLTETQGTGAC-HSSCKISSPSCSKADS 691
Dd 695 HSPLDATPHTLVQPIPATLAS-----DPASCPCQHEGDRRPSGLSTDS 739
QY 692 GACGPDSCPYCARTGAGEPESADHMPDSDSEAVYEFTQDAQHSDLRDPHSRRRRQSLGP 751
Dd 740 QOEGSGS---GSSAGGEDEA-----DGDGA---RSSEGDGASSELGKEEEEEQ----- 781
QY 752 DAEPSSVLA---FWRLICDTFRKIVDSKYFGRGIMAILVNLMSMGIEYHEQPE----- 802
Dd 782 -ADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQAASAAQPGRA 840
QY 803 -----ELTNALE-----ISNIV----- 814
Dd 841 CGRGONPDLCTWLKAPCLCHNVPSPGQVLSHPVTPHTAPWRMETGKQGHGCEGPGQR 900
QY 815 FTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFLMRV 874
Dd 901 SSDMFALEMILKLAAPGLFDYLRNPYNIFDSIIVISIWEIVGQADGGLSVLRTFLLRV 960
QY 875 LKLVRLPALQRLVLMKTMNDNVATFCMLLMFIFISILGMHLFGCKFASERD-GDTL 933
Dd 961 LKLVRFMPALRRQLVLMKTMNDNVATFCMLLMFIFISILGMHIFGCKFSLRDTGDTV 1020
QY 934 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 993
Dd 1021 PDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSPWASLYFVALMTFGNYVLFNLLV 1080
QY 994 AILVEGFQAE-----GD 1005

Dd 1081 AILVEGFQAEVTVVLAEEAPPQGLRKTGRGRGGLDGGGLQPKLLAGNLSLKEGVADEVGD 1140
QY 1006 ATKSESEPDFFSPSV-----DGDGRKKRLALVALGSHAELRKSLLPLLIHT-- 1053
Dd 1141 ANRSYDEDEQSSNIEEFDKLQEGLDSSDPK--LCPIMPTNGHLDPSL--PLGGHLGP 1196
QY 1054 --AATP-----MSHPKSSSTGVG-----EALGSGSRRTSSSGSA----- 1085
Dd 1197 AGAAGPAPRLSLQDDPMLVALGSRKSSVMSLGRMSYDQRLVGLGRATAGVQAAFGHLVP 1256
QY 1086 EP-----GAAHMKCPPSARSPSPHSPWSAASSWTSSRRSSRNSLGRAPSLKRRSPSGERR 1140
Dd 1257 QPWWCLWGADPNNGNSFQSSSRSSYYGPWGRSAAWASRRSSWN-----SLKHKPPSAEHE 1310
QY 1141 SLLSGE-GQESQDEFESEEE--DRASPAGSDH-----RHRGSLEREAKSS 1182
Dd 1311 SLLSAERGGGARVCEVAADGPPRAAPLHTPHAAHHVHGHPLAHRHRRHRTLSLDNRDS 1370
QY 1183 FDLPDTLQVPGHLHRTASGRSS--ASEHQDCNKKSASGRRLARTLT--DDPQLDGGDDND- 1237
Dd 1371 VDLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRMPS--IAKOVFTKMGDRGDRGEDEEEI 1428
QY 1238 -----EGNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFR-----LLC--- 1280
Dd 1429 DIVSGGGAEGDLTLCFVRVKMIDVYKPDWCCEVRDWSVYLFSPENRLDLGWSVLECCQK 1488
QY 1281 -----HRIITHKMFHDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSN 1325
Dd 1489 VGDLVVVYVYQRRQRQRTIIAHKLFYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSN 1548
QY 1326 YIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKIL 1385
Dd 1549 YIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVLDGFLVFSIIDIVVSLASAGGAKIL 1608
QY 1386 GMLRVLLRLTLRPLRVISRAQGLKLVVETLMSSLKPDIGNIVVICCAFFIIFGILGVQLF 1445
Dd 1609 GVLRVLRLLRLTLRPLRVISRAPGLKLVVETLISSLKPEIGNIVLICCAFFIIFGILGVQLF 1668
QY 1446 KGKFFVCQGEDTRNITNKSDCAEASRYRVRHKYNFNDLGOALMSLFLVASKDGVWDIMYD 1505
Dd 1669 KGKFYHCLGVDTRNITNRSDCAANYRWVHHKYNFNDLGOALMSLFLVASKDGVWNIMYN 1728
QY 1506 GLDAGVVDQOPIMNHNPMMLLYFISFLLIVAFVFLNMFVGVVVENFHKCRHQHEEEARR 1565
Dd 1729 GLDAGAVDQOPVTNHNPMMLLYFISFLLIVSFFVLNMFVGVVVENFHKCRHQHEEEARR 1788
QY 1566 REEKLRLRLKKRRSKEQMAEAOCKPYSDYSRFRLLVHHLCTSHYLDLDFITGVLGNV 1625
Dd 1789 REEKLRLRLKKRR-----KAQLPYATYATYCHTRLLIHSMTCTSHYLDIFITFIICLVN 1841
QY 1626 VTMAHEHYQQP 1636
Dd 1842 VTMSLEHYNQP 1852
RESULT 13
US-10-369-493-6836
; Sequence 6836, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374									
; SEQ ID NO 6836									
; LENGTH: 1657									
; TYPE: PR									
; ORGANISM: Caenorhabditis elegans									
US-10-369-493-6836									
Query Match 29.5%; Score 3553; DB 14; Length 1657;									
Best Local Similarity 42.2%; Pred. No. 5.3e-226;									
Matches 800; Conservative 234; Mismatches 436; Indels 426; Gaps 42;									
QY	66	AGSTEKDPG-----SADSEAEGLPYPALAPVVFYLSQDSRPRSCWCLRTVCN	112						
Db	88	ASSEASPSRWEGRQIEWGNEEQIEESE-LPYPGFAEPALRCFYQARPPRKWALQVMS	146						
QY	113	PWFERVSMVLINCVTLGMFRPCD-IACDSQRCRILQAFDDFIFAFFAVEMVVMVAL	171						
Db	147	PWFDRITMAVIMINCVTLGMYRPCEDGDCDTRYCQILDIIIDNCIFVYFAFEMVIKIMAL	206						
QY	172	GIFGKKCYLGDWTNRDLDFIVIAGMLEYSLDLQ--NVSFSAVRTVRVLRPLRAINRVPS	228						
Db	207	GFYGPAAVMSDTWNRLDFFIVMAGIAEFVLHEYLGGNINLTAIRTVRLRPLRAVNRIPS	266						
QY	229	MRILVTLILLDTLPMGLNVLLLCFFVFIFGIVGVQLWAGLLRNRCF--LPENFS-----L	281						
Db	267	MRILVNLILLDTLPMGLNVLLLCFFVFIFGIVGVQLWAGLLRNRCVINLPKTISENQSAL	326						
QY	282	PLSVLDLEPYQTENEDESPFCISQPRENGMRSCRSVPTLRGEGGGPPCSDLDETYSNSS	341						
Db	327	FNNVXLTRFYIPE-DTSLEYICSPDANGLHTCSNLPPYTVD---GVKCNLTLDYDKVT	382						
QY	342	NTTCVNNQYNTNCAG-----EHNPKGAINFDNIGYAWIAIFQVIT	384						
Db	383	NDSCINWNIYYNECQVNIYPSLMTIAISCFIKVMQRNPPQGSVSFDNIGFAWIAIFLVIS	442						
QY	385	LEGWVDIMYFVMDAHSFYNYFIYILLIIVGSFFMINCLVVIATQESETKQRESQLMREQ	444						
Db	443	LEGWTDIMYVQDAHSFNNWIIYFVLLIVIGAFFMINCLVVIATQFAETKRETERMLQE	502						
QY	445	RVRFLSNASTLASFSEPG-----SCYEELKVLVILRKAARRLAQVSRAGVVRAG	495						
Db	503	RKMLNRRDSISCTGSEIGGASSKEEGDTVYAAAFVRFIGHTFRRTKRAAKKYTAY----	557						
QY	496	LLSSPVARSQEPQPSGSCSTRSHRRLSVHLVHHHHHHHHHHLGNGTLRVPRASPEIQD	555						
Db	558	-----MEERAERKSSERQORRKSCL-----DDMATLSRIEKAED	592						
QY	556	RDANGSRRLMLPPPSTPTSGGPPRGAESVHSFYHADCHLEPVRCAQAPPRCPSASGRT	615						
Db	593	EE-----DETTITRENGDDQIEQN-----	611						
QY	616	VSGKVYPTVHTSPPHILKDKALVEVAPSPGPTLTSTFNIPPGPFSSMHKLETSQSTA	675						
Db	612	-GDGVRIKRVKIEEPKI-----	628						
QY	676	CHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVVEFTQDAQHS	735						
Db	629	-----KIGNSNSNGPHYKHSSEES-----DEDGEED	656						
QY	736	DLRDPHSRRRQSLGDAEPSSVLAFWRLLCDTFRKIVDSKYFGRGIMIAILLVNTLSMGI	795						
Db	657	QVYDGEAEKK-----STPSKL--WW--FREKIQKFVICDHFTRGILVAILVNTLSMGV	706						
QY	796	EYHEQPEELTNALEISNIVFTSLFALEMLLKLIVPGFYKPNYNIPFDGVIIVISVWEI	855						
Db	707	EYHQOPEILTIVILEYNSLFFFTALFALEMLLKIIASGLFGYADGNLFDGGIVALSVEL	766						
QY	856	VGOQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATFCMLLMFIFISIL	915						
Db	767	FOEGKGLSVLRTFRLRLILKVRFPALRYQLVVMRLTMDNVTVFFGLLVLFIFISIL	826						
QY	916	GMHLFGCKFASERD---GDTLP--DRKNFDSLWAIIVTVFQILTQEDWNKVLVNGMASTS	970						

RESULT 14

US-10-627-370-2

; Sequence 2, Application US/10627370

; Publication No. US20040081988A1

; GENERAL INFORMATION:

; APPLICANT: Johnson, Jason M.

Db	827	GMNLFCKVEKFLGGLAKCKERNFDTLLWALITVFQILTQEDWNMVLNMGMAQTN	886
QY	971	SWAALYFIALMTFCGNYVLFNLLVAILVEGFAEGADATKSESEPDFSPSVGDGDRKKRL	1030
Db	887	PWAALYFVALMTFCGNYVLFNLLVAILVEGFAEGADATKSESEPDFSPSVGDGDRKKRL	946
QY	1031	ALVALGEHAELKSLPLPLIHTAATPMHPKSSSTGVGEALGSGSRRTSSSGSAEPGAA	1090
Db	947	ELII-----AKTTSPAFNNGVA	963
QY	1091	HHEMKC--PPSARSSPHSPWSAASSWTSSRRNSLGRAPSLKRRSPSG-----ERRSLL	1143
Db	964	PAECTCQRPSPPEEP-SPRLLSANY-----HPSPERKHSANLDAIIDKRLVL	1010
QY	1144	SGEGQESQDEESESSEEDRASAPGSDHRHSGSLEREAKSSFDLPDTLQVPLHRTASGRSS	1203
Db	1011	-----RNSAPFDR-SPV-SEGRDDSRLLNRHA--SLVLPVANGVP-----	1045
QY	1204	ASEHQDCNGKSASGRRLARTLRDTPQLDGGDDNDDEGNLSKGERIQAWVRSRL-PACCRER	1262
Db	1046	-YRRQRVHSWKASQELKQALAEERNEAKQN-----TFVRKLLKKTCLHNR	1091
QY	1263	DSWSAYJFPQSRFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLT	1322
Db	1092	TEFSLFLMGPKNPLRIKCLQTQKKWFDYTVLFFIGINCTIAMERPSIPPDSEFERQFLH	1151
QY	1323	LSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVSMVSDSGT	1382
Db	1152	ISGYIFTVIFTGEMMK-----	1168
QY	1383	KILGMLRVLRLRLTLRPLRVISRAQGLKLVVETILMSSLKPIGNIVVICCAFFIIFGILGV	1442
Db	1169	-----VSHRIPTLKPIGNIVLICCTFFIIFGILGV	1198
QY	1443	QLFKGKFFVCOGEDTRNITNKSDCAEASYSR--WVRHKYNFDNLGQALMSLFLVASKDGV	1500
Db	1199	QLFKGMYHCIGPEVGNVTTKADCIE-DYRNKWNHRYNFDNLGQALMSLFLVSSKDGW	1257
QY	1501	DIMVDGLDVGVDQOPIMNHNPNMMLLYFISFLLIIVAFVLMFVGVVVENPHKCRHQEE	1560
Db	1258	SIMYQIDAVGVDVQPIENYNEWMIYFISFLLVGVFVLMFVGVVVENPHKCKEALEK	1317
QY	1561	EEARRREEKRLRLEKKRKSKEKQMAEAQCK-----PYYSYSRF	1600
Db	1318	EMREKEKEKRLKR-KLKRQKFEESMAGRKRNRIWAGSAIKSIFSVERNYPYHYDGH	1376
QY	1601	RLLVHHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQILDEALKICNYIFTVIFVESVF	1660
Db	1377	RLFLHGIVTSKYFDLATAAIVGINVISMAEFYMMPMGLKYVLKALNYFFTAFTLEAAM	1436
QY	1661	KLVAFAFRFFQDRWNQDLAIVLLSIMGITLEEIEVNLSPINPTIIRMRVLRIARVL	1720
Db	1437	KJIALGFKRFFIEKWNRLDMFIVILSIAGIIFEEFEA-LELPINPTIIRVMRVLRIARVL	1495
QY	1721	KLLKMAVGMRALHTVMQALPOVGNLGLLFLMLFFIFAALGVLEFGDLECDETHPCGLG	1780
Db	1496	KLLKMAKGIRSLDVTVEALPOVGNLGLLFLFFIFAALGVLEFGDLECDETHPCDGLG	1555
QY	1781	RHATFRNFGMAFLTFRVSTGDNWNGIMKDPSPR-DCD-----QESTCYNTVISPIYFVSF	1834
Db	1556	EHAHFKNFGMAFLTFRATGDNWNGIMKDALRDDCDSSDHCECTCCVDPILAPCFFVIF	1615
QY	1835	VLTAQFVLNVVIAVLMKHLEESNKEAKEAEAELEAE	1870
Db	1616	VLISQFVLNVVAVVAVLMKHLEESN---KRDAEGPAE	1648

```

; APPLICANT: Castle, John C.
; APPLICANT: Armour, Christopher D.
; TITLE OF INVENTION: SPLICE VARIANT ISOFORMS OF HUMAN CALCIUM CHANNEL CACNA1B
; FILE REFERENCE: RS0202Y
; CURRENT APPLICATION NUMBER: US/10/627,370
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2264
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-627-370-2

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QY	871	LMRVLKLVRFLPALORQVLVLMKMTDNDVATFCMLMLFIIFISILGMHLFGCKFASERDG	930
Db	582	LLRIFKVKYWSLRNLVSVLLNSMKSIISLLFLFLFIVV FALLGMQLFGGQNFQDET	641
QY	931	DTLPDRKNPDSLLWAIWTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFIALMTFGN	985
Db	642	PT---TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGVSKGMFSSFYFIVLTLFGN	697
QY	986	YVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGRKKRLALVALGEHAELRKSL	1045
Db	698	YTLNVLFAIAVDNLANAQELTXDEEEMEEAA-----NQKLALQAKEVAEV--SP	746
QY	1046	LPPLIIHTAATPMShPKSSSTGVGEA-----	1071
Db	747	MSAANISIAARQONSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLR	806
QY	1072	-----LGSGRRRTSSGSAEPGAA-----HH-----EMKCP-----	1097
Db	807	PDMKTHLDRPLVVELGRDGARGPVGGKARPEAAEAPEGVDPRRHRHRDKDCTPAAGDQ	866
QY	1098	-----PSARSS---PHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSL	1142
Db	867	DRAEAPKAESGEGAREERPRPHRSHSKAAA--GPPEARSERGRGP-----GPEGGRHH	919
QY	1143	LSGEGQESQDEE-----ESSEEDRASPGSDHRRHRSLE--REAKSSFDLPTL	1189
Db	920	RRGSPEEAEREPRRHRHRHQDPSPKACAGKERRARRHGGPRAGPREAESG-----	972
QY	1190	QVPG-LHRTASGRSSASE--HQDCNGKSASGRLA-----RTLRTDDPQLDGGDDNDE	1238
Db	973	EEPARRHRARHKAQPAHEAAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS	1032
QY	1239	GNLSKGERIQAWVRSLPACCRER-----DSW-----	1265
Db	1033	GTIVTGP-----MHTLPSTCLQKVEEQPEDADNQNVTRMGSPQPDNTIVHIPVMLTG	1086
QY	1266	-----SAYIFPPQSRFRLLCHRI	1283
Db	1087	PLGEATVVPVSGNVLDLESAEGKKEVEADDVMRSGPRPIVPYSSMFCLSTNLLRRFCHYI	1146
QY	1284	ITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL	1343
Db	1147	VTMYFEVILVIALSSIALAAEDP-VRTDSPRNALKYLDYIFTGVTFEMVIK MIDL	1205
QY	1344	GWCFGEQAYLRSSWNVDGLLVLSVIDILVSMV-SDSGTKILGLMLRVLRLTLRPLRV	1402
Db	1206	GLLLHPGAYFRDLWNILD----FIVVSGALVAFAPSGSKGKDINTIKSLRVLRLRPLKT	1261
QY	1403	ISRAQGLKLVVETLMSLPKIPGNIWVICCAFFIIFGILGVQLFKGKFFVCCOGE-----D	1456
Db	1262	IKRPLKAVFDCVVNSLKNVLNLIIVMLFMFIFAIVAVQLFKGKFFYCTDESKELE RD	1321
QY	1457	TRN--ITNKSDCAEASYR-WVRHKYNFDNLGQALMSLFLVASKDGWVDIMYDGLDAVGVD	1513
Db	1322	CRGQYLDYEKEEVEAQPRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE	1381
QY	1514	QQPIMNHNPMWLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRQHOOEEEEARRRREKRLRR	1573
Db	1382	QGSPSPGYRMELSIYFVVVFVVPFFVFVNI FVALIIITF-----QE QGDKVMSE-----CS	1431
QY	1574	LEKKRRSKEQMAEAQCKPYYSDYSR--FRLLVHHLCTSHYLDLFTIGVIGLNVVVTMAME	1631
Db	1432	LEKNERACIDFAISAKPLTRYMPQNRQSFQYKTTWTFVVSPPFEYFIMAMIALNTVVLMMK	1491
QY	1632	HYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAPRRFFQDRWNQLDLAIVLLSIMGIT	1691
Db	1492	FYDAPYEXELMKCLNIVFTSMFSMECVLKI AFGVLNVYFRDAWNVDFVTVLGSITDIL	1551
QY	1692	LEEIE-----VNLSLPINPTIIRIMEVRLIARVLKLLKMAVGMRALHTVTMQALPQVGNL	1746
Db	1552	VTEIAETNNFINLS-----FLFLFRAARLIKLLRQGYTIRILLTWTFFVQSFKALPVY	1602

Db 730 NOKLALQKAKEVAEV--SPMSAANISIAARQNSAKARS--VMEQRASQLRLQNLRASCE 785
QY 1078 -----RTSSSGSAEPGAAHH-----EMKOPPSARSSPHSPWSAASS 1113
Db 786 ALYSEMDPEERLRYASTHRVRPDMKTHMDRPLVVEPGRDGLRGFVGSKSKPEGTEATESA 845
QY 1114 WTSRRSSRN-----SLGRAP-----SLKRRSPSGE----- 1138
Db 846 DLPRRHHRRDRDKTSATAPAGGEQDRTESTETGAREERARPRRSHSKETPGADTQVRCE 905
QY 1139 --RRSLLSGEGQESQDEE-----ESSEEDRAS---PAGSDH-RHRG--SLEREA 1179
Db 906 RSRHRHRRGSPPEATEEREPRRHRRAHQDSKEGTAPVLVPKGERRARHRGPRTGPREA 965
QY 1180 KSSFD-----LPDTLQVPLHRTASGRSSASE-----HQDCNGKSAS 1216
Db 966 ENNEEPTRRHRARHKVPPTLQPPPE-REAAEKESNAVEGDKETRHNHQPKPHCDLEAIAVT 1024
QY 1217 G-----RLARTL--RTDDPQLDGGDDND----- 1237
Db 1025 GVGPLHMLPSTCLQKVDEQPEDADNQNVNTRMGSQSDPSTTVHVVPVTLTGPPGETPVVP 1084
QY 1238 EGNL-----SKGER-----IQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIIT 1285
Db 1085 SGNMNEGQAEGKKEAEADDVLRGRPRPIVPYS-----SMFCLSPTNLLRRFCHYIVT 1137
QY 1286 HKMFDHVVLVILFNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGW 1345
Db 1138 MRYFEMVILVIALSSIALAAEDP-VRTDSFRNNALKYMDYIFTGVFTFEMVIKMDLGL 1196
QY 1346 CFGEQAYLRSSWNVLGGLVLISVIDI-LVSMVSDSGTKILGMLRVLRLTLRPLRVIS 1404
Db 1197 LHHPGAYFRDLWNILDFIVVSGALVAFAPSSFMGGSKGKDINTIKSLRVLRLPLKTIK 1256
QY 1405 RAQGLKLIVETLMSLKPIGNIVVICAPFIIFGILGVQLFKGFFVCOGE-----DTR 1458
Db 1257 RLPKLKAVFDVCVNSLKNVLNILIVYMLFMFIFAVIAVQLFKGFFYCTDESKELERDCR 1316
QY 1459 N--ITNKSDCARASYSR-WVRHKXNFDNLGOALMSFLVASKDGVVDIMYDGLDAVGVDQ 1515
Db 1317 GQYLDYERKEEVEAQPRQWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEEQG 1376
QY 1516 PIMHNPNMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRRREKKLRRL 1575
Db 1377 PSPGFRMELSFIVVYFVVFVFFVFVFIIPVVALIITF-----QEQGDKVMSE-----CSLE 1426
QY 1576 KKRRSKEQMAEAOCKPYYSYSR--FRLLVHLCTSHYLDLFTITGVIGLNVVTWAMEHY 1633
Db 1427 KNERACIDFAISAKPLTRYMPQNKQSFQYKTYFWVSPPEFYFIMAMIALNTVVLMMKFY 1486
QY 1634 QQPQILDEALKICNIVFTVIFVFESVKLVAFARFRFFQDRWNQLDLAIVLLSIMGITLE 1693
Db 1487 DAPYELMLKCLNIVFTSMFSMECILKIIAFGVNLNFERDANNVDFVTVLGSITDILVT 1546
QY 1694 EIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVMQALPOVGNLGLLFMLL 1753
Db 1547 EIANNF---IN---LSPLRLFRAARLIKLRQGYTIRILLWTTFVQSFKALPYVCLLIAML 1600
QY 1754 FFIFAALGVELFGDCEDETHPCCEGLGRHATFRNFGMAFLTFLFRVSTGDNWNGIMKD--P 1811
Db 1601 FFIIYALIGMQVFGNIALDDDD---TSINRHNHRTFLQALMLLFRSATGEAWHEIMLSCLG 1657
QY 1812 SRDCD---QESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLM-----KH 1853
Db 1658 NRACDPHANASEC-GSDFAYFYFVSFIFCLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHH 1716
QY 1854 LEE----- 1856
Db 1717 LDEFIRVWAEYDPAACGRISVNDMFEMLKHMSPPILGKKPCPARVAYKXLRVMNMPISNE 1776
QY 1857 -----SNKEAKEEALEAEL-----ELEMKTLS--PQPHS 1884

Db 1777 DMTVHTSTLMALIRTALEIKLAPAGTKHQHQCDAELRKEISSVWANLPQKTLDLLVPPHK 1836
QY 1885 P-----LGSPF-----LWPGVEGVNSTDSPKPGAPHTTAAHGAASGFSLEHPTMVPHEEVP 1936
Db 1837 PDEMTVGKVVAAALMIFDFYKQNKTTTRDQTHQAPGGLSQMGFVSLF---HPLKATLEQOTQP 1893
QY 1937 VPLGPDLLTVRKSGSVSRTHSLPNDSYNCRNGSTAESRSLGHRGWG----- 1980
Db 1894 AVLRGARVFLRQKSAT---SLNNGGAIQTQESGIKESL---SWGTRQTDALYEARAPLE 1947
QY 1981 -----LPKAQSGSI-----LSVHSQPADTSC 2001
Db 1948 RGHSAEIPVGQSGTLAVDVQMNMTLRGPDGEPQPGLESQGRAASMPRLAAETQPAPNAS 2007
QY 2002 ILQLPKDVHYLL-QPHGAPTWGAIPKLPDPG-----RSPLAQRPRLRQAART 2048
Db 2008 --PMKRSISTLAPRPHGTQLCSTVLDRLPPPSQASHHHHHRCHRRDRKKQRSLEKGP SLSV 2065
QY 2049 DSLDVQGLGSRREDLLSEVSGPSCPLTRSSSFWGSSSIQVQQRSGIQSKVSKHIRLPAPCP 2108
Db 2066 DP-----EGAPSTAAGPLPHGEGSTACRRDRKQERGRSQERRQPSSSSSEKQRFY 2116
QY 2109 GLEPSWAKDPPESTRSSLELDTLSWISGDLPLSPSQEEPLFRDLKCKCYSVETQSCRRRPG 2168
Db 2117 SCDRFGSREPPQ-----LMPSLSSHPTSP----- 2140
QY 2169 FWLDEQRRHSIAVSCLDGSGQPRCLCPSPSSLGQPL-----GGPGSRPKKKLSP 2217
Db 2141 -----TAALEPAPHQ---GSGSVNGSPMLMSTSGASTPGRGGRRLPQTPLTP 2185
QY 2218 -PSIS-----IDPPESQGSRRPPCSPG-----VCLRRRAPASD-----SKD 2251
Db 2186 RPSITYKTANSSPVHFAEGSGGLPAFSPGRLSRGLSEHNALLQKEPLSQPLAPGSRIGSD 2245
QY 2252 PSVSSPLDSTAASPSPKKDTLSL-----SGLSS 2279
Db 2246 PYLGQLDSEASHTLPEDITLTFEEAVATNSGRSS 2280

Search completed: November 18, 2004, 13:58:59
Job time : 208.328 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:21 ; Search time 50.7329 Seconds
(without alignments)
4337.375 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRPRCVRTPTPLRGSAR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	11657	96.9	2254	2	T09053	low voltage-activated
2	3553	29.5	1657	2	T15838	hypothetical protein
3	1720.5	14.3	1810	2	T31092	probable voltage-gated
4	1676	2339	2	A42566	omega-conotoxin-se-	
5	1665.5	13.8	2259	2	S29236	calcium channel pr-
6	1653.5	13.7	2272	2	C54972	voltage-dependent
7	1652.5	13.7	1891	2	T43262	calcium channel al-
8	1652.5	13.7	2178	2	S29237	calcium channel pr-
9	1650.5	13.7	2288	2	S41080	calcium channel al-
10	1642	13.7	2223	2	A47447	calcium channel pr-
11	1640.5	13.6	2237	2	T45115	N-type calcium cha-
12	1638	13.6	2251	2	B54972	voltage-dependent
13	1637.5	13.6	2270	2	A54972	voltage-dependent
14	1636	13.6	1993	2	T30902	sodium channel SCA
15	1632.5	13.6	2222	2	A37490	voltage-dependent
16	1632.5	13.6	2336	2	A45386	omega-conotoxin-se-
17	1631	13.6	2181	2	A38198	calcium channel al-
18	1628	13.5	1873	2	A30063	dihydropyridine re-
19	1622	13.5	2161	2	JH0564	calcium channel al-
20	1619.5	13.5	1911	2	T43048	calcium channel al-
21	1616	13.4	1852	2	A37860	calcium channel pr-
22	1614.5	13.4	1977	2	S54771	sodium channel alp-
23	1613	13.4	2203	2	T42742	voltage-dependent
24	1610	13.4	2143	2	JH0427	voltage-dependent
25	1603	13.3	1610	2	A46227	voltage-dependent
26	1595.5	13.3	1783	2	T37258	probable voltage-d-
27	1595	13.3	2166	2	S11339	calcium channel pr-
28	1592.5	13.2	2139	2	A44467	voltage-dependent
29	1587.5	13.2	1646	2	JH0422	voltage-dependent

30	1587.5	13.2	1873	2 A55645	calcium channel, v
31	1585.5	13.2	2016	2 A38195	sodium channel pro
32	1580	13.1	1917	2 C88728	protein C48A7.1 fi
33	1577.5	13.1	1559	2 T30535	calcium channel al
34	1574	13.1	2171	2 S05054	calcium channel al
35	1573	13.1	2108	2 S72458	sodium channel pro
36	1567.5	13.0	1687	2 S41742	calcium channel al
37	1565	13.0	1957	2 S68453	sodium channel pro
38	1557.5	12.9	2220	2 A45290	calcium channel pr
39	1556	12.9	2019	2 A33996	sodium channel pro
40	1551.5	12.9	1840	1 CHRTM1	sodium channel pro
41	1549	12.9	1976	2 I56555	sodium channel pro
42	1546.5	12.9	1983	2 A60054	sodium channel pro
43	1546	12.9	2262	2 T30890	calcium channel al
44	1544.5	12.8	1951	2 S00320	sodium channel pro
45	1544.5	12.8	2005	2 A46269	sodium channel alp

ALIGNMENTS

RESULT 1

T09053
low voltage-activated, T-type calcium channel alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09053
R;Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox, Nature 391, 896, 1998
A;Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium A;Reference number: Z16538; MUID:98154730; PMID:9495342
A;Accession: T09053
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2254 <PER>
A;Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g37 A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Map position: 17
A;Note: CACNA1G
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: calcium channel; voltage-gated ion channel

Query Match	96.9%;	Score 11657;	DB 2;	Length 2254;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 2219;	Conservative	0;	Mismatches 6;	Indels 0;
Gaps	0;			
QY	62	GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPFERVSML	121	
Db	30	GRQPGSGTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPFERVSML	89	
QY	122	VILLNCVTGLGMRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG	181	
Db	90	VILLNCVTGLGMRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG	149	
QY	182	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRLAINRVPSMRILVTLLDTP	241	
Db	150	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRLAINRVPSMRILVTLLDTP	209	
QY	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSDVLEPYQTENEDESPF	301	
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSDVLEPYQTENEDESPF	269	
QY	302	ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLDETYSNSSNTTCVNNQYTTNCSAGEHN	361	
Db	270	ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLDETYSNSSNTTCVNNQYTTNCSAGEHN	329	
QY	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL	421	
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL	389	
QY	422	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSFSGCYEELKYLVLIRKAAR	481	

Db 390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 449

QY 482 RLAQVSRATGVRAGLLSSPVARSQEPQPSGSCSTRSHRRLSVHLLVHHHHHHHHYHLGN 541

Db 450 RLAQVSRATGVRAGLLSSPVARSQEPQPSGSCSTRSHRRLSVHLLVHHHHHHHHYHLGN 509

QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPPTPTPSGGPPRGAEVSHSFYHADCHLEPVRQC 601

Db 510 GTLRVPRASPEIQDRDANGSRRLMLPPPTPTPSGGPPRGAEVSHSFYHADCHLEPVRQC 569

QY 602 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTLSFNIPGPF 661

Db 570 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTLSFNIPGPF 629

QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPPDS 721

Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPPDS 689

QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTERKIVDSKYFGRG 781

Db 690 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTERKIVDSKYFGRG 749

QY 782 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN 841

Db 750 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLKLLVYGPFGYIKNPYN 809

QY 842 IFDGVIWISWEIVGQGGGLSVLRTFRLMRVLKLVRFPLPALORQLVVLMTMDNVATF 901

Db 810 IFDGVIWISWEIVGQGGGLSVLRTFRLMRVLKLVRFPLPALORQLVVLMTMDNVATF 869

QY 902 CMLLMFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTVFQILTQEDWNKV 961

Db 870 CMLLMFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTVFQILTQEDWNKV 929

QY 962 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFFSPSVD 1021

Db 930 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFFSPSVD 989

QY 1022 GDGDRKKRLALVALGEHAELRKSLPLPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081

Db 990 GDGDRKKRLALVALGEHAELRKSLPLPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1049

QY 1082 SGSAEPGAAHHEMKPPSARSSPHSPWSAASWTSRSSRNSLGRAPSLKRRSPSGERRS 1141

Db 1050 SGSAEPGAAHHEMKPPSARSSPHSPWSAASWTSRSSRNSLGRAPSLKRRSPSGERRS 1109

QY 1142 LLSGEGQESQDEEESSEEDRASPGSDHRHRSGLEREAKSFDLPDTLQVPLHRTASGR 1201

Db 1110 LLSGEGQESQDEEESSEEDRASPGSDHRHRSGLEREAKSFDLPDTLQVPLHRTASGR 1169

QY 1202 SSASEHQDCNGKSASGRLARTLRDTPQLDGDNDNDEGNLSKGERIQAWVRSRLPACCRE 1261

Db 1170 SSASEHQDCNGKSASGRLARTLRDTPQLDGDNDNDEGNLSKGERIQAWVRSRLPACCRE 1229

QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSAERIFL 1321

Db 1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSAERIFL 1289

QY 1322 TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSG 1381

Db 1290 TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSG 1349

QY 1382 TKILGMLRVLLRLTLRPLRVISRAQGLKVETLMSSLKPIGNIIVVICCAFFIIFGILG 1441

Db 1350 TKILGMLRVLLRLTLRPLRVISRAQGLKVETLMSSLKPIGNIIVVICCAFFIIFGILG 1409

QY 1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASRWRHRYNFNDLQALMSLFLVASKDGWVD 1501

Db 1410 VQLFKGKFFVCQGEDTRNITNKSDCAEASRWRHRYNFNDLQALMSLFLVASKDGWVD 1469

QY 1502 IMYDGLDVGVDQOQPIMNHNPNWMLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRHQHEE 1561

Db 1470 IMYDGLDVGVDQOQPIMNHNPNWMLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRHQHEE 1529

QY 1562 EARRREKRLRLEKKRRSKEKQMAEAQCKPYYSYRFRLLVHHLCTSHYLDLFTITGVI 1621

Db 1530 EARRREKRLRLEKKRRSKEKQMAEAQCKPYYSYRFRLLVHHLCTSHYLDLFTITGVI 1589

QY 1622 GLNVVTMAHEHYQOQIILDEALKICNYIFTVIVFVSVFKLVAFARFRFFQDRWNQDLA 1681

Db 1590 GLNVVTMAHEHYQOQIILDEALKICNYIFTVIVFVSVFKLVAFARFRFFQDRWNQDLA 1649

QY 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLIARVLKLLKMAVGMRALHTVMQALP 1741

Db 1650 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLIARVLKLLKMAVGMRALHTVMQALP 1709

QY 1742 QVGNLGLLEFLLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTG 1801

Db 1710 QVGNLGLLEFLLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVSTG 1769

QY 1802 DNWNGIMKDPSCRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVVIAMKMLEESNKEA 1861

Db 1770 DNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVVIAMKMLEESNKEA 1829

QY 1862 KEEAELEAELELEMKTLSPQSPHSPGLSPFMPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921

Db 1830 KEEAELEAELELEMKTLSPQSPHSPGLSPFMPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1889

QY 1922 SLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLHGRWGGL 1981

Db 1890 SLEHPTMVPHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLHGRWGGL 1949

QY 1982 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAI PKLPPGRSPLAQRP LR 2041

Db 1950 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAI PKLPPGRSPLAQRP LR 2009

QY 2042 RQAAIRTDSDLVQGLGSRDILLSEVSGPSCPLTRSSSFWGGSSIQVQQRSIGISKVSKHI 2101

Db 2010 RQAAIRTDSDLVQGLGSRDILLSEVSGPSCPLTRSSSFWGGSSIQVQQRSIGISKVSKHI 2069

QY 2102 RLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLSSQEEPLFPRDLKCCYSVETQ 2161

Db 2070 RLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLSSQEEPLFPRDLKCCYSVETQ 2129

QY 2162 SCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSSSSLGGQPLGGPGSRPKKLSPPSIS 2221

Db 2130 SCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSSSSLGGQPLGGPGSRPKKLSPPSIS 2189

QY 2222 IDPPESQSRPPCSPGVCLRRRAPASDSKDPSSVSSPLDSTAASPSPKDTLSLGLSSDP 2281

Db 2190 IDPPESQSRPPCSPGVCLRRRAPASDSKDPSSVSSPLDSTAASPSPKDTLSLGLSSDP 2249

QY 2282 TDMDP 2286

Db 2250 TDMDP 2254

RESULT 2

T15838
hypothetical protein C54D2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
C;Accession: T15838
R;Minx, P.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid C54D2.
A;Reference number: Z18415
A;Accession: T15838
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1657 <MIN>
A;Cross-references: EMBL:U37548; NID:g1017804; PID:g1017809; PIDN:AAA79201.1; CESP:C54D
C;Genetics:
A;Gene: CESP:C54D2.5
A;Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 370/2; 439/3; 470/3; 51
C;Superfamily: sodium channel protein

Query Match		29.5%;	Score 3553;	DB 2;	Length 1657;
Best Local Similarity		42.2%;	Pred. No. 1.3e-217;		
Matches 800;		Conservative 234;	Mismatches 436;	Indels 426;	Gaps 42;
QY	66	AGSTKDPG-----SADSEAEGLPYPALAPVVFYLSQDSRPSRWCLRTVCN	112		
Db	88	ASSEASPSRWEGRQIEWGNEEQIEESE-LPYGFAEPALRCFYQARPPRKWALQVMS	146		
QY	113	PWFERSMLVILNCVTLGMFRPCED-IACDSQRCRILQAFDEIFAPFAVEMVVMVAL	171		
Db	147	PWFDRITMAVIMNCVTLGMYRPCEDGDCDITYRCQILDIDNCIFVFYFAFEMVIMAL	206		
QY	172	GIFGKKCYLGTWNRDLFFIVIAIGMLEYSLDQ--NVFSAVRTVRVLRPLRAINRVPS	228		
Db	207	GFYGPAAVMSDTWNRDLFFIVMAGIAEFVLHEYLGNINLTARTVRVLRPLRAVNRIPS	266		
QY	229	MRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCF--LPENFS-----L	281		
Db	267	MRILVNLTLTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCVINLPKTISENQSA	326		
QY	282	PLSVDLPEYYQTENEDESPFCISQPRENGMRSCRSVPTLRGEGGGPPCSDLDETYSNS	341		
Db	327	FNNVCLTRFYPE-DTSLEYICSQPDANGLHTCSNLPPYTVD---GVKCNLTLDYDKVT	382		
QY	342	NTTCVNNQYTYTNCAG-----EHNPEKGAINFNDNIGYAWIAIFQVIT	384		
Db	383	NDSCINWNIIYNECQVNIYPSLMTIAISCFIKVMQRNPFQGSVFDNIGPAWVAIFLVIS	442		
QY	385	LEGWVDIMYFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQ	444		
Db	443	LEGWTDIMYVQDAHSFWMWLYFVLLIVIGAFFMINCLVVIATQFAETKRRETERMLQE	502		
QY	445	RVRFLSNASTLASFSEPG-----SCYEELLKVLVYLKARRLAQVSRAGVVRAG	495		
Db	503	RKMLNRRDSISCTGSEIGGASSKEEGDVTYAAVFVFGHTFRRTKRAAKKYTAY-----	557		
QY	496	LLSSPVARSQEQPQSGSCTRSHRRLSVHHLVHHHHHHHHYHLNGTLRVPRASPEIQD	555		
Db	558	-----MEERAERKSERQRRKSKL-----DDMATLSRIEKAED	592		
QY	556	RDANGSRRLMLPPPTPTPGSGPPRGAESVHSFYHADCHLEPVRCQAPPSPRCPSEASGR	615		
Db	593	EE-----DETTITRENGDDQIEQN-----	611		
QY	616	VGSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSTFNIPPGPSSMHKLTQSTGA	675		
Db	612	-GDGVRIKRVKIEEPKI-----	628		
QY	676	CHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHS	735		
Db	629	-----KICNGNSNGPHYKHSSDEES-----DEDGEED	656		
QY	736	DLRDPHSRRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGI	795		
Db	657	QVYDGEAEAKK-----STPSKL--WW--FREKIQKFVICDHFTRGILVAILVNTLSMGV	706		
QY	796	EYHEQPEELTNALIEISNIVFTSLFALEMLLKLIVYGPFYIKNPYNIFDGVIVVISVWEI	855		
Db	707	EYHQQPEILTVILEYSNLFFTALFALEMLLKIASGLFGYLADGFNLDGGINVLSVLEL	766		
QY	856	VGOQGGGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATFCMLLMFLIFIFSIL	915		
Db	767	FOEGKGLSVLRTFRLRLKLVRFMPALRYQLVLMRLTMDNVTVFFGLLVLFIFIFSIL	826		
QY	916	GMHLFGCKFASERD---GDTLP--DRKNFDSLLWAIVTVFQILTQEDWNKVLVNGMASTS	970		
Db	827	GMNLFQCKFKVEEKFGLGLAKKCKERNFTLLWALITVFQILTQEDWNVLFNGMAQTN	886		
QY	971	SWAALYFIALMTFGNYVLFNLLVAILVEGFQAGDATKSESEPDFFSPSVDGDKRKKRL	1030		
Db	887	PWAALYFVALMTFGNYVLFNLLVAILVEGFQESKEEKRLQLEEDARKQAVEEEDERKREL	946		

QY	1031	ALVALGEHAELRKSLPLPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSSSGSAEPGAA	1090		
Db	947	ELII-----AKTTSAPFNNGVA	963		
QY	1091	HHEMKC--PPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSG-----ERRSLL	1143		
Db	964	PAECTCORPSSPEESP-SPRLLSANY-----HPSPERKHSANLDAIIDKRLVL	1010		
QY	1144	SSEGQESQDEESSEEDRASAGSDHHRHSGSLEREAKSSFDLPTLQVPLHRTASGRSS	1203		
Db	1011	-----RNSAPFDR-SPV-SEGDDSRNLNRHA--SLVLPVANGVP-----	1045		
QY	1204	ASEHQDCNGKSASGRRLARTLTDDPQLDGGDDNDEGNLSKGERIQAWVRSL-PACCRER	1262		
Db	1046	-YRRQVRVHSWKASQELKQALAAEEKRNKQN-----TFVRKLLKKTCLHNR	1091		
QY	1263	DSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLVIIFLNCITIAMERPKIDPHSAERIFLT	1322		
Db	1092	TEFSLFLMGPKNPLRIKCLQTTQKKWFDYTVLFFIGINCITLAMEPSPIPDSFQFLH	1151		
QY	1323	LSNYIFTAVFLAEMTVKVVALGWCQGEQAYLRSSWNVLDSLVLISVIDILVSMVSDSGT	1382		
Db	1152	ISGYIFTVFTGEMMK-----	1168		
QY	1383	KILGMLRVLRLLRTLRLPLRVISRAQGLKLVTETLMSILKPIGNIVVICCAFFIIFILGV	1442		
Db	1169	-----VSHRIPILKPIGNIVLICCTFFIIFILGV	1198		
QY	1443	QLFKGKFFVCQGEDTRNITNKSDCAEASR--WVRHKYNFDNLGQALMSLFLVASKDGVV	1500		
Db	1199	QLFKGMMYHCIGPEVGNVTTKADCIE-DYRNKWNHRYNFDNLGQALMSLFLVSSKDGWV	1257		
QY	1501	DIWYDGLDVGVDQOPIMHNHPWMLLYFISFLLVAFVFLNMFVGVVVENFHKCRHQEE	1560		
Db	1258	SIMYQIGIDAVGVDVQPIENYENWRMIYFISFLLVGVFFVFLNMFVGVVVENFHKCEALEK	1317		
QY	1561	EEARRREEKRLRLEKKRRSKEKQMAEAOCK-----PYYSYSRF	1600		
Db	1318	EMREKEKEKRLKR-KLKQKQFEESMAGRKKNRIVWAGSAIKSIFSVERNYPYHYDYGHT	1376		
QY	1601	RLLVHHLCTSHYLDLFTIGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFSVF	1660		
Db	1377	RLFLHGIVTSKYFDLAIAAVIGINVISMAFEMFMMGLKYVLKALNYFFTAVFTLEAAM	1436		
QY	1661	KLVAFAFRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPIIRIMRVLRVARVL	1720		
Db	1437	KLIALGFKRFFIEKWNRLDMFIVILSIAGIIFEEFEA-LELPINPIIRVMRVLRVARVL	1495		
QY	1721	KLKMAVGMRALHTVMOALPOVGNLGLLFLMLFFIFAALGVLEGLDCEHPCDGLG	1780		
Db	1496	KLKMAKGIRSLDVTGEALPOVGNLGLSFLFLFFIFAALGVLEGLDCEHPCDGLG	1555		
QY	1781	RHATFRNFGMAFLTFRVSTGDNWNGIMKDPSPR-DCD-----QESTCYNTVISPIYFVSF	1834		
Db	1556	EHAHFKNFGMAFLTFRVSTGDNWNGIMKDALRDDCCSDHCHETNCCVDPILAPCFFVIF	1615		
QY	1835	VLTAQFVLNVVVIKLVLMKHLEESNKEAKEAELEAE	1870		
Db	1616	VLISQFVLNVVVAVLMKHLEESN---KRDAEGPAE	1648		

RESULT 3

T31092

probable voltage-gated sodium channel - Aiptasia pallida

C;Species: Aiptasia pallida

C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C;Accession: T31092

R;White, G.B.; Pfahnl, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.

submitted to the EMBL Data Library, January 1998

A;Description: Structure of a putative sodium channel from the sea anemone Aiptasia pallida

A;Reference number: Z20975

A;Accession: T31092

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1810 <WHI>

A;Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AA89

C;Genetics:

A;Gene: Nal

C;Superfamily: sodium channel protein

Query Match 14.3%; Score 1720.5; DB 2; Length 1810;

Best Local Similarity 25.8%; Pred. No. 6.2e-101;

Matches 509; Conservative 342; Mismatches 694; Indels 429; Gaps 65;

QY	110	V	C	N	P	W	F	E	R	V	S	M	L	L	N	C	V	T	L	G	M	F	R	P	C	E	D	I	A	C	D	S	Q	R	C	R	I	L	Q	A	F	D	D	F	I	F	A	F	A	V	E	M	V	V	K	M	168																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
Db	110	I	T	N	Q	F	F	E	F	I	L	L	T	I	V	N	C	I	F	L	A	L	-----	R	D	A	P	E	Q	B	E	V	F	A	A	I	Y	T	F	E	M	L	L	K	I	155																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
QY	169	V	A	L	G	-	I	F	G	K	K	C	Y	L	G	D	T	W	N	R	L	D	F	F	I	V	I	A	G	M	L	E	S	L	D	L	Q	N	V	S	F	S	A	V	T	R	V	L	R	P	L	R	A	I	N	R	V	P	227																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
Db	156	I	A	K	L	V	M	H	E	Y	A	L	R	D	P	W	N	L	D	F	V	V	I	L	G	Y	T	L	V	P	N	V	A	N	L	-----	S	G	I	R	I	F	R	V	L	R	A	L	R	T	I	S	A	V	E	213																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
QY	228	S	M	R	I	L	T	L	L	D	T	L	P	M	L	G	N	V	L	L	C	F	F	V	F	I	F	G	I	V	G	V	Q	L	M	A	G	L	L	R	N	C	F	L	P	E	N	F	S	L	P	L	S	V	D	L	287																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
Db	214	G	L	K	T	M	N	A	L	L	K	S	M	K	M	L	S	D	V	L	I	T	T	F	L	C	F	A	L	V	G	M	Q	L	F	V	G	S	L	R	N	K	V	L	K	P	L	N	T	I	D	Y	S	273																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
QY	288	-----	E	P	Y	Q	T	E	N	E	D	E	S	P	I	C	S	Q	P	R	E	N	G	M	R	S	C	R	S	V	P	T	L	R	G	E	G	G	P	P	C	S	L	D	Y	E	T	N	S	S	N	T	343																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
Db	274	P	V	T	N	E	S	H	W	H	H	P	D	T	D	T	P	I	T	C	-----	G	N	S	T	A	G	P	C	P	L	N	Y	-----	306																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
QY	344	T	C	V	N	W	N	Q	Y	T	N	C	S	A	G	E	H	N	P	K	G	A	I	N	F	D	N	I	G	Y	A	I	F	Q	V	I	T	L	E	G	V	D	I	M	Y	F	V	M	D	A	H	S	F	Y	N	403																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
Db	307	T	C	L	-----	A	N	I	G	-	N	N	P	N	Y	G	T	N	L	D	N	F	G	W	A	V	I	T	A	Q	L	V	T	L	D	Y	W	E	N	V	N	Y	V	L	S	M	G	S	W	Y	357																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
QY	404	F	I	F	E	L	L	I	I	V	G	S	F	F	M	I	N	C	L	V	I	A	T	Q	F	S	E	T	K	Q	R	E	S	Q	L	M	R	E	Q	R	V	R	F	L	S	N	A	S	T	L	A	S	F	E	P	G	S	463																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
Db	358	I	F	Y	F	F	M	V	I	F	G	S	F	Y	L	L	N	L	V	L	A	V	A	V	S	Y	-----	Q	Q	E	V	L	A	L	Q	D	R	E	N	Y	N	N	L	K	G	V	A	S	L	Y	S	F	H	G	412																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
QY	464	C	Y	E	E	L	L	K	V	L	V	I	L	R	K	A	R	L	A	Q	V	S	R	A	I	G	V	R	A	G	L	-	L	S	P	V	A	R	S	G	O	E	P	Q	P	S	C	T	R	S	H	R	R	L	S	522																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
Db	413	C	-----	V	V	P	K	L	R	N	S	K	S	T	K	S	L	A	S	K	C	K	M	S	F	C	V	P	C	F	S	I	G	K	O	P	E	H	S	N	G	-----	453																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
QY	523	V	H	L	V	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H

Db 1552 VTEIAETNNFINLS-----FLRLFRAARLIKLRQGYTIRILLTWTFFVQSPKALPYV 1602

QY 1747 GLLEMLLFFIFAALGVLEFGLCEDETHPCBGLGRHATFRNFGMAFLTLFRVSTGDNWNG 1806

Db 1603 CLLIAMLFFIYAIIGMQVFGNIALDDD---TSINRHNNFRFTLOALMLLFRSATGEAWHE 1659

QY 1807 IMKD--PSRCDQE--STCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHEENKEAK 1862

Db 1660 IMLSCLSNQACDEQANATECGSDFAFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS 1719

QY 1863 -----EEAELEAELE-----LEM-KTSLSPQPHSPLG-----SPFLWPGV 1895

Db 1720 ILGPHHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMS?-----PLGLGKKCPARVAYKRL 1775

QY 1896 EGVNSTDSPKGPAPHTTAHIGAASGFSLE-----HPTMVPHPEEVPV----- 1937

Db 1776 VRNMPIISNEDMTVHFTSTLMALIRTALEIKLAPAQTKHQCDAEHLKEISVVWANLPQK 1835

QY 1938 -----PLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAESLHGRGWGLPKAQSGSIL 1990

Db 1836 TLDLLVPPHKPDENTVGKVYAA---LMIEDFY--KQKTTTRDQMQAAPGGL--SQMGPV 1888

QY 1991 SVH-----SQPA-----DTSCILQ-----LPKDVHYLLQ-----P 2015

Db 1889 LFHPLKATLEQTQPAVLRGARVFLRKQSTSLNGGAIQNESGIKESVSWQTQTDAP 1948

QY 2016 HGAPTWGAIPKLPPGGRSPLAQRPLRRQAAIRTDSDVQ-----GLGSRE 2060

Db 1949 HEA-----RPPLERGHSTEIPVGRSGAL---AVDVQMOSITRRQDDQEPQPGLESQ 1997

QY 2061 DLLS--EVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDP 2118

Db 1998 RAASMPRLAAETQPTVDASPMKRSISTLAQPRG-----THLCSTTP-----DRPP 2043

QY 2119 PETRS-----SLELDTLSWISGDLPLSSQEEPLFP-----RDL 2152

Db 2044 PSQASSHHHHRRCHRRDRKQSRLEKGPSSL-ADMDGAPSSAVGPGLPGEQPTQCRRE 2102

QY 2153 KKCVSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGSPRLCPSPS----- 2197

Db 2103 ERRQERGRSQERRQPSSSSEKQRF---YSCDRFGGRHPPKPKPSLSSHPTSTAGQEPG 2159

QY 2198 -----SLGGQPL-----GGGSR---PKKLSLSP-PSIS-----IDPPESQGS 2230

Db 2160 PHPOGSGSVNGSPLLSTSGASTPGRGQRRQLPQTPLTPRPSITYKTANSSPIHFAQAQTS 2219

QY 2231 RPPCSPG-----VCLRRRAPASD-----SKDPSVSSPLDSTAASPSPKKDTLS 2273

Db 2220 LPAFSPGRSLRGLSEHNALLQRLDPLSQPLAPGRIGSDPYLQORLDSEASVHALPEDILT 2279

QY 2274 L-----SGLSS 2279

Db 2280 FEEAVATNSGRSS 2292

RESULT 5

S29236

calcium channel protein BII-1, brain - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S29236

R;Niidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.

FEBS Lett. 308, 7-13, 1992

A;Title: Molecular cloning and characterization of a novel calcium channel from rabbit b

A;Reference number: S29236; MUID:92354772; PMID:1379552

A;Accession: S29236

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2259 <NII>

A;Cross-references: UNIPROT:Q02343; EMBL:X67855; NID:g1472; PIDN:CAA48040.1; PID:g1473

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C;Keywords: transmembrane protein

Query Match 13.8%; Score 1665.5; DB 2; Length 2259;

Best Local Similarity 23.8%; Pred. No. 2.6e-97;

Matches 606; Conservative 379; Mismatches 844; Indels 719; Gaps 87;

QY 62 GAAGAGSTEKDPGSADS--EAEGLPYPALA-----PV----- 91

Db 5 GEAAAGRPASGESGDSQGRNLPCTVPVPASGAAAYKQSKAQRARTMALYNPIPVQNCFT 64

QY 92 ---VFFYLSQDSRPRSWCLRTVCNPFWRVSMVLVILLNCVLTGMFR--PCEDIACDQRC 146

Db 65 VNRSFIPEGEDNIVRYAKKLIDWPPFEYMLATIIANCIVLALEQHLPEDDDKTPWSRR- 123

QY 147 RILQAFDDFIFAFFAVEMVMVMVALG-IFGKKCYLGDWTNRDLDFEIVIAGMLEYSLLDQN 205

Db 124 --LEKTEPYFIGIFCFEAGIKIVALGFIHKGSYLRNGWNVNDPIVVLGILATAGTFN 181

QY 206 --VSFSAVRTVRVLRLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFIGVGVQ 263

Db 182 THVDLRTLRAVRVLRLKLVSGIPSLQIVLKSIMKAMVPLQLGLLFFAILMFAIIGLE 241

QY 264 LWAGLLNRCLPENFSLPLSVDLEPYQTENEDESPFICSPRENGMRSCRSVPTLRGE 323

Db 242 FYSGLHRACFVNN-----SGVLEGF-----DPPHPC----- 268

QY 324 GGGGPPCSLDYETINSSNTTCVNNQYVYNCISAGEHNPKGAINPDNIGYAWIAIFQVI 383

Db 269 --GVQGCAPGYE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCI 306

QY 384 TLEGVVDIMYFVMDA-HSFYNIYFIYILLIIVGSFFMINCLVVIATOFSETKQRESQLMR 442

Db 307 TMEGWTTVLYNTNDALGATWNWLYFIPLIIGSFFVLNLVLGVLGSGEFAKERERV--- 361

QY 443 EQVRFLSNASTLASFSPEGSCYEELLYLVILRKAARRLAQVSRAT-GVRAGLLSSPV 501

Db 362 ENRRAFMK-----LRRQQIERELNGYRAWIDKAAE 392

QY 502 ARSQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGS 561

Db 393 VMLAEBENKNSGTSALEVLRAT-----IKRSRTAMTRDSS-- 428

QY 562 RRLMLPPPSTPTSPGGPPRGAESVHSFYHADCHLEBPVRCQAPPRCPSEASGRTVSGKV 621

Db 429 -----DEHCVDIS-----S 437

QY 682 ISSPCSKADSGACGPDSCPYCARTGAGEPESADHVPDSDSEAVYEFTQDAQHSDLRDPH 741

Db 438 VGTPLARASIKSAKVDGASY-----FRHKE----- 462

QY 742 SRRRQORSLGDAEPSSVLAFWRLLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQP 801

Db 463 -----RLLRISVRHAVKSQVYWIIVLSLVALNTACVAIVHNQP 501

QY 802 EELTNALIEISNIVFTSLFALEMLKLIVYGPFGYIKNPYNITFDGVIVVISVWEIVGQ--- 858

Db 502 QWLTHLLYYAEFLFLGLFLEMSLKMVGMPRLYFHSSFCDFGVTVGSIFEVVAIFR 561

QY 859 --QGGGLSVLRTFRIMRVLKLVRFLPALQRLVLMKTMNDNVATFCMLLMFLIFIFSLG 916

Db 562 PGTSFGISVLRALRLRIFKITKYWASLRNLVLSMSSMKSIISLLFLFLFVVFALLG 621

QY 917 MHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKVLNGM-----ASTSS 971

Db 622 MQLFGGRF-NFNDG--TPSANFDTFPPAINTVFQILTGEDWNWYNGIRSQGVSSGM 677

QY 972 WAALYFIALMTFGNVVLENLLVAILVEGFAEGDATKSE-SEPDPFS----- 1017

Db 678 WSAVYFIVLTLFGNYTLNVLNVLAIAVDNLANAQELTKDEQEEEEAFNQKHALQKAKEVSP 737

QY 1018 -----PSVDGDGDRKKRLAL-----VALGEHAEL 1041

QY	331	SLDYETYNSSNTTTCVNWNQYNTNCSAGEHNPPKGA	INFDNIGYAWIAIFQVITLEGWVD	390	Db	1105	ETKEEEVEKKKKQKKEKRETKGAMVPHSSMEIFST	NTNPIRRACHYIVNLRYPFEMCILL	1164				
Db	275	PAGYE-----CKDW-----	IGPNDGITQFDNILFAVLTVFQCITMEGWTT	314	QY	1296	IIFMNCITIAMERP	KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRS	1355				
QY	391	IMYFVMDA-HSFYNFIYFILLIIVGSFFMINLCLVVIATQFSETKQRESQOLMREQVRFL	449	Db	1165	VIAASSIALAAEDPVL	TNSERNKV-LRYFDYVFTGVTPEMVIK	MIDQGLJLQDGSYFRD	1223				
Db	315	VLYNTNDALGATWNWLYFIPLIIGSFFVLNLVLGVLGSEFAKERERV-----ENRRAFM	369	QY	1356	SNWLDGLLVLSVIDI-LVSMVSDSGTKILGMLRVLRLTLRPLRVISRAQGLKLWVE	1414	Db	1224	LWNILDFVVVVGALVAFALANALGNTKGRDIKTIKSLRVLRLPLKTIKRLPKLKA	1283		
QY	450	SNASTLASFSEPGSCYBELLKYLVIILRKAARLAQVSRAL-GVRAGLLSSPVARSQEP	508	Db	1415	TLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVC-QGEDTRN-----ITNKS	1466	QY	1284	CVVTSLKNVENILIVYKLFMFIFAVIAVQLFKGKFFYCTDSSKDTEKECIGNYVDHEKNK	1343		
Db	370	K-----LRRQQIERELNGYRAWIDKAEVWMAEEN	400	QY	1467	AEASYR-WVRHKYNFDNLGOALMSLFLVASKDGWVDIMYDGLDAVGVDQQPIMNHNPMWL	1525	Db	1344	MEVKGREWKREHFDYDNI	1403		
QY	509	QPSGCTRSHRRLSVHHLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRLMLPP	568	QY	1526	LYFISFLLIIVAFFVLNMFVVVENFHKCRQHQBEEERREKRLRLEKKRRSKEKQM	1585	Db	1404	IFYVYFVVVFPFFVFNIFVALIITF-----QE	1453		
Db	401	KNSGTSALVLRAT-----IKRSRT	429	QY	1586	ABEQCKPYYSYDSR--FRLLVHHLCTSHYLDL	FITGVIGLNVVTMAMEHYQQPQILDEAL	1643	Db	1454	ISAKPLTRYMPQNRHTFYQYRVWHFVVVSPSEFYTIMAMIALNTVVLMMKYTAPCTYELAL	1513	
QY	569	PSTPTSGGPPRGABSVHSFYHADCHLEPVCQAPPPRCPSEASGRTVSGKVYPTVHTS	628	QY	1644	KICNYIFTVIVFVESVFKLVAFARFRFPQDRWNQDLDAIVLLSIMGITLEEIEVNLSLPI	1703	Db	1514	KYLNIATMVFSLECVLKVIAFGFLNYFRDFTW	1573		
Db	430	-----DEHCVDIS-----SVGTPLAR	445	QY	1704	NPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPOVGNLGLLFFMLFFIFAALGVE	1763	Db	1574	NMSFLKLFR--ARLIKLLRQGYTIRILLWTFVQSF	1630		
QY	629	PPPEILKOKALVEVAPSPGPPTLT	TSFNIPGPFSSMHKLLTQSTGACHSSCKISSPCSK	688	QY	1764	LFQDLECD-ETHPC	EGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD--PSRDCDQEST	1820	Db	1631	VFGNIKLDEESH---INRHNFRSFFGSLMLLFRSATGEAWQEI	1686
Db	430	-----DEHCVDIS-----SVGTPLAR	445	QY	1821	C-----YNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAK-----E	1863	Db	1687	APSGQNESERCGTDLAYVYFVSFIFFC	1746		
QY	689	ADSGACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRS	748	QY	1864	EAELEAELE-----LEMKTL-SPQPHSPLG-----SPFLWPGEVGNSTDSP	1904	Db	1747	FVRVWAEYDRAACGRIHYTEMYLEMTLMSP---	1797		
Db	446	ASIKSTKVDGASY-----FRHKE-----	463	QY	1905	KPGAPHTTAH-----IGAASG-----FSLEHPTMV--PHPEE-----	1934	Db	1798	MPVAEDMTVHFTSTLMALIRTALDIKIAKGGAD	1857		
QY	749	LGPDAEPSSVLAFWRLLCDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNAL	808	QY	1935	VPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGST	AERSLGHGWLPKAQSGSILSVHS	1994	Db	1858	VPMPKASD-LTVGKIYAA---MMIMDYKQSKVKKQ	1905	
Db	464	-----RLLRISIRHMVKSQVYFVIVLSVVALNTACVAIVHHNQOWLTHLL	509	QY	1995	QPADTSCILQLPKDV-----HYLLQPHGAPT	WGAIKPLPPGRSPLAQRPLRROAIR	2047	Db	1906	EPS-----SLPQEI	1955	
QY	809	EISNIVFTSLFALEMLKLLVYGPFGYIKNPYNIPDGVIVVISWEIVGQ-----QGGGL	863	QY	2048	TDSLDVQGLSREDLLSEVSGPSCPL-----TRSSSF	2080	Db	1956	DPADDGQFQEQQSLV--VTDPSMRRSFSTIR	2012		
Db	510	YYABFLGLFLLEMSLKMVMGPRLYFHSSFCNCFDGVTVGSIFEVWVAFRPGTSFGI	569	QY	2081	GGSSIQVQ-----QRSG-----IQSKVSKH	IRLP-APC-----PGLPFSW-	2114	Db	2013	SYHSSLRLSAHRLNSDSGHKSDTHRS	2072	
QY	864	SVLRTFRLMRVLKLVRFLPALQRLVVLKTMNDNVATECMLLMFLFIFISILGMHLFGCK	923	QY	2115	-----AKDPPE	TRSSLELDTLSWISGDLPLSSQEEPLFP	PRDLKKCYSVETQSCRRRPG	2168	Db	2073	SPERRQSRSPSEGRSQTNRQGTGSLSESI	2129
Db	570	SVLRALRLRIFKITKYWASLRNLVLSLMSMKSIISLLFLFLFIVVFPALLGMQLFGGR	629	QY	2169	FWLDEQRRHSIAVSCLDGSGQPRLCPS	SPSSILGGQPLGGGSRPRKKK-LSPPSISIDPPES	2227	QY				
QY	924	FASERDGTLPDRKNFDSLWAIWTVVFQILTQEDWNKVLYNGM-----ASTSSWAALYFI	978	QY									
Db	630	F-NFNDG---TPSANEDT	FPAAIMTVFQILTGEDWNEVYNGIRSQGGVSSGMMWSAIYFI	685	QY								
QY	979	ALMTFGNYVLNLLVAILVEGFAEGDATKSE-SEPDEFS-----P	1018	QY									
Db	686	VLTLFGNYTLNLVFLAIAVDNLANAQELTKDEQEEEAEPNQKHALQKAEVSPMSAPNMP	745	QY									
QY	1019	SVDGDGDKRKLAL-----VALGEHAELRKSLLPP	1048	QY									
Db	746	SIERDRRRRHMSWMEPRSSHLRERRRRHHMSVWEQRTSOLRRHMQMSQAEALNKEEAPP	805	QY									
QY	1049	LIHTAATPMS-----HP---KSSSTGVGEALGSGRRRTSSSGSAEPGAAHHEMKCPP	1098	QY									
Db	806	MNPLNPLNPLNPLNAHPSLYRRPRPIEGLALGLGKCEERISRGGSLKGDIGGLT	865	QY									
QY	1099	SARSSPHSPWSAAS---SW-----TSRRSSRNSLGR	1126	QY									
Db	866	SALDNQRSPLSLCKREPPWLP	PRSCHGNCDPIQEQAGGETVTVTFEDRARHRQSQR	925	QY								
QY	1127	APSLKRRSPSGERRSLLSGEGQESQDEESSEEDRAS	PAGSDHHRGSLEREAKSSFDL-	1185	QY								
Db	926	RVRTEGKOSASGRS-RSASQERSLDEGVSGEKEHEP	HSRSHRSKEPTIHEERTQDLR	984	QY								
QY	1186	-PDTLOVP---GL-----HRTASGRSSASEHQDCN	GKSASGRL-----1219	QY									
Db	985	RTNSLMVPRGSLVGALDEAETPLVQPOPELEV	GKDAALTEQEAEGSSEQALLGDVQLDV	1044	QY								
QY	1220	-----ARTLRTD-----DPQLD-----GDDND	EGNLSKG	1244	QY								
Db	1045	GRGISQSEPDLSMTANMDKATTESTSVTVAIPDV	DLVDSTVNVINSKTDGEASPLKEA	1104	QY								
QY	1245	E--RIQAWVRSRLPACCRERDSWA-----YIFPPQSR	FRLLCHRIITHKMFHDVVVLV	1295									

Db 2130 LSYSLMRHTGGISPPDGSE-----GGSPLASQALSNACLTSSNSLHPQQG 2179

QY 2228 QGSRPP---CSPGVCLRRRAPASD 2248

Db 2180 QHPSPQHYISEPYLALHEDSHASD 2203

RESULT 7

T43262

calcium channel alpha-1 chain, L-type - Stylophora pistillata

C;Species: Stylophora pistillata

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T43262

R;Zoccola, D.; Tambutte, E.; Senegas-Balas, F.; Michiels, J.F.; Failla, J.P.; Jaubert, J

Gene 227, 157-167, 1999

A;Title: Cloning of a calcium channel alpha1 subunit from the reef-building coral, Stylo

A;Reference number: Z22375; MUID:99148007; PMID:10023047

A;Accession: T43262

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1891 <ZOC>

A;Cross-references: UNIPROT:O97017; EMBL:U64465; NID:g4204977; PID:g4204978; PIDN:AAD114

C;Genetics:

A;Gene: CACHL

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.7%; Score 1652.5; DB 2; Length 1891;

Best Local Similarity 24.8%; Pred. No. 1.4e-96;

Matches 523; Conservative 331; Mismatches 623; Indels 633; Gaps 60;

QY 115 PERVSMVLVILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIF-AFFAEMVVMKVALG- 172

Db 83 FDMVILITIFANCAALAEPLPE--KDSSEINDLEVAEYVFLAVFTMEAVLKIIAYGF 140

QY 173 IFGKKCYLGDWTNRLLDFFVIAG---MLEYSLDLQNVSFSAVRTVRLRPLRAINRVPS 228

Db 141 LFHPGAYLRNGWNILDFVIVVGLATILVKATLSGSPDVKALRAFRVLRPLRLVSGVPS 200

QY 229 MRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLE 288

Db 201 LQVNLNIIKALIPLEHIALLVFVVIYAIIGVELFMRLHKTCT--DNVTGAESFE-E 257

QY 289 PYYQTENEDESPFICQPRENGMRSCRSVPTLRGEGGGPPCSDYETVNSSNTTCVNV 348

Db 258 PH-----PCS-----SGSSGFQCDKA 273

QY 349 NQYNTCSAGEHNPFKAINFDNIGYAWIAIPQVITLEGWVDIMVFVMDA-HSFYNFIYF 407

Db 274 AGQV--CEGWKGNHIGITNFDNIGLACMTVPQCITLEGWTDVLYWINDAVGNSWPWYF 331

QY 408 ILLIIVGSFFMINCLVVIATQFSETKQ-----ESQLMREQR-----VRFLSNAS 453

Db 332 VTLLIIGSFFVLNLVLGVLGSEFAKEKARRQKSGEFQKREKQVEDAYNGYLDWITQAE 391

QY 454 TLASFSEPGSCYEELLKYLIVYLKAAARLAQVSRAGVRAGLLSSPVARSGQEPQPSGS 513

Db 392 DIEGDSESESGDES-----KASKK-----TSSRQSR-----EDIEM 423

QY 514 CTRSHRRLSVHHLVHHHHHHHHHHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTPT 573

Db 424 IDRNERQDSI-----SQHDTHY-----

QY 574 PSGGPPRGAEVSHFYHADCHLEPVRCAQPPRCPCSEASGRTVSGKVYPTVHTSPPEI 633

Db 442 -----

QY 634 LKDKALVEAPSPGPTLTSTFNIIPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGA 693

Db 442 -----GWCHNEKKV-----

QY 694 CGPDCPYCARTGAGEPESADHVMFSDSEAVYEFTQDAQHSDLRDPHSRRRQSLGPDA 753

Db 451 -----LKKWHHRQTE----- 461

QY 754 EPSSVLAFWRLLCDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 813

Db 462 -----LRKAVKTAQFYWIVVVFVFLNSLTALAEHYDQPDWLTCKFLDIANK 506

QY 814 VFTSLFALEMLLKLIVYGPFGYIKPNYNIFDGVIVV-----ISVWEIVQQGGGLSVLRT 868

Db 507 LFLGIFTIEMIVKMYCLGFHGYFASLFRNFDCLVVISSLELAITEALKQPPIGISVLRC 566

QY 869 FRLMRVLKLVRFPLPALQRLVLMKMDNVATFCMLLMFLTIFISILGMHLFGCKFASER 928

Db 567 IRLLRIFKVTTRYWSSLSNLVASLLNSMRSTIAGLLLLSLFLMLICSLLMQIFGGKF--NT 624

QY 929 DGDTPDKNFDSSLWAIIVTVFQILTQEDWNKVLYNGMAS-----TSSWAALYFTALM 981

Db 625 DDDEIP-RSNFDSFWRALITVFQILTGEDWNAVYDGIKAWGGIGEGGSAIALYFIFLV 683

QY 982 TFGNYVLENLVAILVEGFAEGDATKSESEPDPFFSPVDGDRKKRLALVALGEHAEL 1041

Db 684 VVGNYILLNVFLAIAVDNLADAENLTEMEE-----KSKKK-----EKARE 724

QY 1042 RKSLPLLIHTAATPMSPKSSSTGVGEALGSGSRRTSSSGSAEPGAHHMKCPPSAR 1101

Db 725 KEAL-----KMGSVDSQG-----RIDQGAIVPN----- 749

QY 1102 SSPSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESESSEDR 1161

Db 750 ---HS-----SASRSNVTLDKSTQELHSTG----- 771

QY 1162 ASPAGSDHRHRGSLEREAKSSFDLPTLQVPGHRTASGRSSASEHQDCNGKSASGLAR 1221

Db 772 -----TLNGGVARTAS-----HDDVEAQS----- 791

QY 1222 TLRTDDPQLDG-----DDNDEGNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRF 1276

Db 792 ---TDISEIVGSKSAVSNNESASASSDDID--RAPMP-----PESALFIFSPTNIF 839

QY 1277 RLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPDKIDPHSAERIFLTLNFIYTAFLAEM 1336

Db 840 RVVCYKIATNTYFVNFILCLIIIVSSILLAAEDP-LNASAKRNQVLNVDYFFTSVFTFEI 898

QY 1337 TVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRLVRLLR 1396

Db 899 LVKFISYGLILHKGSCFSAFNLLDLLVSVSVISISLR-----TSQFSVVRILRLVR 952

QY 1397 LRPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGED 1456

Db 953 LRPLRAINRAKGLKHVVQSVFVAVKTIKNTKMLFQFLFAVIGVQLFKGTFFSCNDE- 1011

QY 1457 TRNITNKSDCAEASY-----RWRHKYNFDNLQALMSLVFLASKDGV 1500

Db 1012 --KILTAEEC-QGNYIDFKGPGLSNPVVKERWRRRHDFNDVGNAMTLFTVMTFEGWP 1068

QY 1501 DIMYDGLDAVGVDQPIPMNHNPMWLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQEE 1560

Db 1069 GILENSIDSTEVDKGPNNRNPWVAIYIYIIIIAFEMVNI FGVIVTF----- 1119

QY 1561 EEARREKRLRLLEKRRSKEKQMAEAOCKPYYSYDSYFRLLVHLLCTSHYDLFITGV 1620

Db 1120 -QSEGREEFKGCELDKNQRCIEFALKAKPLKRYIPENRLOPHIWPVVTQAFFEYLIFAF 1178

QY 1621 IGLNVVTMAHEHYQOQIILDEALKICNYIFTVIFVFESVFKLVAFARRFFQDRWNQDL 1680

Db 1179 IVCNTVVLMMQYQEPKLYTRVLDGFNIGFTAVFLLECILKLIAPKKNYFTDRWNLDF 1238

QY 1681 AIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIARVLKLLKMAVGMRLHTVM--- 1737

Db 1239 IIVVGSIIIDITMNEVSSEQMFAFG-----FFRLFRALRLVLLNQSGIKTLWTFKSF 1293

QY 1738 QALPQVGNLGLLFFLFFIFAALGVLEFGDLECDETHPCPEGLGRHATFRNFGMAFLTFR 1797

Db 1294 QALPYV---ALLIVMMFFIYAVIGMQMFGRIANSD---TAINRNNNFQTFPQSLMVLFR 1347

QY	1798	VSTGDNWNGIMK-----DPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVVI	1847
Db	1348	SATGENWQIMLACTHRDDVKCDQADPQEPGLGSEFAFYFVSFYSICSFLINLFV	1407
QY	1848	AVLMKHLFESNKEAEAELEAEMKTLSPQPHSPGLSPFLMPGVEGVNSTDSPKPG	1907
Db	1408	AVIMDNFDYLTRD-----WSILGPHHL---DEYVRVWSEYDDP	1442
QY	1908	APHTTAHIGASGFSLEHPTM-----VPHPEE---VPVPLGPDLLTVRKSGV-----	1951
Db	1443	AHGCVKHVDIVTVLKRIAPPLGFGKFCFHREACKRLVTWNG-----LTKDGMVDFNATL	1497
QY	1952	-----SRTHSLPNDSYMCRNGSTAERSLHRGWGLPKAQSGSLSVHSQPADTSCILQL	2005
Db	1498	FGLIRSSLNIRPEGKSIDKANEEVRNIIIRW--PKT-SMELLDKVVQPSGVRDDVTV	1554
QY	2006	PK-DVHYLLQ-----PHGAPTGAIPKLPP-PGRSPLAQRLRRQAA	2045
Db	1555	GKFYATYLIQYFRFRPKARQKAQNAQNEPHGNSTMALQAGRLTLHGLGPQLRRRAISGQLG	1614
QY	2046	I-----RTDSDLVQGLGSREDLLSEVS-GPSCPLTRSSSF-----WGGSSIQVQQ	2089
Db	1615	SDDDELFLKEDDSQKAHDKGFWESLKSAVSVSPRHSFRSSASRLSAFLGKNGSGLETCK	1674
QY	2090	RSGLQSKVSK	2099
Db	1675	KSSSMNLSE	1684
RESULT 8			
S29237			
calcium channel protein BII-2, brain - rabbit			
C:Species: Oryctolagus cuniculus (domestic rabbit)			
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004			
C:Accession: S29237			
R:Niidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.			
FEBS Lett. 308, 7-13, 1992			
A:Title: Molecular cloning and characterization of a novel calcium channel from rabbit b			
A:Reference number: S29236; MUID:92354772; PMID:1379552			
A:Accession: S29237			
A>Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-2178 <NII>			
A:Cross-references: UNIPROT:Q02343; EMBL:X67856; NID:g1474; PIDN:CAA48041.1; PID:g1475			
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain			
C:Keywords: transmembrane protein			
Query Match 13.7%; Score 1652.5; DB 2; Length 2178;			
Best Local Similarity 23.8%; Pred. No. 1.7e-96;			
Matches 601; Conservative 376; Mismatches 850; Indels 699; Gaps 83;			
QY	62	GAAGAGSTEKDPGSADS--EAEGLPYPALA-----PV-----	91
Db	5	GEAAAGRPASGEGSDQGRNLPGTVPFASGSAAYKQSKAQRARTMALNPVPRQNCFT	64
QY	92	---VFFYLSQDSRPRSWCLRTVCNPFERVSMLVILLNCVTLGMR--PCEDIAQDSQRC	146
Db	65	VNRSLFIFGEDNIVRKYAKKLIDWPPFEYMIATIIANCIVLALEQHLPEDDKTPMSRR-	123
QY	147	RILQAFDDFFIAFFAVEMVVKMVALG-IFGKKCYLGDWTNRLLDFFIVIAGMLEYSLDLQN	205
Db	124	--LEKTEPYFIFGFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVVLSGILATAGTFN	181
QY	206	--VSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQ	263
Db	182	THVDLRTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLQLIGLLFFAILMFAIIGLE	241
QY	264	LWAGLLNRNCFLENFSLPSVDLEPYQYOTENEDESPFICSQPRENGMRSCRSVPTLRGE	323
Db	242	FYSGKLHRACFVNN-----SGVLEGF-----DPFHPC-----	268
QY	324	GGGGPPCSLDYETYNSNTTCVNNQYNTNCSAGEHNPFGKAINFDNIGYAWIAIQVI	383

Db	269	--GVQCPAGYE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCI	306
QY	384	TLEGWVDIMYFVMDA-HSFVNIYFIILLIIVGSEFFMINCLVVIATQFSETKQRESQLMR	442
Db	307	TMEGTTVLYNTNDALGATWNWLYFIPLIIIGSFFVLNLVGLSGEFAKERERV-----	361
QY	443	EQRVRFLSNASTLASFSEPGSCVEELLKYLVIILKAARLAQVSRAI-GVRAGLLSSPV	501
Db	362	ENRRAFMK-----LRRQQIERELNGYRAWIDKAE	392
QY	502	ARSGQEPQSGSCTSRHRLSVHHLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGS	561
Db	393	VMLAEENKNSGTSALEVLRAT-----IKRSRTEAMTRDSS--	428
QY	562	RRLMLPPPSTPTSPGGPPRGAESVHSFYHADCHLEPVRCAQAPPRCPSEASGRTVGSCKV	621
Db	429	-----	428
QY	622	YPTVHTSPPEILKDKALVEVAPSPGPPTLTSTFNIPPGPFSSMHKLLTQSTGACHSSCK	681
Db	429	-----DEHCVDIS-----S	437
QY	682	ISSPCSKADSGACGPDSCPYCARTGAGEBESADHVPDSDSEAVYEFTQDAQHSDLRDPH	741
Db	438	VGTPLARASIKSAKVDGASY-----FRHKE-----	462
QY	742	SRRRQSLGPDAPESPVLAFWRLICDTRFKIVDSKYFGRGIMIALIVNLTSLMGIEYHEQP	801
Db	463	-----RLLRISVRHAVKSQVFIWIVLSVALNTACVAIVHNQP	501
QY	802	EELTNALEISNIVFTSLFALEMLLKLLVYGPPIKPNYPNIFDGVIVVISVWEIVGQ---	858
Db	502	QWLTHLLYYAEFLFLGLFLEMSLKMYGMGRPLYFHSSFCDFGTVGSIFFVWAIFR	561
QY	859	--QGGGLSVLRTFRLMRVLKLVFLPALQRLVVLMTMDNVATFCMLLMFIFIFISILG	916
Db	562	PGTSFGISVLRALRLRIPKITKYWASLRNLVLSLSSMKSIISLLFLFLFIWVFALLG	621
QY	917	MHLPGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKVLYNGM-----ASTSS	971
Db	622	MLFGGRF-NFNDG---TPSANFDTFPAIIMTVFQILTGEDWNEVMYNGIRSQGVSSGM	677
QY	972	WAALYFIALMTFGNYVLFNLVAILVEGFAEGDATKSE-SEPDFS-----	1017
Db	678	WSAVYFIVTLTFGNYTLNLNVELAIAVDNLANAQELTKDEQEEEAFAFNQKHALOKAVEVSP	737
QY	1018	-----PSVDGDGDRKKRLAL-----VALGEHAEL	1041
Db	738	MSAPNVPSIERDRRRHHMSWEPRSSHLRERRRRHHMSVWEQRTSQLRRHQSSQEAL	797
QY	1042	RKSLPLPLIHTAATPMS--HPKSSSTGV-----GEALGSGSRRTSSSGSAEPGAHHE	1093
Db	798	NKEEAPPNPLNPLNPLSPLNPLNAHPSLYRRPRRMEGLALGLEKCEEEHVSRGGSILKA	857
QY	1094	MKCPPS-----ARSSPHSPWSA-----ASSWT-----SRRSRNSLGR	1126
Db	858	LDCQSPSLGRREP--PWLARPCHGNCEPALQETAGETVTVTFEDRARHRQSRRSRHR	915
QY	1127	APSLKRRSPSGHRRSLLSGEQESQDEEESSEEDRASPGSDHRRGS-----LEFE	1178
Db	916	RVRTEAKESSSASRS-----RSVQSERSLDEGASTEGEDHEARGSHGGKEPTIHEEE	968
QY	1179	AKSFDLPDLTQVP-----GLHRTAS-----GRSSASEHQDCNGKSASGRL--	1219
Db	969	RAQDLRRTDSLMVPKSGLAGGLDEAGTPLVLSPEGVGKEAAFTQHADGSGGEPALLGH	1028
QY	1220	-----ARTLRDTPDL-----DGDNDNDE-----GNLSKGE--	1245
Db	1029	VQLDVGRAISQSEPDLSCVTATTDKVTTESTDVTVAIPDAEPLVDSVTVHIGNKTDGEAS	1088
QY	1246	-----RIQAWVRSLPACCRERDSWA-YIPPPQSRFRLLCHRIITHKMFHDV	1292
Db	1089	PQEAEMKEAEQETEKQKKERPASGKAMVPHSSMFIFTSNPIRRACHYVNVNLYFEMC	1148

QY 737 LRDPHSRRQRSLGPDAPSSVLAFWRLLCDTFRKIVDSKYFGRGIMIAILVNTLSMGIE 796
Db 465 -----RRKEK-----MREFF-----IRRMVKAQSFYVWVLCVVALNTLCVAMV 502
QY 797 YHEQPEELTNALIEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIV 856
Db 503 HYNQPORLTTALYFAEFVFLGLFLEMSLKMVGLGPRSYFRSSFNCFDFGVIVGSIPEVV 562
QY 857 GQ-----QGGGLSVLRTFRLMRVLKLVRFPLPALORQLVVLMTMDNVATFCMLLMLEFI 911
Db 563 WAAIKPGTSFGISVLRALRLRIFKVTKYWNSLRNLVSLNSMKSIISLLFLFLFIVV 622
QY 912 FSILGMHLFGCKFASERDGDTLPLDRKNFDSILLWAIIVTFQILTQEDWNKVLYNGM----- 966
Db 623 FALLGMQLFGGQNFQDETPT---TIFDTFPAAILTVFQILTBEDWNAVMYHGIESQGG 678
QY 967 ASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFFSPSVDGDGR 1026
Db 679 VSKGMFSSFYFIVLTLFGNYTLLNVFLAIVDNLANAQELTKDEEEMEEAA----- 729
QY 1027 KKRLALVALGEHAELRKSLPLPPLIIHTAATPMSPKSSSTGVGEALGSGSR----- 1077
Db 730 NQKLALQAKEVAE-----VSPMSAANISIAAQNSAKARSVWEQASQLRLQNLRASCE 784
QY 1078 -----RTSSGSAEPGAHH-----EMKCPPSARSSPHSPWSAASS 1113
Db 785 ALYSEMDPEERLRYASTHRVRPDMKTHMDRPLVVEPRDGLRGPVGSKSKEGTEATESA 844
QY 1114 WTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGESQDEEESSEEDRASP-----A 1165
Db 845 DLPRRHRHR--DRDKTSATAPAG-----GEQDRTESTETGPREERARPRRSHSKETP 895
QY 1166 GSD-----HRRHRSLE----- 1176
Db 896 GADTVRCERSRRHRRGSPPEATEREPRCHRAHRHAQDSSKEGTVPLVPKGERRARHR 955
QY 1177 -----REAKSSFD-----LPDTLQVPLGHLRTAS-----GRSSASEHQDCNG 1212
Db 956 GPRTGPRAENNEEPTRRHRARHKVPPTLOPP--ERAAEKESNPVEGDKETRHNQKPEP 1013
QY 1213 KSASGRLART-----LRTDDPQLDGDND----- 1237
Db 1014 HCDLEAIAVTDVGPLHMLPSTCLQKVDEQPEDADNQNVTRMGSQSPDSPSTTVHVPVTLT 1073
QY 1238 -----EGNL-----SKGER-----IQAWVRSRLPACCRERDSWSAYIFPPQSR 1275
Db 1074 GPPGETPVVPSGNMNLGQAEKGKAEADVDLRRGRPRIVPYS-----SMFCLSPTNL 1126
QY 1276 FRLLCRRITTHKMFHDVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAE 1335
Db 1127 FRRECHYIVTMRYLEMVILVIALSSIALAAEDP--VRTDSPENNALEYMDYIFTGVFTCE 1185
QY 1336 MTKVKVALGWCFGQAYLRSSWNVLGGLVLISVIDILVSMV--SDSGTKILGMLRVLRL 1394
Db 1186 MVIKIMIDLGLLHPGAYFRDLWNILD----FIVVSGALVAFAPSGSKGKDINTIKSLRVL 1241
QY 1395 RTLRLRVISRAOGLKLVVETLMSSSLKPIGNIWICCAFFIIFGILGVQLFKGKFFVCQG 1454
Db 1242 RVLRLPKTIKRLPKLPVDSVNSLKNVLNLIIVMLFMFIFAVIAVQLFKGKFFYCTD 1301
QY 1455 E-----DTRN--ITNKSDCAEASYR--WVRHKYNFDNLGQALMSLVFLASKDGMVDIMYD 1505
Db 1302 ESKELERDCRGQYLDYEKEEVEAQPROWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKH 1361
QY 1506 GLDAVGVDQQPIMNHNPMWMLLYFISFLLIIVAFVFLNMVGVVVVENFHKCRHQHEEEARR 1565
Db 1362 SVDATYEEQGPSGPFERMELSILYVVYFVVPFFVFNIFVALIITP-----QEQQDKUM 1415
QY 1566 REEKRLRLEKKRRSKBKQMAEAQCKPYYSYSR--FRLLVHLCTSHYLDLFTITGVIGL 1623
Db 1416 SE----CSLEKNERACIDFAISAKPLTRYMPQNKQSFQYKWTWTFVVSPPFEYFIMAMIAL 1471
QY 1624 NVVTVAMEHYQQPQILDALKICNYIFTVIFVFESVFKLVAFARFRFQDRWNQLDLAIV 1683

Db 1472 NTVVLMMKFYDAPYEYELMKCLNIVFTSMFMECILKIIAFGVLYNFRDANNVDFVTV 1531
QY 1684 LLSIMGITLEEIE-----VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRAALLHTVMQ 1738
Db 1532 LGSITDILVTEIAETNNFINLS-----FLRLFRARLIKLLRQGYTIRILLWTFTVQ 1582
QY 1739 ALPOVGNLGLLFFLFFIFAALGVVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRV 1798
Db 1583 SFKALPYVCLLIAMLFFIYAIIGMVQVFGNSALDDD--TSINRHNHNFRTFLOAIMLLFRS 1639
QY 1799 STGDNWNGIMKD--PSRDCD--QESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKH 1853
Db 1640 ATGEAWHEIMLSCLDNACDPHANASEC--GSDFAFYFVFSFLCSFLMLNLFVAVIMDN 1698
QY 1854 LEESNKEAK-----EEAELEAELE-----LEM-KTSLSPQPHSPLG----- 1887
Db 1699 FEYLTRDSSILGPHHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSP-----PLGLGKKC 1754
QY 1888 -SPFLWPGEVGNSTSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGP-DLLT 1945
Db 1755 PARVAYKRLVRMNMPLSNEDMTVHTSTLMALIRTALE-----IKLAPADEMT 1802
QY 1946 V-----RKSGVSRTHSLPNDSYMCRNGSTAESLGRGWGLPKAQSGSIL 1990
Db 1803 VGKUYAALMIFDFYKQNKTRDQTHQAPG-----GL--SQMGFVS 1840
QY 1991 SVHSQPADTSCILQLPKDVHYLLQPHGAPTGAIPKLPPPGRSPLAQR---PLRQAAIR 2047
Db 1841 LFHPLKAT-----LEQTQPAVLRGA-----RVFLRQKSATSLNSGGAIQ 1879
QY 2048 TDSLQVQGLGSR-----EDLLSEVSGP-----SCPLTRSSSFVGSSIQVQQR 2090
Db 1880 T-----QESGSRSRCPGRRRGTDALYEGRAPLERDHSKEIIPVQS-----GTLVVDVQM 1930
QY 2091 S-----GIQS--KVSKHIRLPA---PCPGLEP-----SWA 2115
Db 1931 NMTLRGPDGDPQPGLESQGRAASMLRLAAETQAPNASPMKRSISTLAEPDGTQLCSTV 1990
QY 2116 KDPP-----ETRSLELDETE---LSWISGDLPLSPSQEEPLF 2148
Db 1991 LDRPPPSQASHHHHRRRRDKQKRSLEKGPSSLVDPEGAPSTAAAGPLPHGEGSTAC 2050
QY 2149 PRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSC--LDSGSQPRLCPSPS----- 2197
Db 2051 RRDRKQERGRSQE--RRQPSSSSEKQRF---YSCDRLGAGS--POLMPSLSHPTSPAAA 2104
QY 2198 -----SLGQPL-----GGGSRPKKKLSP-PSIS-----IDPPE 2226
Db 2105 LEPAPHPQSGSVNGSPMLSTSGAITPGRGRRQLPQPLTPRPSITYKTANSPPVHFAE 2164
QY 2227 SQGSRPPCSPG-----VCLRRRAPASD-----SKDPSVSSPLDSTAASPPKK 2269
Db 2165 GQGLPAPSPGRLSRGLSEHNALLQKEPLSQPLAPGSRIGSDPYLGQLDSEASAHTLPE 2224
QY 2270 DTLSL-----SGLSS 2279
Db 2225 DTLTFEEAVATNSGRSS 2241

RESULT 10
A47447
calcium channel protein alpha-1 chain (variant doe-1) - electric ray (discoptye ommata)
C;Species: Discoptye ommata
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47447
R;Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
A;Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray Dis
A;Reference number: A47447; MUID:93248175; PMID:7683405
A;Accession: A47447
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA

A:Residues: 1-2223 <HOR>			QY		
A:Cross-references: UNIPROT:P56699			975		LYFIALMTFGNYLVFNLLVAILVEGFAEGDATKSESEPDFFSPVDGDRKKRLALVA 1034
A>Note: sequence extracted from NCBI backbone (NCBIP:130671)			695		VYFIVLTFLFGNYTLNVLFLAIAVDNLANAQELTKEEQEE-----EA 736
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain			QY		1035
Query Match 13.7%; Score 1642; DB 2; Length 2223;			737		INQKHALQKA-----KEVSPMSAPGFPSTEREFRHRHKHSIWEARTSQLRRRMQSS 788
Best Local Similarity 24.0%; Pred. No. 8.1e-96;			QY		1085
Matches 598; Conservative 373; Mismatches 841; Indels 682; Gaps 78;			Db		789
			QY		1135
			Db		849
			QY		1186
			Db		906
			QY		1230
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			QY		1275
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A:Cross-references: UNIPROT:P56699			QY		
A>Note: sequence extracted from NCBI backbone (NCBIP:130671)			975		LYFIALMTFGNYLVFNLLVAILVEGFAEGDATKSESEPDFFSPVDGDRKKRLALVA 1034
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain			695		VYFIVLTFLFGNYTLNVLFLAIAVDNLANAQELTKEEQEE-----EA 736
Query Match 13.7%; Score 1642; DB 2; Length 2223;			737		INQKHALQKA-----KEVSPMSAPGFPSTEREFRHRHKHSIWEARTSQLRRRMQSS 788
Best Local Similarity 24.0%; Pred. No. 8.1e-96;			QY		1085
Matches 598; Conservative 373; Mismatches 841; Indels 682; Gaps 78;			Db		789
			QY		1135
			Db		849
			QY		1186
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A:Residues: 1-2223 <HOR>			QY		
A:Cross-references: UNIPROT:P56699			37		RRMERAPRSRDSFVASRSSTTCGPGGAAGAGSTEKDPGSADSEAEGLPYPA-----LAPV 91
A>Note: sequence extracted from NCBI backbone (NCBIP:130671)			Db		
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain			21		RSRHQVPVTGETAVAAAAAUVAGAAQGSAGFKQTRAQARTMALYNPIPVHRNCLTANR 80
Query Match 13.7%; Score 1642; DB 2; Length 2223;			QY		
Best Local Similarity 24.0%; Pred. No. 8.1e-96;			Db		
Matches 598; Conservative 373; Mismatches 841; Indels 682; Gaps 78;			81		SLFLFGEDNIVRKSARRVIEWPPPEYMIATIANCVVLALEQHLPGND---KTPMAKSL 137
			150		QAFDDFIFAFFAVEMVVMKVALG-IFGKKCYLGDWTNRLDFFIIVAGMLEYSLDLQNVSF 208
			138		EQTEPYFIGFCFEAGIKIVALGFVFKGSYLRNGWNVMDFIVVLSGLL--ATAATHFNL 195
			209		SAVRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGL 268
			196		RTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLIQIGLLFFAILMFAIIGLEFYGYK 255
			269		LRNRCFLPENFSLPLSVDLEPYQYQTENEDESPPFICSQPRENGMRSCRSVPTLRGEGGGP 328
			256		LHRTCYTDDAAAEELDLQF----- 274
			329		PCSLDYETYNSSNTTCVNNQYTYTNCAGEHNPKGAINFDNIGYAWIAIFQVITLEGW 388
			275		PCGTQEPTRLCPNGTVCSYW-----IGPNDGITQFDNILFALLTFVFCITMEGW 323
			389		VDIMYFVMDA-HSFYNYFIYILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVR 447
			324		TTILYNTDDALGAMWNWLYFIPLIIIGSFFVLNLVLGVLGSEFAKERERV-----ENRRS 378
			448		FLSNASTLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAL-GVRAGLLSSPVARSQ 506
			379		FLK-----LRRQQIERELNGYRAWIDKAEVVMLE 409
			507		EPQPSGSTRSH--RRLSVHHLVHHHHHHHHYHLNGFLRVPRASPEIQDRDANGSRRL 564
			410		ENKNAGEKSALHVLRRATIK-----KGRMEM-----IQTESSEDQ--- 444
			565		MLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRCPSASGRTVSGKVYPT 624
			445		-----YTEISSVGSPLARASIKS----- 462
			625		VHTSPPPEILKOKALVEVAPSPGPPTLTSFNIPPGPFSSMHKLLETQSTGACHSSCKISS 684
			463		-----TKLLEGSS----- 470
			685		PCSKADSGACGDCPYCARTGAGEPESADHVMFSDSDSEAVYEFTQDAQHSDLRDPHSRR 744
			471		-----YFRR 474
			745		RQSLGPDABESSVLAFWRLICDTERKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEEL 804
			475		KERML-----RI---SIRHMVKSHAFYWIIVLGLVALNTVCVAVVHDQPLWL 518
			805		TNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIV-----GQQ 859
			519		SNFLYYAEFTFLGLFSSEMFLKMYGCGPRLYFHSSFCNFCGVIIGSIFDVVWVWIIIRPET 578
			860		GGGLSVLRTRFRLMRVLKVRFLPALQRLVVLMTMDNVATFCMLLMFLIFIFSILGMHL 919
			579		SFGISVLRALRLRIFKITKYWASLRNLVLSMSSMKSIISLLFLFLFIVVFALLGMQL 638
			920		FGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKVLNGMAS-----TSSWAA 974
			639		FGGQFNTEE--GTPP--TNFDTFPAAIITVFQILTGEDWNEVMYNGIKSQGGVNSGMWSS 694

QY	975	LYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFFSPVDGDGRKKRLALVA 1033
Db	695	VYFIVLTLFGNYTLLNVFLATAVDNLANAQELTKEQEE-----EA 736
QY	1035	LGEHAELRKSLPLLIHTAATPMSHPKSSST-----GVGEALGSGSRRTSSSGS 1084
Db	737	INQKHALQKA-----KEVSPMSAPGFPSTEREFRHKHMSIWEARTSQLRRRMQMS 788
QY	1085	AE-----PGAAHHEMKCPPSARSSPHSPWPSAASSWTSRRSSRNSLGRAPSLKRRS--- 1134
Db	789	REALFTDALQLEGSRYYRRHSRIFEAESLRLAEQQAASHQLGVEGRREAFKSRSLRN 848
QY	1135	---PSG---ERRSLLSGEQE---SQDEESESSEDRASPAGSDHRHRSGLEREAKSSFDL 1185
Db	849	SWQAPAGPDKRSSIKVNGEQGRALGRSVEAGASFRMAEPIRARRRYR-SLYKEAK--MGL 905
QY	1186	PDTLOVPLHRTASGRSSASEHQDCNGKSAAGRLARTLRTDDPQ----- 1229
Db	906	EESAETSLRRPGKNKEGRLLQQLCE-EQESQLTQTPEVMDAQGMKAFSQWQEPHSSS 964
QY	1230	---LDGDDNDDEGNLSK-----GERIOA---WVRSRL----- 1255
Db	965	MTRTPDVTDPGSGNLEKESGRTPENGKEESANTSEQVNEQSNWLNQLNQOATPGDREL 1024
QY	1256	-----PACCRERDSWSAYIFPPQS 1274
Db	1025	TTGTRDTKQDKTQEQTEIDVDCENTETPMDSLVTPGNAYSSSSSVKEDEKSKAIIPYTS 1084
QY	1275	RF-----RLCHRRIITHKMFHDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNY 1326
Db	1085	MFLFRKTNPIRVCHFIVNLRYFEMCILLVIAASSVALAEDP-IHKDSARNQVLRIFYD 1143
QY	1327	IFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDI-LVSMVSDSGTKIL 1385
Db	1144	VFTGVFTFEMVIKIDIGLVFHEGSYFRDVMNILDVIVSGALVAFATNLIGGSSGKI 1203
QY	1386	GMLRVLRLLRTLRLPRVISRAOGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLF 1445
Db	1204	NTIKSLRVLRVLRPLKTIKRLPKLKAVDVCVVTSLKNVFNLLIVYKLFMFIFAVIAQLF 1263
QY	1446	KGKFFVCOGEDTRNITNKSDCABASYRWVRHK-----YNFDNLGQALMSLFVL 1493
Db	1264	KGKFFYC--TDSSKMT-KQDC-RGQFVLYRQRTKLSIENGNTVTFHYDNVWVALLTFTV 1319
QY	1494	ASKDGVVDIMYDGLDAVGVDQDQIPMNNHNPWMLLYFTSFLIVAFVFLNMFVGVVVENFHK 1553
Db	1320	STGEGWPQVLQHSVDVTEADQGPPIGNRMEMSIIFYIVFWVFPFFVFNIFVALIITF-- 1377
QY	1554	CRHQEHEEARRREKRLRLEKKRRSKEQMAEACKPYYSYDYSR--FRLLVHHLCTSH 1611
Db	1378	-----QEQQDKMLEES---SLEKNERACIDFAISAKPLTRYMPQNQRTFQYRVWQFVVSP 1429
QY	1612	YLDLFIITGVIGLVNVTMAHEHYQQPQILDEALKICNYIFTVIVFVESVFKLVAFARRFF 1671
Db	1430	SFEYILTMIALNTVLMMKHSPPPGFASVLKLMNIAFTITFTLECILKILAFGLNYF 1489
QY	1672	QDRWNQLDLAIVLLSIMGITLEEIE---VNLSPINPTIIRIMRVLRJARVLKLLQMAVG 1728
Db	1490	RDSWNVDFVTVVGSISEIIVTECNLKFVNL-----FLKLFRAARLIKLLRQGIT 1540
QY	1729	MRALLHTVMQALPQVGNLGLLMLFFIFAALQVELFGDLECEDETHPCBGLGRHATFRNF 1788
Db	1541	IRILLWTVFQSFKALPYVCLLIAMLFFIYAIIGMQLFNGIGLDDHTP---INRHNHFTF 1597
QY	1789	GMAFLTLFRVSTGDNWNGIMKD--PSRDCD--QESTCYNTVISPIYFVSFVLTAQFVLVN 1844
Db	1598	FNALMLLFRSATGESWQEIIMLACLSGKEGTREPSG-GTDVAYFYFVSFIFLCSFLMLN 1656
QY	1845	VVIAVLMKHLBSNKEAK-----EBAELEAELE-----LEMKTL-SPQPH 1883
Db	1657	LFVAVIMDNFEYLTRDSSILGPHLDFVRVWAEYDRAACGRJIHYTDMYQMLTLMSP--- 1713
QY	1884	SPLGSPFLWPGV-----EGVNSTDSPKPGAPHTTAHIGAASGFSLEHPT 1927

Db	1714	-PLGLKKCPKSVAYKRLVLMNMPVETDKTVHFT-STLMGLIRTAIQIKLARGCA-----	1766
QY	1928	MVPHPEEVPVPLGPDLLTVRKSGVSRTHSL--PNDSYMCNRNGSTAERSLGRGWGLPKAQ	1985
Db	1767	---DKQQLDAELRKEIMTIWPHLSQKTLDLLVPMHTY-----SDLTVG-----KIY	1809
QY	1986	SGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTGAIPKLPPPGRSPLAQR-----PLR	2041
Db	1810	AAMMIMDYKQSKNKKYQKLQEE-----QSRTPMFQRMESSLP	1848
QY	2042	RQAAIRTDSDV--QGLGSRDRLLSVSGPSCPLTRSSSFWGSSIQVQORSGIOQKYSK	2099
Db	1849	PQIISSTKGLPYLQGTGPDVDSRSEFT-PLVPLPPVMFQQGRTSSQGEIHKQRPKELK	1907
QY	2100	HIRLPAP-----CPGLEPSWAKDPPETRRSLEL-----DTLSWISGDL	2139
Db	1908	KIKLEYPHYGHYLPIENQGRAVSMRLEIESAEDTSPLKRSLSSTFAANHSNSTWLNEYS	1967
QY	2140	PSSQEEPLFPRDLKKCVSVETQSCRRRPGFWLDEQRRHSIAVCLDSGSPRLCPSPSSL	2199
Db	1968	-----ERAGPEDLYKRWS-----RRP-----LRP-----PSRSSN	1992
QY	2200	GGQPLGGPSRPKKLSPPSISI-----DPESQG-----SRPPGSPGVCLRRRAPAS	2247
Db	1993	AGSRERG-RSRERKHLSPERSVCSTGQCAHPQSHRGLDQRLSRSP-SPGYSHRPREQVN	2050
QY	2248	DSKDPSSVSSPLDSTAASPSPKKDTLSLSGLSSDP	2281
Db	2051	SSVS---ESPVPSSSGTSPPKQGORQLPQTPSKP	2081
RESULT 11			
T45115			
N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human			
C:Species: Homo sapiens (man)			
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004			
C:Accession: T45115			
R:Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McQ			
Science 257, 389-395, 1992			
A>Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type			
A:Reference number: A42566; MUID:92335886; PMID:1321501			
A:Accession: T45115			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-2237 <WIL>			
A:Cross-references: UNIPROT:Q00975; EMBL:M94173; NID:g179759; PIDN:AAA51898.1; PID:g1797			
A:Experimental source: cell line IMR32; neuroblastoma			
C:Genetics:			
A>Note: CCHL1A2			
C:Function:			
A:Description: calcium influx			
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain			
Query Match 13.6%; Score 1640.5; DB 2; Length 2237;			
Best Local Similarity 23.5%; Pred. No. 1e-95;			
Matches 614; Conservative 350; Mismatches 815; Indels 839; Gaps 82;			
QY	59	PGGAAGAGSTEKDPSADSEAEGLPYPALAPV-----VFFYLSQDSRPRSWCLET	109
Db	32	PGFGLQPGQORVLYKQSIQARARTMALYNPIPVKQNCFTVNRSLVFSEDNVVRKYAKRI	91
QY	110	VCPNPFERVSMLVILLNCVTILGMFRPCEDIACDSQRCRILQAFDD---FIFAFFAVEMVV	166
Db	92	TEWPPFEYMILATIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIFGFCFEAGI	147
QY	167	KWVALG-IFGKKCYLGDWTNRDLDFIVIAGLEYS---LDLQNVSFSAVRTVRLRPLRA	222
Db	148	KIIALGFVFKGSYLRNGWNVMDFFVVLTGILATAGTDFDLR-----TLRAVRLRPLKL	202
QY	223	INRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCFLPENFSLP	282
Db	203	VSGIPSLQVWLKSIKAMVPLLIQIGLLLLFFAILMFAIIGLEFFYMGKFKACF-----P	255

QY	283	LSVDLEPYQYQTEDESPFICSQPRENGMRSCRSPVTLRGEGGGPPCSDLYETYNSSN	342
Db	256	NSTDAEPV-----GDFPCGKEAPARLCEGD	280
QY	343	TTCVNWNQYITNCAGEHNPFKAINFDNIGYAWIALFQVITLEGWVDIMYFMD-AHSF	401
Db	281	TEC---REYWP-----GPNFGITNFDNIFAILTVFCITMEGWTDILYNTNDAAGNT	330
QY	402	YNFIYFILLIIVGSFFMINCLVVIATQFSETKQES-----QLMREQVRFLSNASTL	455
Db	331	WNWLYFIPILIIIGSFFMLNLVLGVLGSEFAKERERVENRRAPLKLRRQQIE-----	382
QY	456	ASFSEPGSCYBEELLYLVILRKARRLAQVSRAGVRAGLLLSPVARSGQEPQPSGCT	515
Db	383	-----RELNGYLEWIFKAEVMLAEED-----RNAEEKSPLDVLK	417
QY	516	RSHRRLSVHLLVHHHHHHHHHHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPS	575
Db	418	RAATKKSRNDLIH-----AEEGEDRFAD-----	440
QY	576	GGPPRGAESVHSFYHADCHLEPVRCAAPPRCPSEASGRTVGSGKVYPTVHTSPPPEILK	635
Db	441	-----	440
QY	636	DKALVEVAPSPGPPTLTFSNIPPGPFSSMHKLLTQSTGACHSSCKISSPCSKADSGACG	695
Db	441	-----LCAVGSPPFARAS-----	452
QY	696	PDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHRRRRQRLSGPDAEP	755
Db	453	-----LKSGKTESSSYF-----RRKEK-----	469
QY	756	SSVLAPWRLLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHEQEPEELTNALEISNIVF	815
Db	470	--MFRFF-----IRRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLTYFAEFVF	521
QY	816	TSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QGSGISVLRTFR	870
Db	522	LGLFLTEMSLKMVYGLGPRSYFRSSFCDFGVIVGSVFVWAAIKPGSSSFISVLRLR	581
QY	871	LMRVLKLVRFLPALQRLVVLTKTMDNVATFCMLLMFLIFISILGMHLFGCKFASERDG	930
Db	582	LLRIFKVTKYWSSLRLNVVSLNSMKSIISLLFLFLFIVV FALLGMQLFGCGQNFQDET	641
QY	931	DTLPDRKNFDSLLWAIIVTVFOILTQEDWNKVLNGM-----ASTSSWAALYFIALMTFGN	985
Db	642	PT---TNFDTTPAAIILTVFOILTGEDWNAMVYHGIESGGVSKGMSSFFIVLTLFGN	697
QY	986	YVLFNLLVAILVEGFQAEGDATKSESEPdffpsvDGDGRKKRLALVALGEHLRKSL	1045
Db	698	YTLNVLAIADVNLANAQELTKDEEEMEEAA-----NQKLALQAKEVAEV--SP	746
QY	1046	LPPLIIHTAATPMSPKSSSTGVGEA-----	1071
Db	747	MSAANISIAARQONSAKARSVWEQARSQLRLQNLRASCEALYSEMDPEERLRFATTHLR	806
QY	1072	-----LGSGSRRTSSGSAEPGAA-----HH---EMKCP-----	1097
Db	807	PDMKTHLDRPLVVELGRDGARGVVGKARPEAAEAPGVDPRRHHRHDKDKTPAAGDQ	866
QY	1098	-----PSARSS---PHSPWSAASWTSSRRSSNSLGRAPSLKRRSPSGERRSL	1142
Db	867	DRAEAPKAESGEPGAREERPRPHRSKBA--GPPEARSERGCP-----GPEGGRHH	919
QY	1143	LSGEGQESQDEE-----ESSEEDRASPGSDHRRHRSLE---REAKSSFDLPDIL	1189
Db	920	RRGSPEEAAERPRRHRHRHQDPKCECAKGERARRHRHRRGGPRAGPREAESG-----	972
QY	1190	QVPG-LHRTASGRSSASE--HQDCNGKKSAGRLA-----RTLRTDDPQLDGGDDNDE	1238
Db	973	EEPARRHRARHKAQPAHEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETS	1032

QY 1239 GNLSKGERIQAWVRSLPACCRER-----DSW----- 1265
Db 1033 GTVTVGP-----MHTLPSTCLQVEEQEDADNQRNVTMRGQPPDPNTIVHIPVMLTG 1086
QY 1266 ----- 1266
Db 1087 PLGEATVVPSSNVLDLESAEGKKEVEADDVMSRGPRIPIVYSSMFCLSPTNLLRRFCHYI 1146
QY 1284 ITHKMFHDHVLVIFLNCITIAMERPKIDPHSAERIFLTLSNVIPTAVFLAEMTVKVVAL 1283
Db 1147 VTMRYFEVILVIALSSIALAAEDP-VRTDSPRNALKYLDYIFTGVFTFEMVIKIDL 1205
QY 1344 GWCFFGEQAYLRSSWNVLDGLLVLSVIDILVSMV-SDSGTKILGMLRVLRLRLRPLRV 1402
Db 1206 GLLHPGAYFRDLWNILD----FIVVSGALVAFAGSGSGKDINTIKSLRVLRLPLKT 1261
QY 1403 ISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCQE-----D 1456
Db 1262 IKRLPKLKAVIDCVNSLKNVNLILIVYMLFMFIFAVIAVQLFKGFFYCTDESKELERD 1321
QY 1457 TRN--ITNKSDCAEASYR-WVRHKYNFDNLGOALMSLFLVASKDGVNDIMYDGLDAVGVD 1513
Db 1322 CRGOVLDEKEEVEAQPROWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEE 1381
QY 1514 QQPIMNHNPMMLLYFISFELLIVAFVFLNMVGVVVVNFPHKCRHQHEEAEARRREKRLRR 1573
Db 1382 QGSPSGYRMELSIFVYVVFVFFVFVIFVALIITF-----QEQGDKMSE----CS 1431
QY 1574 LEKRRSKEKQMAEAQCKPYSDYSR--FRLLVHHLCTSHYLDLFTITGVIGLNVVTMAME 1631
Db 1432 LEKNERACIDFAISAKPLTRYMPQNRQSFQYKXTWTFVVSPPFEYFIMAMIALNTVVLMMK 1491
QY 1632 HYQQOILDEALKICNYIFTVIFVFESVFKLVAFAPRRFFQDRWNQLDLAIVLLSIMGIT 1691
Db 1492 FYDAPYEYELMKCLNIWFTSMFSMECVLKIIAFGVNLVFRDANVDFVTVLGSITDIL 1551
QY 1692 LEEIE-----VNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALPOVGNL 1746
Db 1552 VTEIAETNNFINLS-----FLRLFRAARLIKLRQGYTIRILLWTFVQSFKALPYV 1602
QY 1747 GLLFMLLFFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFLTFRVSTGDNWNG 1806
Db 1603 CLLJAMLFFIYAIIGMQVFGNIALDDD---TSINRHNFRFTLQALMLLFRSATGEAWHE 1659
QY 1807 IMKD--PSRDCDQE--STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLM----- 1851
Db 1660 IMLSCLSNQACDEQANATECGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS 1719
QY 1852 ----KHLEE----- 1856
Db 1720 ILGPHHLDFTRWAEYDPAACGRISYNDMFEMLKHMSPPPLGLGKKCPARVAYKRLVRMN 1779
QY 1857 -----SNKEAKEEAELAEAL-----ELEMKTLS- 1879
Db 1780 MPISNEDMTVHTSTLMALIRTALEIKLAPAGTKQHQCDAELRKEISVVWANLPQKTLDL 1839
QY 1880 -PQPHSP----LGSPF----LWPGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVP 1930
Db 1840 LVPPHKPDDEMTVGKYAALMIFDFYKQNKTRDQMQQAPGGLSQMGPVSLF---HPLKAT 1896
QY 1931 HPEEVPVPL-CPDLLTVRKSGVSRTHSLPNDSYMCNRNGSTAERSLGHGWGLPKAQSGSI 1989
Db 1897 LEQTQPAVLRGARVFLRQKSS-----SLNNGGAIQNESGIKESV---SWGTRTQDA-- 1947
QY 1990 LSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPGRSPLAQRLRRQAIRT 2049
Db 1948 -----PHEA-----RPLERGHSTEIPVGRSGALAVD 1974
QY 2050 -----SLDVQGLSREDLLSEVSGPSCPLTRSSSFWGSSSIQVQORSG 2092
Db 1975 VQMQSITRRGPDGEPQPGLESQG--RAASMPRLAAETQPVTDASPMKRSISTLAQPRG 2031
QY 2093 IQSKVSKHIRLPAPCPGLEPSNAKPPETRS-----SLELDTLSWIS 2135

RESULT 12

B54972

voltage-dependent calcium channel alpha 1E-1 - human

C;Species: Homo sapiens (man)

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999

C;Accession: B54972

R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mill J. Biol. Chem. 269, 22347-22357, 1994

A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel

A;Reference number: A54972; MUID:94350992; PMID:8071363

A;Accession: B54972

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-2251 <WIL>

A;Cross-references: GB:L29384; NID:g495867; PIDN:AAA59204.1; PID:g495868

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match

Best Local Similarity 13.6%; Score 1638; DB 2; Length 2251;

Matches 600; Conservative 391; Mismatches 818; Indels 724; Gaps 86;

QY 73 PGSADSEA-----EGLPYPALA-----PV-----VFFY 95

Db 12 PGSGDGDSDQSRNRQGTVPVPSAGQAAAYKQTKAQRARTMALYNPIVRQNCFTVNRSLFI 71

QY 96 LSQDSRPRSWCLRTVCNMPWFERSVLMVILLNCVTLMFR--PCEDIACDSQRCRILQAFD 153

Db 72 FGEDNIVRKYAKLIDWPPFEYMIATIANCIVLALEQHPDDKTPMSRR---LEKTE 128

QY 154 DFIFAFEAFAVEMVVKWVALG-IFGKKCVLGDWTNRLDFFIVIAGMLEYSLDLQN--VSFSA 210

Db 129 PYFIGIFCFEAGIKIVALGFIFHKGYLRNGWNVMDFIVVLSGILATAGTHFNTHVDLRT 188

QY 211 VRTVRVLRLRAINRVPSMRILVTLDDTLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLR 270

Db 189 LRVRVLRPLKLVSGIPSLQIVLSIMKAMVPLLQIGLLFFAILMFAIIGLEFYSGKLH 248

QY 271 NRCFLPENFSLPLSVLDLEPYQOTENEDESPFICSQPRENGMRSRCSVPTLRGEGGGPPC 330

Db 249 RACFMNN-----SGILEGF-----DPPHPC-----GVQGC 273

QY 331 SLDYETYNSSSNTTCVNWNQVYTNCISAGEHNPPKGAJNFDNIGYAWIAIFQVITLEGWVD 390

Db 274 PAGYE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITMEGWTT 313

QY 391 IMYFVMDA-HSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFL 449

Db 314 VLYNTNDALGATWNWLYFIPILIIGSFFVLNLVLGVLSEFAKERERV-----ENRRAFM 368

QY 450 SNASTLASFSEPGSCYEELLYLVILRKAARLAQVSRAI-GVRAGLLSSPVARSQEP 508

Db 369 K-----LRRQQIERELNGYRAWIDKAEVWLAEN 399

QY 509 QPSGSCTRSHRRLSVHVLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPP 568

Db 400 KNAGTSALEVLRRAT-----IKRSRTAMTRDSS----- 428

QY 569 PSTPTSGGPRGAESVHSFYHADCHLEPVRCQAPPPRCPSEASGRTVGSGKVYPTVHTS 628
Db 429 ----- 428
QY 629 PPEILLKXALVEVAPSGPPTLTSENIPPGPFSSMHKLLTQSTGACHSSCKISSPCSK 688
Db 429 -----SVGTPLAR 444
QY 689 ADGACGPDSCPYCARTGAGEPESADHWMPDSDSEAVYFTQDAQHSDLRDPHSRRQRS 748
Db 445 ASIKSAKVDGSY-----FRHKE----- 462
QY 749 LGPDAEPSSVLAFWRLICDTRFKIVDSKYFGRGIMIALVNTLSMGIEYHEQPEELTNAL 808
Db 463 -----RLLRISIRHMVKSQFYFWIVLSLVALNTACVAIVHHNQOWLTHLL 508
QY 809 EISNIVFTSLFAEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVMEIVGQ-----QGGGL 863
Db 509 YYAEFLFLGLEMSLKMYGMGPRLYFHSFNCDFGVTVGSIFEVWVAIFRPGTSFGI 568
QY 864 SVLRTFRMLRVLKLVPFLPALORQLVLMKTMNDNVATFCMLLMFLFIFSILGMHLFGCK 923
Db 569 SVLRALRLLRIFKITYKAWASLRNLVSLMSSMKSIISLLFLFLFIVVFALLGMQLFGGR 628
QY 924 FASERDGDRTLPRKNPDSLLWAIIVTFQILTOEDWNKVLYNGM-----ASTSSWAALYFI 978
Db 629 F-NFNDG---TPSANEDTTPAAIMTVFQILTGEDWNEVMYNGIRSQGGVSSGMWSAIYFI 684
QY 979 ALMTFGNYVLNLLVAILVEGFOAEGDATKSE-SEPDPFS-----P 1018
Db 685 VLTIFGNYTLNVLTAIVDNLANAQELTKDEQEBEEAFNQKHALQKAKEVSPMSAPNMP 744
QY 1019 SVDGDGDRKKRLALVALGHAELRKSL-----LPPLIIHTAATPM-S 1059
Db 745 SIERERRRRHMS-VWEQRTSQLRKHQMSSQEBALNREEAPTNNPLNPLNLSLNPLNA 803
QY 1060 HP-----KSSSTGV-----GEALGSGSRRTS-----SSGSAEPG 1088
Db 804 HPSLYRRPRAIEGLALGLEKEFEERISRGGSLKGDGDRSSALDNQRTPLSLGQREPP 863
QY 1089 --AAHEMKCPPSARSSPHSPWSAASSWTSSRSSRSLGRAPSLKRRSPSGERRSLLSGE 1146
Db 864 WLARPCHCNCDPTQOEA--GGGEAVVTFEDRARHRQSRRS--RHRRVRTEGKESSAS 918
QY 1147 GOESQDEEESSEEDRASPAGSDHHRG-----SLERHAKSSFDLPDTLQVPLHRTAS 1199
Db 919 RRSASQERSLDEAMPTGEKDHLELRGNHGAKEPTIQEERAQDLRRTNSLMVSRGSLAG 978
QY 1200 GRSSAS-----EHQDCNGKSASGLAR-----T 1222
Db 979 GLDEADTPLVLPHEVGHVLTQEPEGSSEQALLGNVQDMGRVISQSEPDLSGIT 1038
QY 1223 LRTD-----DPQLDG-----DDNDEGNLSK 1243
Db 1039 ANTDKATTESTSVTVVAIPDVPDPLVDSVTVVHISNKTGDEASPLKEAIREDEEVEKKQK 1098
QY 1244 GERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLVIIFLNCIT 1303
Db 1099 KEKRETG-KAMVPHS-----SMFIFSTNPIRRACHYIVNLRVYFEMCILLVIAASSIA 1150
QY 1304 IAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDDL 1363
Db 1151 LAADPVLTNSENKV-LRYFDYVFTGVTFEMVIKMDIQLQDGSYFRDLWNILDFV 1209
QY 1364 LVLSVIDI-LVSMVSDSGTKILGMLRVLRLTLRPLRVISRAQGLKLVVETLMSLLKP 1422
Db 1210 VVVGALVAFALANALGNTKGRDIKTIKSLRVLRLPLKTIKRLPKLKAVFDCVVTSLKN 1269
QY 1423 IGNIWICCAFFIIFGILGVQLFKGKFFVC--QGEDTRN-----ITNKSDCAEASYR-W 1473
Db 1270 VENILIVYKLFMF1FAVIAVQLFKGKFFYCTDSSKOTEKECIGNYVDHEKNKMEVKGREW 1329
QY 1474 VRHKYNFDNLGQALMSLFLASKDGWVDIMVDGLDAVGVDQQPIIMNHPWMLLYFISFLL 1533

Db 1330 KRHEFYDNIWALLTLFTVSTGEGWPQVLQHSVDVTEDRGPSRNRMEMSIFVYVYFV 1389
QY 1534 IVAFFVLNMFVGVVWFENFKCRQHQQEERARRREKRRLRLEKKRRSKEKQMAEAQCKPY 1593
Db 1390 VFPFFVFNIFVALIITF-----QEQDKMEE--CSLEKNERACIDFAISAKPLTR 1439
QY 1594 YSDYSR--FRLIVHHLCTSHYLDLFTITGVIGLNVVTMAMEHYQQOQILDEALKICNYIFT 1651
Db 1440 YMPQNRHTFYQVRVWHFVVVSPSFYTIMAMIALNTVLMMKYSAPCTYELALKYLNIAFT 1499
QY 1652 VIFVESVFKLVAFARFRFFQDRWNQLDLAIVLLSIMGITLBEIEVNLSLPINPTIIRIM 1711
Db 1500 MVFSLECVLKVIAGFLNYFRDWNIFDFTIVIGSITEIILTDKLVNTSGFNMSFLKLF 1559
QY 1712 RVLRIARVLKLLKXAVGMRALLHTVWQALPQVGNLGLLFFLMLFFIFAALGVELFGDLECD 1771
Db 1560 RA--ARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAMLEFFIYAIIGMQVFGNIKLD 1616
QY 1772 -ETHPCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKD--PSRDCDQESTC----- 1821
Db 1617 EESH---INRHNFRSFFGSLMLLFRSATGEAWQEIIMLSCLGKGCPEPDTTAPSGQEN 1672
QY 1822 --YNTVISPIYFVSFVLTAQFVLNVNVIIVMLKHLSESNKEAK-----EEAELEAE 1871
Db 1673 ERCTDLAYVYFVSPIFFCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDDEFVRVWAEY 1732
QY 1872 E-----LEMKTL-SPQHPSPLG-----SPFLWPVGVEGVNSTDSPKPGAPHTT 1912
Db 1733 DRAACGRIHYTEMYEMLTLMSP---PLGLGKRCPSKVAYKRLVLMN-----MPVAEDMT 1783
QY 1913 AH-----IGAASG-----FSLHEPTMV--PHPEE-----VPVPLGPD 1942
Db 1784 VHTSTLMALIRTALDIKIAKGADRQQLDSELQKETLAIWPHLSQKMLDLLVMPKASD 1843
QY 1943 ILTVRKSQSVRTHSLPNDSYMCRNGSTAERSLCHRGWGLPKAQSGSILSVHSQPADTSCI 2002
Db 1844 -LTVGKIYAA--MMIMDYKQSKVKKQKQOQL-----EEQKNAPMEQMEPS----- 1886
QY 2003 LQLPKDV-----HYLLQPHGAPTWGAIPKLPPGRSPLAQRLRRQAAIRTDSDLVQG 2055
Db 1887 -SLPQEIIANAKALPYLOD---PVSGLSGRSGYPSMSPLSPQDIFQLACM--DPADDGQ 1940
QY 2056 LGSREDLLSEVSGPSCPL-----TRSSSFVGSSIQVQQRSGIQSKVSKHIRLPAPC 2107
Db 1941 FQERQSLV--VTDPSMRRSFSTIRKRSNSW-----LEEFSEMERSS----- 1981
QY 2108 PGLEPSWAKDPPETRSSLELDT-ELSWISG---DLLPSSQEEPLFPRDLKKCYSVETQSC 2163
Db 1982 ---ENTYKSRRRSYHSSRLSAHRLNSDSGHKSDTHPSGGRERRRRSKERHLLSPDVSR 2038
QY 2164 ---RRPFGWLDEQRHRSIAVSCLDGSGQRLCPSPSLGGQPLGGPGSRPKKLSPPS 2219
Db 2039 NSEERTQADWESPERRQS-----RSPSEGRSQTNRQGTGSLSESSIPS 2083
QY 2220 IS--IDPPESQGSRRPPCSPG-----VCLRRRA-----PASDSKD--PSVSSPLDSTAA 2263
Db 2084 VSDTTPRRRRQLPPVPPKPRLLSYSSLIRHAGSISPADGSEEGSPLTSQALSNNA 2143
QY 2264 -----SPSPKK 2269
Db 2144 WLTESSNSPHPQQ 2156

RESULT 13
A54972
voltage-dependent calcium channel alpha 1E-3 - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accession: A54972
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mi
J. Biol. Chem. 269, 22347-22357, 1994
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel

Db 1674 GEKGCEPDTTAPSGQNERCGLDLYVYFVSFIFFCSFLMLNLFVAVIMDNFEYLTRDS 1733

QY 1862 K-----EBAELEAELE-----LEMKTL-SPQHSPLG-----SPFLWPG 1894

Db 1734 SILGPHHLDDEFVRVWAEYDRAACGRHYHYTEMYEMLTLMSP-----PLGLGKRCPSKVAYKR 1789

QY 1895 VEGVNSTDSPKPGAPHTTAH-----IGAASG-----FSLEHPTMV--P 1930

Db 1790 LVLMN-----MPVAEDMTVHFTSTLMALIRALTALDIKIAKGGADRQQLDSELQKETLAIWP 1844

QY 1931 HPEE-----VPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHARGWGLPKA 1984

Db 1845 HLSQKMLDLLVMPKASD-LTVGKIYAA---MMIMDYKQSKVKQKQQL-----EE 1892

QY 1985 QSGSILSVHSQPADTSCILQPKDV-----HYLLQPHGAPTWGAIPKLPPLPPGRSPLAQ 2037

Db 1893 QKNAPMFQRMERS-----SLPQEIIANAKALPYLOQD---PVSGLSGRSGYPMSPLSP 1943

QY 2038 RPLRRQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPL-----TRSSSFVWGGSSIQVQQ 2089

Db 1944 QDIFQLACM--DPADDDQFQERQSLV--VTDPSSMRRSFSTIRDKRNSSW-----LEE 1993

QY 2090 RSGTQSKVKSHIRLPAPCPGLEPSWAKPPETRRSLELDT-ELSWISG---DLLPSSQEE 2145

Db 1994 FSEMRSS-----ENTYKSRRRSYHSSLRLSAHRLNDSGHKSDTHPSGGRE 2039

QY 2146 PLFPRDLKCYSVETQSC---RRRPGFWLDEQRHSHIAVCLDSGSPRLCPSPSSLGG 2201

Db 2040 RRRSKERKHLSPDVSRCNSEERGTQADWESPERRQS-----RSPSEGRS 2084

QY 2202 QPLGGGSRPKKLSPPSIS--IDPPESQSGSRPPCSPG-----VCLRRRA-----PAS 2247

Db 2085 QTPNRQGTGSLSESSIPSVSDTSPRRSRRLQPPVPKPRPLLSYSSLIHAGSISPPAD 2144

QY 2248 DSKD--PSVSSPLDSTAA-----SPSPKK 2269

Db 2145 GSEEGSPLTSALESNNAWLTESNSPHFPQQ 2175

RESULT 14

T30902

sodium channel SCAP1 alpha chain - California sea hare

C;Species: Aplysia californica (California sea hare)

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T30902

R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.

DNA Cell Biol. 16, 347-356, 1997

A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.

A;Reference number: Z20929; MUID:97238630; PMID:9115644

A;Accession: T30902

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1993 <DYE>

A;Cross-references: UNIPROT:P90670; EMBL:U66915; NID:G1842248; PID:G1842249; PIDN:AAC474

C;Superfamily: sodium channel protein

Query Match 13.6%; Score 1636; DB 2; Length 1993;

Best Local Similarity 25.8%; Pred. No. 1.7e-95;

Matches 518; Conservative 348; Mismatches 702; Indels 442; Gaps 69;

QY 94 FYLSQDSRPRSWCLRTVCNPFWERVSMVLVILNCVTLGM--FRPCEDIACDSQRCRILQA 151

Db 119 FLLSPFPNPIRRIAYILVHPIFSLVMMTILVNCVFMAITSYTP-----PA 164

QY 152 FDDFFIF-AFFAVEMVVMVALGIFGKK-CYLGDTWNRLDFFIV-IAGMLEYSLDLQNVSF 208

Db 165 FVEHIFLGIYTVAEAVVKVLSRGFVLKPFTYLRDPNWLDFVVISIAYMTMTVKSEGNL-- 222

QY 209 SAVRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIGIVGVQLWAGL 268

Db 223 QALRTFRVLRAKLTISVIPGLKTIIVGALLEAVRRLRDVMIITVFLVSIFALIGMQLYSGA 282

QY 269 LRNRCTLPENFSLPLS-----VDLEPYQTENEDESPFICSQPRENGMRSCRSVPT 319

Db 283 LRQKCVLNPVPELGTNITHDEWMDWNWNNESHQKDFYDEWQ-VC----- 325

QY 320 LRGEGGGGPPCSDLDETYSNTTTCV-NWNQYITNCAGEHNPFKGAINFDNIGYAWIA 378

Db 326 --GNGTGAGKCG--NGTINGTAEWLCLPNIGQ-----NPNHDTSFDFNFGMALLC 371

QY 379 IFQVITLEGWVDIMYFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRES 438

Db 372 AFRMLTQDFWESLYHLVLRVAGSAHCLYFVLVILLGSFYLVNLIILAIAMSYDET-QKQD 430

QY 439 QLMREQVRFLSNASTLASFSEPGSCYHELLKYLVIILRKAARLIA-QVSRAIGVRAGLL 497

Db 431 QADAEAEA-----AERQE-----EARKEALSIMTKSPSNSWNNDFEAGVR--- 472

QY 498 SSPVARSGQEPQPSGSCSTRSHRRLSVHHLVHHHHHHHHHHLGNGTLRVPRASPEIQDRD 557

Db 473 ---TAGDKAEKERLSLTSDSHATS AHLKPSRLNQRH-----SLSLP-GSPYIHRRN 521

QY 558 ANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCAAPPSPCPSEASGRTVG 617

Db 522 SRGSQYSWRKPVPTAKRS-----PYCPDR----- 545

QY 618 SGKVYPTVHTSPPEILKDKALVEVAPSPGPPLTSTF---NIPPG---PFSSMHKLLET 670

Db 546 QPLVHHTLENLPLP-FADDSAAV---TPSSEDLNCFSFIRNMPNRRRFPASQRRPDGT 600

QY 671 QSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGE-----PESA-D 714

Db 601 GRSGRRSS--FASNHSRASRTSRG-----SQQDRTKTQTLNFKKKGKVPDVVLD 649

QY 715 HVMPPDSDEAVYEFTQDAQHSDLRDPHSRRR---QRSLGPAEPPSSVLA----- 760

Db 650 KSKLDDDDQDSV--SSGSGCHCPEKDKASENPFSLSPGGPNVEMKDMVMLKDILDDQASG 707

QY 761 -----FWRLIC-----DTRFKI-----VDSKYFGRGIMAILVN 789

Db 708 HRRSFVSMTSIHQRTMKDIMWKYFCTWDCHPNFQKLRQLVSLFIMDAFVDFITICILVN 767

QY 790 TLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVYGGFYIKNPYNIPDGVIIV 849

Db 768 TAFMAMEHYDMEDDLKAVSNAANLVFTAFAVEAFKLALSPVIYFKDGNIFDLSIIVA 827

QY 850 ISVWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDNVATFCMLMLFLI 909

Db 828 LSLMELSMTKLPGLSVLRAFRLRLRVFKLAKSWPTLNLMLIAIVGRTMGALGNLIIVLGIII 887

QY 910 FIFSILGMHLFGCKFAS-ERD-----GDTLPDRKNFDSLWAIIVTFQILTQEDW 958

Db 888 FIFAVMGQQLFSSDYKTYEREIDAWGNVTINKDKMP-RWPNDFLHSMIVFRVLCGE-W 945

QY 959 NKVLYNGMASTSSWAAL-YFIALMTFGNYVLFNLLVAILVEGFQAEG-DATKSESEPDFF 1016

Db 946 IESMW-GCYLVSGWACVPFFLLTYVGNLVVNLFLALLSSFGSESLQRSESDDEPSKI 1004

QY 1017 SPSVDGDGDRKKRLA-----LVALGHEAELRKSLPPLIHTAATPMShPKSSSTGVG 1069

Db 1005 AEAI---DRFXRFGNWVKIIVCIKVKLQKQKWRPP-----PTTGQS 1045

QY 1070 EALGSGSRRTSSSGSAEPGAAHHEMKCPSPARSSPHSPWSAASWTSRRSRNSLGRAPS 1129

Db 1046 EVNG-----KDPAAVVDGTVVSMKTPDPDFDGPCCPAQAAC----- 1082

QY 1130 LKRRSPSGERRSLLSGEGQESQDEESESDEDRASPAGSDHRHRSLEAKSSFDLPDTL 1189

Db 1083 -----SAKDKLKSPPSGS-HSNSGS----- 1100

QY 1190 QVPLHRTASGRSSASEHQDCNGKSASGRUAARTLRTDDPOLDGGDDNDENLKGRIQA 1249

Db 1101 -----SHCSSCSLSESAQTKID---LEADHEINEVEI-----V 1132

QY 1250 WVR-----SRLPACCRERDS-----WSAYIFPPQSRFRLLCHRIITHKMFHDVV 1293

Db 1133 YVKEPDDCFYMCYKRCPCWCVKVEKSKIGRAWA-----VRCFFYRLTENKYFDSFI 1184

QY 1294 LVILFLNCITIAMERPDKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYL 1353

Db 1185 IAMILASSCALAEDAYLHEKPIKLEIDYDKVFTAFIIEMLIKWLA---FGFKTYF 1240

QY 1354 RSSWNVLGGLLVISVIDILVSM-VDSGTFKILGMLRVLRLRLRLPLRVISRAOGLKLV 1412

Db 1241 TDAWCWLDFTIIVMLSVLADLTASEEGGSMWMSMRTLRALPLRAVSRWEGMRVV 1300

QY 1413 VETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGE-----DTRNITNKSDCA 1467

Db 1301 VNALFKAIPISICNVLLVCLVFLWLFIMGVQLFNGKFHACRDEKGDYKYPREEVPNKTVCI 1360

QY 1468 EASYRWRHRYKYNFDNLQALMSLFLVLASKDGVVDIMYDGLDAVGVDQOQIMNHNPMWMLLY 1527

Db 1361 DKGYNWTNAQINFHDVLSAYLALFQVATYKGWIDIMNNAIDSTEIGQQPSREENVIMYLF 1420

QY 1528 FISFLIVAFVFLNMFGVVVVENFH--KCRQHQEEEEARRREKRLRLLEKRRSKEKQM 1585

Db 1421 FVLFIVCFSFTLNLFIGVIIENFNSQKKKAGGSLEMFMTEDQKKYNAKRMQSKSPQ- 1479

QY 1586 AEAQCKPYSDYSRFRLLVHLCTSHYLDLFTITGVLNVVMTAMEHYQQPQILDEALKI 1645

Db 1480 -KSIPRPKY---KLAGLIFDITTDQKFDIAIMVIIILNMLTMMFEHGHMSAQMKNILGI 1534

QY 1646 CNYIFTVIFVFESVFKLVAFARFRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINP 1705

Db 1535 FNLIFITFAECVLKIGLRW-YFKIPWNVEDFVVVLSILASSLSEFED--SFFISP 1591

QY 1706 TIIRMRVLRIARVLKLLKMAVGMRAALLHTVMQALPQVGNLGLLFLMLFFIFAALGVLELF 1765

Db 1592 TLLRVRIRVRGVRVLRLVKSAGIRTLLFSMAVSLPALFNIGLLGLIMFIYAIMGMNFF 1651

QY 1766 GDLECDETHPCEGLRHATERFNGMAFLTLFRVSTGDNWNGIMKDPSCDQESTCYNTV 1825

Db 1652 --MGAEQKY---GLDDAFNFTFLRSFILLFQMCTSAGMSDVLNGLIARCAPEGTCKDYN 1706

QY 1826 ISPIYFVSFLTAQFVLNVVIVAVLMKHLSESNKEAEAEAELEMEKTLSPQHPSP 1885

Db 1707 VATIYLATYLVSVFLVVVNMVIAVILENFSQATED--EQQLTPD-DFDMYVEKWEKYDP 1763

QY 1886 LGSFPLMPGVEGVNSTDSPKPGAPHTTAHIGAASEF--SLEHPTMVPHP-----EVPVP 1938

Db 1764 KASKYI-----PLDQLSDFDVDYLEEPLRLPKENHFLVCLKDIP 1801

QY 1939 LGP-----DLLTVRKSGVSRTHSLP 1958

Db 1802 ICENDRCYCRDILDALTAKNPLGTGETSDIP 1831

RESULT 15

A37490

voltage-dependent calcium channel alpha 1E - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A37490

R;Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P.

Science 260, 1133-1136, 1993

A;Title: Structure and functional expression of a member of the low voltage-activated ca

A;Reference number: A37490; MUID:93262464; PMID:8388125

A;Accession: A37490

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-2222 <SOO>

A;Cross-references: UNIPROT:Q07652; GB:L15453; NID:g310082; PIDN:AAA40855.1; PID:g310083

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIP:132101)

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.6%; Score 1632.5; DB 2; Length 2222;

Best Local Similarity 23.6%; Pred. No. 3.3e-95;

Matches 587; Conservative 389; Mismatches 819; Indels 697; Gaps 81;

QY 94 FYLSQDSRPRSRLWCLRTVCNPFWEERVSMLVILLNCVTLGMFR--PCEDIACDSQRCRILQA 151

Db 21 FIFGEDNIVRKYAKKLIIDWPPFEYMLATIIANCIVLALEQHLPEDDKTTPMSRR---LEK 77

QY 152 FDDFIFAFAFVEMVVKMVALG-IFGKKCYLGDWTNRLDFFIVTAGMLEYSLDLQN--VSF 208

Db 78 TEPYFIFGCFEAGIKIVALGFIFHKGSYLRGNWNVMDFIVVLSGILATAGTHFNTHVDL 137

QY 209 SAVRTVRVLRLRAINRVPSMRILVTLDDTLMLGNVLLLCFFVFFIFGIVGVQLWAGL 268

Db 138 RTLRAVRVLRLKLVSGIPSLQIVLKSIMKAMVPLLIQIGLLFFAILMFAIIGLEFYSGK 197

QY 269 LRNRCFLPENFSLPLSVDLPEYYQTENEDESPFICSPRENGMRSCRSVPTTLRGEGGGP 328

Db 198 LHRACFMNN-----SGILEGF-----DPPHPC-----GVQ 222

QY 329 PCSLDYETYNSSNTTCVNNWNYTNCSSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGW 388

Db 223 GCPAGYE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITMEGW 262

QY 389 VDIMYFVMDA-HSFYNYFIYFILLIIVGSFFEMINCLVVIATQFSETKQRESQLMRQRVR 447

Db 263 TTVLYNTNDALGATWNWLYFIPLIIGSFFVLNLVLGVLGSEFAKERERV-----ENRRA 317

QY 448 FLSNASILASPEPGSCGYEELLKYLVIILKAARLAAQVSRAT-GVRAGLLSSPVARSQ 506

Db 318 FMK-----LRRQOIERELNGYRAWIDKAEVMLAE 348

QY 507 EPQPSGSTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLML 566

Db 349 ENKNSGTSALEVLRAT-----IKRSRTEAMTRDSS-----379

QY 567 PPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQAPPPRCPSEASGRVTGSGKVYPTVH 626

Db 380 -----DPPHPC-----379

QY 627 TSPPEILKDKALVEVAPSPGPTLTSTFNIPPGFSSMHKLETTQSTGACHSSCKISSPC 686

Db 380 -----DEHCVDIS-----SVGTPL 393

QY 687 SKADSGACGPDSCPYCARTGAGEPESADHVMDDSDSAVYEFTQDAQHSDLRDPHSRRRQ 746

Db 394 ARASIKSTKVDGASY-----FRHKE-----413

QY 747 RSLGPDAAEPSSVLAFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTN 806

Db 414 -----RLRISIRHMVKSQFYWIVLSVALNTACVAIVVHNQPLWTH 457

QY 807 ALEISNIVFTSLFALEMLLKLIVYGPFGYIKPNYINIFDGVIVVISVWEIVGQ-----QGG 861

Db 458 LLYYAEFLFLGLFLEMSLKMGMGPRLYPHSSFCDFGVTVGSIFEVVWAIFRPGTSF 517

QY 862 GLSVLRTFRLMRVLKIVRFLPALQRLVVLMTMDNVATFCMLLMFIFIFISILGMHLFG 921

Db 518 GISVLRALRLLRIFKITKYWASLRNLVSLSMKSIISLLFLLFVIVVALLGMQLFG 577

QY 922 CKFASERDGDITLDRKNFDSLIIWAIIVTVFQILTQEDWNKVLNMG-----ASTSSWAALY 976

Db 578 GRF-NFNDG---TPSANFDTFPAAMTVFQILTGEDWNEVMYNGIRSGQGVSSGMWSAIY 633

QY 977 FIALMTFGNYVFLNLLVAILVEGFOAEGDATKSE-SEPDFS-----1017

Db 634 FIVLTIFGNVTLNVFLAIAVDNLANAQELTKDEQEEEAFAFNQKHALQKAKEVSPMSAPN 693

QY 1018 -PSVDGDGDRKKRLAL-----VALGEHAELRKSL 1046

Db 694 MPSIERDRRRHHMSMWEPSSHLRERRRRHHMSVWEQRTSQLRRHMQMSSQEALNKEEA 753

QY 1047 PPLIIHTAATPMS-----HP---KSSSTGVGEALGSG-----SRRTSSSGSAE-----1086

Db 754 PPMNPLNPLNPLSPLNPLNAHPSLYRRRPPIEGLALGLEKCEERISRGGSLUKDIGG 813

QY	1087	-----PGAAHEMKCPPSARSSPHSPW-----SAASSWTSRRS	1119
Db	814	LTSVLDNQRSPLSGKREPPWLPKRSCHG--NCDPTQOETGGGETVVTTFEDRARHRQSQR	871
QY	1120	SRNSLGRAPSLKRSPSGERRSLLSGEGQESQDEEESSEEDRASAGSDHRRHGLSLEA	1179
Db	872	SRHRRVRTEGESASASRSR-----SASQERSLDEGVSIDGEKEHEPQSSHRKSKEPTIHEE	927
QY	1180	KSSFDL--PDTLQVP--GL-----HRTASGRSSASEHQDCNGKSAASRL	1219
Db	928	ERTQDLRRTNSLMSVPRSGVLGALDEAETPLVQPQPELEVKGDAALTEQEAEGSSEQALL	987
QY	1220	A-----RTLRTDDPQL-----DG-	1232
Db	988	ADVQLDVGRGISQSEPDLSGMTNMDKATTESTSVTVVAIPDVDPVLDSTVVNISNKTGDE	1047
QY	1233	-----DDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYIFPPQSRFRLLCH	1281
Db	1048	ASPLKEAETKEEEEEVEKKQKKEKRETG-KAMVPHS-----SMFIFSTNPIRKACH	1099
QY	1282	RIITHKMFHDVVLVIIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAVELAEMTVKV	1341
Db	1100	YIVNLRXFEMCILLVIAASSIALAAEDPVLTNSENKVV-LRYFDYVFTGVFTFEMVIKMI	1158
QY	1342	ALGWCFGEQAYLRSSWNVLGLLVLISVIDI-LVSMVSDSGTKILGMLRLVRLRLTLRPL	1400
Db	1159	DQGLILQDGSYFRDLWNILDFVVVVGALVAFALANALGTNKGDRDIKTIKSLRVLRLRPL	1218
QY	1401	RVISRAQGLKLVETLMSLKPICNIWVICCAFFIIFGILGVQLFKGKFFVC--QGEDTR	1458
Db	1219	KTIKRLPKLKAVIDCVVTSLNKNVFNILIVYKLFMFIAPAVIAVQLFKGKFFYCTDSSKDE	1278
QY	1459	N-----ITNKSDCAEASR--WVRHKYNFDNLGQALMSILFVLASKDGVIMYDGLDAVG	1511
Db	1279	KECIGNYVDHEKNKMEVKGREWKRHEPHYDNIIWALLTLFTVSTGEGWPQVLQHSVDTE	1338
QY	1512	VDQOPIMNHPWMLLYFISFLLIIVAFVFLNMFGVVVVENPHKCRQHQQHEEEAARRREKRL	1571
Db	1339	EDRGPSSNRNMEMSIFYVYFVVPFFVFVNFVALIITF-----QEOGDKMEE--	1388
QY	1572	RRLEKRRSKEKQMAEAOCKPYYSYGR--FRLLVHHLCTSHYLDLFTITGVIGLNVVTMA	1629
Db	1389	CSLEKNERACIDFAISAKPLTRYMPQNKRHTFOYRVWHFVVSFSEYTIMAMIALNTVVM	1448
QY	1630	MEHYQQPQIILDEALKICNYIFTVIFVESVFKLVAFARFPQDRWNQLDLAIVLLSIMG	1689
Db	1449	MKYASAPWTVELALKYLNIAFTMVFSLECVLKVIAFGFLNYFRDWTWNIFDFITVIGSITE	1508
QY	1690	ITLEEIEVNLSLPINPTIIRIMRVLRJARVLKLLKMAVGMRALHTVMQALPOVGNLGLL	1749
Db	1509	IILTDSKLVNTSGFNSFLKLFRA---ARLIKLLRQGYTIRILLWTFTVQSFKALPYVCLL	1565
QY	1750	FMLLFFIFAALGVFLGDLECD-ETHPCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIM	1808
Db	1566	IAMLFFIYAIIGMQVFGNIKLDEESH---INRHNFRSFFGSLMLLFRSATGEAWQEI	1621
QY	1809	KD--PSRDCDQESTC-----YNTVISPIYFVSFVLTAQFVLNVNVIIVLVMKHLERS	1857
Db	1622	LSCLGKGECPDTTAPSGQNESERCGLTDLAYVYFVSFIFFCSFLMLNLFVAVIMDNFEYL	1681
QY	1858	NKEAK-----EEAELEAELE-----LEMKTL-SPQPHSPLG-----SPF	1890
Db	1682	TRDSSILGPHHLDEFVRVWAEYDRAACGRIHYTEMVEMLTLMSP-----PLGLGKRCPSKV	1737
QY	1891	LWPGVEGVNSTDSPKGPAPHTTAH-----IGAAAG-----FSLEHPTM	1928
Db	1738	AYKRLVLMN-----MPVAEDMTVHFTSTLMALIRTDALDIKIAKGGADPQQDSELQKETL	1792
QY	1929	V--PHPEE-----VPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTABERSLGRGWG	1980
Db	1793	AIWPHLSQKMLDLLVPMPKASD-LTVGKIYAA---MMIMDYKQSKVKKQRQQL-----	1842
QY	1981	LPKAQSGSILSVHSQPAD-TSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQR	2039

Search completed: November 18, 2004, 13:34:36
Job time : 94.7329 secs

Db	1843	--EEQKNAPMFQMEPSSLPQEIISNAKALPYLQOD--PVSGLSGRSGYPSMSPLSPQE	1897
QY	2040	LRRQAAIRTDLSLDVQGLGSRREDLLSEVSGPSCPL-----TRSSSFW-----	2080
Db	1898	IFQLACM--DPADDGQFQEQQLV--VTDPPSSMRRSFSTIRDKRSNSSWLEEFMSERSSE	1953
QY	2081	-----GGSSIQVQ-----QRSG-----IQSKVSKHIRLP--APC----	2107
Db	1954	NTYKSRRRSYHSSURLSAHRLNSDSGHKSDTHRSGRGRGRSKERKHLSPDVSRCSNSEE	2013
QY	2108	PGLPSW-----AKDPPETRSSLLELDTLSWISGDLPLPSSQEEPLFPRLDKKCYSVET	2160
Db	2014	RGTQADWESPERRQSRSPSEGRSQTPNRQGTGSLSESSIPSIDTSTPRRSRRQLPPVPP	2073
QY	2161	QSCRRRPGFWLDEQRHHSIAVSCLDGSGQPRLCPSPSSLGQPLGGPGSRPKK-LSPPS	2219
Db	2074	--KPRPLLSYSSLMRHTGGISPPPDGSE-----GGSPLASQALESNSACLTESS	2120
QY	2220	ISIDPPESQGSRPP---CSPGVCLRRRAPASD	2248
Db	2121	NSLHPQQGQHPSPQHYISEPYLALHEDSHASD	2152

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:06:30 ; Search time 254.167 Seconds
(without alignments)
5177.235 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPRCVRTPLRGSAR.....KKDTLSLSGLSSDPTMDPZ 2287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11657	96.9	2254	1 CCAG RAT	O54898 rattus norv
2	11657	96.9	2254	2 AAG35186	Aag35186 rattus no
3	11532	95.9	2288	2 Q9WUB8	Q9wub8 rattus norv
4	11372.5	94.6	2295	2 Q9WUT2	Q9wut2 mus musculu
5	11263	93.6	2248	2 Q6PFV8	Q6pfv8 mus musculu
6	11263	93.6	2248	2 AAH57399	Aah57399 mus muscu
7	10732.5	89.2	2377	1 CCAG HUMAN	O43497 homo sapien
8	6809.5	56.6	1389	2 Q6ZPX4	Q6zpx4 mus musculu
9	6809.5	56.6	1389	2 BAC98104	Bac98104 mus muscu
10	6226	51.7	2359	1 CCAH RAT	Q9eq60 rattus norv
11	6222	51.7	2353	1 CCAH HUMAN	O95180 homo sapien
12	6190	51.5	2365	1 CCAH MOUSE	O88427 mus musculu
13	5418	45.0	2223	1 CCAI HUMAN	Q9p0x4 homo sapien
14	5354	44.5	1835	1 CCAI RAT	Q9z0y8 rattus norv
15	4750.5	39.5	1994	2 Q7Z6S8	Q7z6s8 homo sapien
16	4188.5	34.8	1762	2 Q7PQV4	Q7pqv4 anopheles g
17	4137.5	34.4	2893	2 Q9W433	Q9w433 drosophila
18	3856.5	32.1	1837	2 Q967R4	Q967r4 caenorhabdi
19	3849	32.0	1852	2 Q7Z002	Q7z002 caenorhabdi
20	3849	32.0	1852	2 AAR25651	Aar25651 caenorhab
21	3830	31.8	1844	2 Q7YZR6	Q7yze6 caenorhabdi
22	3830	31.8	1844	2 AAR25653	Aar25653 caenorhab
23	3824.5	31.8	1885	2 Q7Z003	Q7z003 caenorhabdi
24	3824.5	31.8	1885	2 AAR25652	Aar25652 caenorhab
25	3665	30.5	1460	2 Q80TJ2	Q80tj2 mus musculu
26	2941.5	24.5	1418	2 Q7JPB4	Q7jpb4 caenorhabdi
27	2941.5	24.5	1418	2 AAR30210	Aar30210 caenorhab
28	2813.5	23.4	1942	2 Q869H0	Q869h0 lymnaea sta
29	2098.5	17.4	1211	2 Q8MQ95	Q8mq95 caenorhabdi
30	1727	14.4	541	2 Q6PE92	Q6pe92 mus musculu
31	1727	14.4	541	2 AAH58206	Aah58206 mus muscu

32	1720.5	14.3	1810	2	O44930	O44930 aiptasia pa
33	1678	14.0	2327	1	CCAB_MOUSE	O55017 mus musculu
34	1674	13.9	2339	1	CCAB_HUMAN	Q00975 homo sapien
35	1673	13.9	2331	2	Q9TTA4	Q9tta4 bos taurus
36	1666.5	13.9	1599	2	Q7PNK9	Q7pnk9 anopheles g
37	1665.5	13.8	2259	1	CCAE_RABIT	Q02343 oryctolagus
38	1661	13.8	2333	2	O89089	O89089 rattus norv
39	1660	13.8	2295	2	Q923K6	Q923k6 rattus norv
40	1656	13.8	2304	2	Q9BMQ4	Q9bmq4 blattella g
41	1653.5	13.7	2272	1	CCAE_MOUSE	Q61290 mus musculu
42	1652.5	13.7	1891	2	O97017	O97017 stylophora
43	1650	13.7	2312	1	CCAE_HUMAN	Q15878 homo sapien
44	1649.5	13.7	1984	2	Q28644	Q28644 oryctolagus
45	1646.5	13.7	1847	2	Q6RKB0	Q6rkb0 brachydanio

ALIGNMENTS

RESULT 1
CCAG RAT STANDARD; PRT; 2254 AA.
AC O54898;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-gated calcium channel alpha subunit Cav3.1).
GN Name=Cacnalg;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98154730; PubMed=9495342;
RA Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J., Williamson M.P., Fox M., Rees M., Lee J.-H.;
RT "Molecular characterization of a neuronal low-voltage-activated T-type calcium channel.";
RL Nature 391:896-900(1998).
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1G gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Moderate expression in heart; low expression in placenta, kidney and lung.
CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.
CC -!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AF027984; AAC67372.1; --
DR PIR; T09053; T09053.
DR RGD; 68942; Cacnalg.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR005445; TVDCCAlphal.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR01629; TVDCCALPHAL.
KW Calcium channel; Calcium-binding; Glycoprotein; Ion transport;
KW Calcium channel; Multigene family; Phosphorylation; Repeat;
KW Ionic channel; Voltage-gated channel.
KW Transmembrane; Voltage-gated channel.
FT REPEAT 68 398 I.
FT REPEAT 730 968 II.
FT REPEAT 1242 1519 III.
FT REPEAT 1564 1822 IV.
FT DOMAIN 1 80 Cytoplasmic (Potential).
FT TRANSMEM 81 101 S1 of repeat I.
FT DOMAIN 102 119 Extracellular (Potential).
FT TRANSMEM 120 141 S2 of repeat I (Potential).
FT DOMAIN 142 150 Cytoplasmic (Potential).
FT TRANSMEM 151 170 S3 of repeat I.
FT DOMAIN 171 175 Extracellular (Potential).
FT TRANSMEM 176 193 S4 of repeat I.
FT DOMAIN 194 213 Cytoplasmic (Potential).
FT TRANSMEM 214 234 S5 of repeat I (Potential).
FT DOMAIN 235 370 Extracellular (Potential).
FT TRANSMEM 371 395 S6 of repeat I.
FT DOMAIN 396 744 Cytoplasmic (Potential).
FT TRANSMEM 745 765 S1 of repeat II (Potential).
FT DOMAIN 766 778 Extracellular (Potential).
FT TRANSMEM 779 800 S2 of repeat II (Potential).
FT DOMAIN 801 806 Cytoplasmic (Potential).
FT TRANSMEM 807 825 S3 of repeat II (Potential).
FT DOMAIN 826 833 Extracellular (Potential).
FT TRANSMEM 834 857 S4 of repeat II (Potential).
FT DOMAIN 858 868 Cytoplasmic (Potential).
FT TRANSMEM 869 889 S5 of repeat II (Potential).
FT DOMAIN 890 940 Extracellular (Potential).
FT TRANSMEM 941 965 S6 of repeat II (Potential).
FT DOMAIN 966 1251 Cytoplasmic (Potential).
FT TRANSMEM 1252 1274 S1 of repeat III (Potential).
FT DOMAIN 1275 1292 Extracellular (Potential).
FT TRANSMEM 1293 1313 S2 of repeat III (Potential).
FT DOMAIN 1314 1323 Cytoplasmic (Potential).
FT TRANSMEM 1324 1343 S3 of repeat III (Potential).
FT DOMAIN 1344 1357 Extracellular (Potential).
FT TRANSMEM 1358 1379 S4 of repeat III (Potential).
FT DOMAIN 1380 1389 Cytoplasmic (Potential).
FT TRANSMEM 1390 1413 S5 of repeat III (Potential).
FT DOMAIN 1414 1490 Extracellular (Potential).
FT TRANSMEM 1491 1516 S6 of repeat III (Potential).
FT DOMAIN 1517 1578 Cytoplasmic (Potential).
FT TRANSMEM 1579 1599 S1 of repeat IV (Potential).
FT DOMAIN 1600 1613 Extracellular (Potential).
FT TRANSMEM 1614 1635 S2 of repeat IV (Potential).
FT DOMAIN 1636 1642 Cytoplasmic (Potential).
FT TRANSMEM 1643 1661 S3 of repeat IV (Potential).
FT DOMAIN 1662 1675 Extracellular (Potential).
FT TRANSMEM 1676 1699 S4 of repeat IV (Potential).
FT DOMAIN 1700 1713 Cytoplasmic (Potential).
FT TRANSMEM 1714 1734 S5 of repeat IV (Potential).
FT DOMAIN 1735 1794 Extracellular (Potential).
FT TRANSMEM 1795 1822 S6 of repeat IV (Potential).
FT DOMAIN 1823 2254 Cytoplasmic (Potential).
FT DOMAIN 290 295 Poly-Gly.
FT DOMAIN 496 506 Poly-His.

FT	DOMAIN	1527	1530	Poly-Glu.
FT	SITE	354	354	Calcium ion selectivity and permeability (By similarity).
FT	SITE	924	924	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1465	1465	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1770	1770	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	173	173	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	246	246	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	306	306	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	310	310	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	322	322	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1427	1427	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1430	1430	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1666	1666	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	2254 AA;	250405 MW;	697BBB06360CF0F6 CRC64;
Query Match 96.9%; Score 11657; DB 1; Length 2254;				
Best Local Similarity 99.7%; Pred. No. 0;				
Matches 2219; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
QY	62	GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERSVMSL	121	
Db	30	GRQPGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERSVMSL	89	
QY	122	VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG	181	
Db	90	VILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG	149	
QY	182	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRLRLRAINRVPSNRILVTLTLP	241	
Db	150	DTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRLRLRAINRVPSNRILVTLTLP	209	
QY	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSLDLEPYQTENEDESPF	301	
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSLDLEPYQTENEDESPF	269	
QY	302	ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSNTTCVNMNQYTNCSAGEHN	361	
Db	270	ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSNTTCVNMNQYTNCSAGEHN	329	
QY	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL	421	
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL	389	
QY	422	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASPSEPGSCYEELKKYLVIILKAAR	481	
Db	390	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASPSEPGSCYEELKKYLVIILKAAR	449	
QY	482	RLAQVSRRAIGVRAGLLSSPVARSQEPQPSGSCSTRHRRLSVHHLVHHHHHHHHYHLGN	541	
Db	450	RLAQVSRRAIGVRAGLLSSPVARSQEPQPSGSCSTRHRRLSVHHLVHHHHHHHHYHLGN	509	
QY	542	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGPPRGAESVHSFYHADCHLEPVRQ	601	
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGPPRGAESVHSFYHADCHLEPVRQ	569	
QY	602	APPPRCPSSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPPGPF	661	
Db	570	APPPRCPSSEASGRTVGSGKVYPTVHTSPPEILKDKALVEVAPSPGPTLTSTFNIPPGPF	629	
QY	662	SSMHKLLTQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHWMPDSD	721	
Db	630	SSMHKLLTQSTGACHSSCKISSPCSKADSGACGPDSCPCYARTGAGEPESADHWMPDSD	689	
QY	722	SEAVYEFTQDAQHSDDLDPHSRRRQRLSGDPAEPSSVLAFWRLLICDTERKIVDSKYFGRG	781	
Db	690	SEAVYEFTQDAQHSDDLDPHSRRRQRLSGDPAEPSSVLAFWRLLICDTERKIVDSKYFGRG	749	
QY	782	IMIAILVNTLSMGIEYHEQPEELTNALIEISNIVFTSLFALEMLKLLVVGPFYIKNPYN	841	

Db 750 IMIALVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFYIKNPYN 809

QY 842 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRFPLPALQRLVLMKTMNDNVATF 901

Db 810 IFDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRFPLPALQRLVLMKTMNDNVATF 869

QY 902 CMLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 961

Db 870 CMLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 929

QY 962 LYNGWASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFSPSVD 1021

Db 930 LYNGWASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEGDATKSESEPDFSPSVD 989

QY 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMShPKSSSTGVGEALGSGSRRTSS 1081

Db 990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMShPKSSSTGVGEALGSGSRRTSS 1049

QY 1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSSRRSSNSLGRAPSLKRSPSGERRS 1141

Db 1050 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSSRRSSNSLGRAPSLKRSPSGERRS 1109

QY 1142 LLSGEGQESQDEEESSEDRASPAGSDHRRHGLSREAKSSFDLPDTLQVPLHRTASGR 1201

Db 1110 LLSGEGQESQDEEESSEDRASPAGSDHRRHGLSREAKSSFDLPDTLQVPLHRTASGR 1169

QY 1202 SSASEHQDCNGKSASGRILARTLRDTPQLDGDDBDDEGNLSKGERIQAWVRSRLPACCRE 1261

Db 1170 SSASEHQDCNGKSASGRILARTLRDTPQLDGDDBDDEGNLSKGERIQAWVRSRLPACCRE 1229

QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFL 1321

Db 1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFL 1289

QY 1322 TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSG 1381

Db 1290 TLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSG 1349

QY 1382 TKILGMLRVLRLRLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441

Db 1350 TKILGMLRVLRLRLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409

QY 1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASVWRVHKYNFDNLGQALMSLFVLASKDGVWD 1501

Db 1410 VQLFKGKFFVCQGEDTRNITNKSDCAEASVWRVHKYNFDNLGQALMSLFVLASKDGVWD 1469

QY 1502 IMYDGLDAVGVDQCPIMNHNPMWLLYFISFLILVAFVFLNMFVGVVVENFHKCRQHQQEE 1561

Db 1470 IMYDGLDAVGVDQCPIMNHNPMWLLYFISFLILVAFVFLNMFVGVVVENFHKCRQHQQEE 1529

QY 1562 EARRREEKRLRLEKRRSKEKQMAEAQCKPYSDYSRFRLLVHLLCTSHYLDLFTITGVI 1621

Db 1530 EARRREEKRLRLEKRRSKEKQMAEAQCKPYSDYSRFRLLVHLLCTSHYLDLFTITGVI 1589

QY 1622 GLNVVTMAMEHYQQPQILDEALKICNIYIFTVIFVFESVFKLVAFAPRRFFQDRWNQLDLA 1681

Db 1590 GLNVVTMAMEHYQQPQILDEALKICNIYIFTVIFVFESVFKLVAFAPRRFFQDRWNQLDLA 1649

QY 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVMQALP 1741

Db 1650 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVMQALP 1709

QY 1742 QVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTG 1801

Db 1710 QVGNLGLLFMLFFIFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTG 1769

QY 1802 DNWNGIMKDPSCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEA 1861

Db 1770 DNWNGIMKDTLRCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEA 1829

QY 1862 KEEAELEAELEEMKTLSPQHPSPGLSPFWGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921

Db 1830 KEEAELEAELEEMKTLSPQHPSPGLSPFWGVEGVNSTDSPKPGAPHTTAHIGAASGF 1889

QY 1922 SLEHPTMVPHPPEEVPLGPDLTLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHGWGL 1981

Db 1890 SLEHPTMVPHPPEEVPLGPDLTLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHGWGL 1949

QY 1982 PKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPGSRPLAQRP 2041

Db 1950 PKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPGSRPLAQRP 2009

QY 2042 RQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFVGGSSIOVQQRSGIQSKVSKHI 2101

Db 2010 RQAAIRTDSDLVQGLGSRREDLLSEVSGPSCPLTRSSSFVGGSSIOVQQRSGIQSKVSKHI 2069

QY 2102 RLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLPSSQEEPLFPRDLKKCYSVETQ 2161

Db 2070 RLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLPSSQEEPLFPRDLKKCYSVETQ 2129

QY 2162 SCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGGSRPKKLSPPSIS 2221

Db 2130 SCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSLGGQPLGGGSRPKKLSPPSIS 2189

QY 2222 IDPPESQGSRRPCCSPGVCLRRRAPASDSKDPSSVSSPLDSTAASPSPKKDTLSLGLSSDP 2281

Db 2190 IDPPESQGSRRPCCSPGVCLRRRAPASDSKDPSSVSSPLDSTAASPSPKKDTLSLGLSSDP 2249

QY 2282 TMDP 2286

Db 2250 TMDP 2254

RESULT 2

AAG35186

ID AAG35186 PRELIMINARY; PRT; 2254 AA.

AC AAG35186;

DT 02-MAR-2004 (TremBLrel. 27, Created)

DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TremBLrel. 27, Last annotation update)

DE Calcium channel alpha-1-G subunit.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=brain;

RX PubMed=11073957;

RA McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,

RA Baillie D.L., Stea A., Snutch T.P.;

RT "Molecular and functional characterization of a family of rat brain T-

RT type calcium channels.";

RL J. Biol. Chem. 276:3999-4011(2001).

DR EMBL; AF290212; AAG35186.2; -

SQ SEQUENCE 2254 AA; 250405 MW; 697BBE06360CF0F6 CRC64;

Query Match

Best Local Similarity 96.9%; Score 11657; DB 2; Length 2254;

Matches 2219; Conservative 99.7%; Pred.No. 0;

Mismatches 6; Indels 0; Gaps 0;

QY 62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPFVYSML 121

Db 30 GRQPGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPFVYSML 89

QY 122 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKCYLG 181

Db 90 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKCYLG 149

QY 182 DTWNRLDFFTVIAGMLEYSLDLQNVSPSAVRTVRVLRPLRAINRVPSMRILVTLTLLDLP 241

Db 150 DTWNRLDFFTVIAGMLEYSLDLQNVSPSAVRTVRVLRPLRAINRVPSMRILVTLTLLDLP 209

QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVDLEPYQOTENEDESPP 301

Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVDLEPYQOTENEDESPP 269

QY 302 ICSQPRENGMRSRCSVPTLRGEGGGPPCSLDYETYNSSSNTTCVWNQYTTNCSAGEHN 361
Db 270 ICSQPRENGMRSRCSVPTLRGEGGGPPCSLDYETYNSSSNTTCVWNQYTTNCSAGEHN 329
QY 362 PFKGAINFDNIGYAWIAIFQVITILEGWVDIMYFVMDAHSFYNFIFYFILLIIVGSFFMINL 421
Db 330 PFKGAINFDNIGYAWIAIFQVITILEGWVDIMYFVMDAHSFYNFIFYFILLIIVGSFFMINL 389
QY 422 CLVVIATQFSETKQRESQOLMREQVRFLSNASTLASFSEPGSCYBELLKYLVIILRKAAR 481
Db 390 CLVVIATQFSETKQRESQOLMREQVRFLSNASTLASFSEPGSCYBELLKYLVIILRKAAR 449
QY 482 RLAQVSRAGIVRAGLLSSPVARSGQBPQPSGSCTRSHRRRLSVHLLVHHHHHHHHYHLGN 541
Db 450 RLAQVSRAGIVRAGLLSSPVARSGQBPQPSGSCTRSHRRRLSVHLLVHHHHHHHHYHLGN 509
QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTSPGGPPRGAESVHSFYHADCHLEPVRQ 601
Db 510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTSPGGPPRGAESVHSFYHADCHLEPVRQ 569
QY 602 APPPRCPSEASGRTVSGKVYPTVHTSPPPPEILKD KALVEAPSPGPPTLTSTFNIPPGPF 661
Db 570 APPPRCPSEASGRTVSGKVYPTVHTSPPPPEILKD KALVEAPSPGPPTLTSTFNIPPGPF 629
QY 662 SSMHKLELTQSTGACHSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPPDS 721
Db 630 SSMHKLELTQSTGACHSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPPDS 689
QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQRLSLGPDABPSSVLAFWRLICDTFRKIVDSKYFGRG 781
Db 690 SEAVYEFTQDAQHSDLRDPHSRRRQRLSLGPDABPSSVLAFWRLICDTFRKIVDSKYFGRG 749
QY 782 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
Db 750 IMTAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809
QY 842 IPDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVVLMTMDNVATF 901
Db 810 IPDGVIVVISWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVVLMTMDNVATF 869
QY 902 CMLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 961
Db 870 CMLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKV 929
QY 962 LYNGMASTSSWAALYFIALMTFCNVVLENLVAILVEGFOAEGDATKSESEPDFFSPSVD 1021
Db 930 LYNGMASTSSWAALYFIALMTFCNVVLENLVAILVEGFOAEGDATKSESEPDFFSPSVD 989
QY 1022 GDGRKKRLALVALGEHAELKSLLPPLIIHTAATPM SHPKSSSTGVGEALGSGSRRTS 1081
Db 990 GDGRKKRLALVALGEHAELKSLLPPLIIHTAATPM SHPKSSSTGVGEALGSGSRRTS 1049
QY 1082 SGSAEPCAAHHEMKCPPSARS SPWSAASSWTSRRSSRNSLGRAPSLKRSPSGERRS 1141
Db 1050 SGSAEPCAAHHEMKCPPSARS SPWSAASSWTSRRSSRNSLGRAPSLKRSPSGERRS 1109
QY 1142 LLSGEGQESQDEEESSEEDRASPGSDHRHRSGLERBAKSSFDLPDTLQVPLHRTASGR 1201
Db 1110 LLSGEGQESQDEEESSEEDRASPGSDHRHRSGLERBAKSSFDLPDTLQVPLHRTASGR 1169
QY 1202 SSASEHODNGKSASGRLARTLRDTPQLDGDNDNDEGNLSKGERIQAWVSRSLPACCRE 1261
Db 1170 SSASEHODNGKSASGRLARTLRDTPQLDGDNDNDEGNLSKGERIQAWVSRSLPACCRE 1229
QY 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIIIFLNCITIAMERPKIDPHSAERIFL 1321
Db 1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIIIFLNCITIAMERPKIDPHSAERIFL 1289
QY 1322 TLSNYYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVL DGLLVLSVIDILVSMVSDSG 1381
Db 1290 TLSNYYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVL DGLLVLSVIDILVSMVSDSG 1349

QY 1382 TKILGMLRVLRLLRTRLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
Db 1350 TKILGMLRVLRLLRTRLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409
QY 1442 VOLFKGKFFVCQGEDTRNITNKSDCAEASYSYRVRHKKYNFNILGQALMSLFLVASKDGWVD 1501
Db 1410 VOLFKGKFFVCQGEDTRNITNKSDCAEASYSYRVRHKKYNFNILGQALMSLFLVASKDGWVD 1469
QY 1502 IMYDGLDAVGVDQQPIIMHNPNMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEE 1561
Db 1470 IMYDGLDAVGVDQQPIIMHNPNMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEE 1529
QY 1562 EARRREEKRLRLEKKRRSKEKQMAEAOCKPYYSYDSYRFRLLVHHLCTSHYLDLFTITGVI 1621
Db 1530 EARRREEKRLRLEKKRRSKEKQMAEAOCKPYYSYDSYRFRLLVHHLCTSHYLDLFTITGVI 1589
QY 1622 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRFFQDRWNQLDLA 1681
Db 1590 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRFFQDRWNQLDLA 1649
QY 1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKXAVGMRALLLHTVMQALP 1741
Db 1650 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKXAVGMRALLLHTVMQALP 1709
QY 1742 QVGNLGLLFMLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTG 1801
Db 1710 QVGNLGLLFMLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTG 1769
QY 1802 DNWNGIMKDP SRDCDOESTCYNTVISPIYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEA 1861
Db 1770 DNWNGIMKDTLRDCDOESTCYNTVISPIYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEA 1829
QY 1862 KEEAELEAELELEMKTLSPQHPSPGLSPFLMPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
Db 1830 KEEAELEAELELEMKTLSPQHPSPGLSPFLMPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1889
QY 1922 SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCNRCNGSTAERSLHGRWG 1981
Db 1890 SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCNRCNGSTAERSLHGRWG 1949
QY 1982 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTGWGAIKLP PPGRSPLAQRP 2041
Db 1950 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTGWGAIKLP PPGRSPLAQRP 2009
QY 2042 RQAAIRTDSDVQGLGSREDLLSEVSGPSCPLTRSSFWGGSSIQVQQRSGIQSKVSKHI 2101
Db 2010 RQAAIRTDSDVQGLGSREDLLSEVSGPSCPLTRSSFWGGSSIQVQQRSGIQSKVSKHI 2069
QY 2102 RLPAPCPGLEPSWAKDPETRSSLDELDTLSWISGDLPLSSQEEPLFPRLDKKCYSVETQ 2161
Db 2070 RLPAPCPGLEPSWAKDPETRSSLDELDTLSWISGDLPLSSQEEPLFPRLDKKCYSVETQ 2129
QY 2162 SCRRPFGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSLGGQPLGGPGSRPKKLSPPSIS 2221
Db 2130 SCRRPFGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSLGGQPLGGPGSRPKKLSPPSIS 2189
QY 2222 IDPPESQGSRRPPCSPGVCLRRRAPASDSKDPSSVSPDLSTAASPSPKKDTLSLGLSSDP 2281
Db 2190 IDPPESQGSRRPPCSPGVCLRRRAPASDSKDPSSVSPDLSTAASPSPKKDTLSLGLSSDP 2249
QY 2282 TDMDP 2286
Db 2250 TDMDP 2254

RESULT 3
Q9WUB8
ID Q9WUB8 PRELIMINARY; PRT; 2288 AA.
AC Q9WUB8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE T-type calcium channel isoform.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=20081696; PubMed=10615950;
RA Zhuang H., Bhattacharjee A., Hu F., Zhang M., Goswami T., Wang L.,
RA Wu S., Berggren P.O., Li M.;
RT "Cloning of a T-type Ca2+ channel isoform in insulin-secreting
RT cells.";
RL Diabetes 49:59-64 (2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
DR EMBL; AF125161; AAD26858.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR002077; Ca_channel_alpha.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR005445; TVDCCalpha1.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR01629; TVDCCALPHA1.
KW Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW Transmembrane; Transport; Voltage-gated channel.
SQ SEQUENCE 2288 AA; 253476 MW; B89DB5A1D81757F CRC64;

Query Match 95.9%; Score 11532; DB 2; Length 2288;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2206; Conservative 1; Mismatches 18; Indels 34; Gaps 2;

QY 62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERVSML 121
DB 30 GRQPGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERVSML 89

QY 122 VILLNCVTGLMFRPCEDIACDSQRCRILQAQFDDFIFAFVAVEMVVKWVALGIFGKKCYLG 181
DB 90 VILLNCVTGLMFRPCEDIACDSQRCRILQAQFDDFIFAFVAVEMVVKWVALGIFGKKCYLG 149

QY 182 DTWNRLDFFIVIAWMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTP 241
DB 150 DTWNRLDFFIVIAWMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTP 209

QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLPEYYQTENEDESPP 301
DB 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLPEYYQTENEDESPP 269

QY 302 ICSPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYTYTNCASGEHN 361
DB 270 ICSPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSNTTCVNNQYTYTNCASGEHN 329

QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 421
DB 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 389

QY 422 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLYLVYILRKAAR 481
DB 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLYLVYILRKAAR 449

QY 482 RLAQVSRAGIVRAGLLSSPVARSQEQPQSGSCSTRSHRRLSVHHLVHHHHHHHHVHLGN 541
DB 450 RLAQVSRAGIVRAGLLSSPVARSQEQPQSGSCSTRSHRRLSVHHLVHHHHHHHHVHLGN 509

QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPGPPRGAESVHSFYHADCHLEPVRQC 601

DB 510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPGPPRGAESVHSFYHADCHLEPVRQC 569
QY 602 APPPRCPSEASGRTVSGKVYPTVHTSPPPPEILKDKALVEAPSPGPPTLTSTFNIPPGPF 661
DB 570 APPPRCPSEASGRTVSGKVYPTVHTSPPPPEILKDKALVEAPSPGPPTLTSTFNIPPGPF 629
QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSDSD 721
DB 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSDSD 689
QY 722 SEAVVEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTERKIVDSKYFGRG 781
DB 690 SEAVVEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTERKIVDSKYFGRG 749
QY 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
DB 750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809
QY 842 IPDGVIVIVISVWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDVATF 901
DB 810 IPDGVIVIVISVWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDVATF 869
QY 902 CMLMLLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIWTVFQILTQEDWNKV 961
DB 870 CMLMLLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIWTVFQILTQEDWNKV 929
QY 962 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAE----- 1003
DB 930 LYNMGASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEHIGKREDASGQLSCIQLP 989
QY 1004 -----GDATESESEPDFFSPSVDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM 1058
DB 990 VNSQGGDATESESEPDFFSPSVDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM 1049
QY 1059 SHPKSSSTGVGEALGSGRRRTSSSGSABPGAAHEMKCPPSARSSPHSPWSAASSWTSRR 1118
DB 1050 SLPKSSSTGVGEALGSGRRRTSSSGSABPGAAHEMKCPPSARSSPHSPWSAASSWTSRR 1109
QY 1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHRHRSGLERE 1178
DB 1110 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHRHRSGLERE 1169
QY 1179 AKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKSASGLARTLTDDPOLDGDNDDE 1238
DB 1170 AKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKSASGLARTLTDDPOLDGDNDDE 1229
QY 1239 GNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIF 1298
DB 1230 GNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIF 1289
QY 1299 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1358
DB 1290 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1349
QY 1359 VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTPLRVISRAQGLKLVVETLMS 1418
DB 1350 VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTPLRVISRAQGLKLVVETLMS 1409
QY 1419 SLKPIGNIWVICCAFFIIFGILGVQLFKGKFFVCOGEDTRNITNKSDCAEASVWRVHKY 1478
DB 1410 SLKPIGNIWVICCAFFIIFGILGVQLFKGKFFVCOGEDTRNITNKSDCAEASVWRVHKY 1469
QY 1479 NFDNLGOALMSLVASKDGVIMYDGLDVGVDQQPIMNHNPMMLLYFISFLLIVAFF 1538
DB 1470 NFDNLGOALMSLVASKDGVIMYDGLDVGVDQQPIMNHNPMMLLYFISFLLIVAFF 1529
QY 1539 VLNMFVGVVVENFHKCRHQHEEAEARRREKRLRREKRR-----SKEKQMAE 1587
DB 1530 VLNMFVGVVVENFHKCRHQHEEAEARRREKRLRREKRRMLDDVIASSSSASAAAE 1589
QY 1588 AQCKPYSDYSRFRLLVHLCCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQLDEALKICN 1647

Db 1590 AQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLVNVTWAMEHYQQPQILDEALKICN 1649

QY 1648 YIFTVIVFESVFKLVAFARFRFFQDRWNQDLDAIVLLSIMGTTLEEIEVNLSPINPTI 1707

Db 1650 YIFTVIVFESVFKLVAFGRFRFFQDRWNQDLDAIVLLSIMGTTLEEIEVNASLPINPTI 1709

QY 1708 IRIMRVLRIRVLKLLKMAVGMRALHTVMQALPOVGNLGLLFMLLFFIFAALGVLEFGD 1767

Db 1710 IRIMRVLRIRVLKLLKMAVGMRALDVTVMQALPOVGNLGLLFMLLFFIFAALGVLEFGD 1769

QY 1768 LECDETHPCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDPDRDCDQESTCYNIVIS 1827

Db 1770 LECDETHPCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDCDQESTCYNIVIS 1829

QY 1828 PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAELEAELEMKTLSPQPHSLPG 1887

Db 1830 PIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEAELEAELEMKTLSPQPHSLPG 1889

QY 1888 SPFLWPGEVGNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEVPVPLGPDLLTVR 1947

Db 1890 SPFLWPGEVGNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHPEVPVPLGPDLLTVR 1949

QY 1948 KSGVSRTHSLPNDSYMCNGSTAERSLGRGWGLPKAQSGSILSVHSQPADTSCILQLPK 2007

Db 1950 KSGVSRTHSLPNDSYMCNGSTAERSLGRGWGLPKAQSGSILSVHSQPADTSCILQLPK 2009

QY 2008 DVHYLLQPHGAPTGAIPKLPPPGRSPLAQRPLRQAAIRTDSDLDVQGLGSREDLLSEVS 2067

Db 2010 DVHYLLQPHGAPTGAIPKLPPPGRSPLAQRPLRQAAIRTDSDLDVQGLGSREDLLSEVS 2069

QY 2068 GPSCPLTRSSSFVGGSSIQVQORSGIOQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSL 2127

Db 2070 GPSCPLTRSSSFVGGSSIQVQORSGIOQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSL 2129

QY 2128 DTELSWISGDLPLSSQEEPLFPRDLKCKYSVETQSCRRRPGFWLDEQRRHSIAVSCLD 2187

Db 2130 DTELSWISGDLPLSSQEEPLSPRDLKCKYSVETQSCRRRPGFWLDEQRRHSIAVSCLD 2189

QY 2188 SQPRLCPSSSLGGQPLGGPGSRPKKLSPPSISIDPPESQGSRRPPGVCVCLRRRAPAS 2247

Db 2190 SQPRLCPSSSLGGQPLGGPGSRPKKLSPPSISIDPPESQGSRRPPGVCVCLRRRAPAS 2249

QY 2248 DSKDPSVSSPLDSTAASPSPKDTLSLGLSSDPTDMDP 2286

Db 2250 DSKDPSVSSPLDSTAASPSPKDTLSLGLSSDPTDMDP 2288

RESULT 4

Q9WUT2 PRELIMINARY; PRT; 2295 AA.

ID Q9WUT2

AC Q9WUT2;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Voltage-gated calcium channel, alpha-1-G subunit.

GN Name=Cacnalg;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=99189326; PubMed=10087148;

RA Klugbauer N., Marais E., Lacinova L., Hofmann F.;

RT "A T-type calcium channel from mouse brain.";

RL Pflugers Arch. 437:710-715(1999).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

CC EMBL; AJ012569; CAB40793.1; -.

DR MGD; MGI:1201678; Cacnalg.

DR GO; GO:0005886; C:plasma membrane; IDA.

DR GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.

DR InterPro; IPR001682; Ca/Na_pore.

DR InterPro; IPR002111; Cat_channel_TrpL.

DR InterPro; IPR002077; Ca_channel_alpha.

DR InterPro; IPR005821; Ion_trans.

DR InterPro; IPR005820; M4channel_nlg.

DR InterPro; IPR005445; TVDCCAlphal.

DR Pfam; PF00520; Ion_trans; 4.

DR PRINTS; PR00167; CACHANNEL.

DR PRINTS; PR01629; TVDCCALPHA1.

KW Calcium channel; Calcium-binding; Ion transport; Ionic channel;

KW Transmembrane; Transport; Voltage-gated channel.

SQ SEQUENCE 2295 AA; 253957 MW; FE817D054ED26984 CRC64;

Query Match 94.6%; Score 11372.5; DB 2; Length 2295;

Best Local Similarity 96.1%; Pred. No. 0;

Matches 2178; Conservative 12; Mismatches 34; Indels 43; Gaps 4;

QY 62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERVSML 121

Db 30 GRQPGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERVSML 89

QY 122 VILLNCVTGLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMKVALGIFGKKCYLG 181

Db 90 VILLNCVTGLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMKVALGIFGKKCYLG 149

QY 182 DTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLD 241

Db 150 DTWNRLDFFIVTAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLD 209

QY 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVDLEPPYQTENEDESP 301

Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVDLEPPYQTENEDESP 269

QY 302 ICSPRENGMRSRCSVPTLRGEGGGPPCSILDYETYNSSNTTCVNNQYTYTNC SAGEHN 361

Db 270 ICSPRENGMRSRCSVPTLRGEGGGPPCGLDYEAYNSSNTTCVNNQYTYTNC SAGEHN 329

QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL 421

Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINL 389

QY 422 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELKLVYLKKAAR 481

Db 390 CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELKLVYLKKAAR 449

QY 482 RLAQVSRAGVGRAGLLSSPVARSQEQPQSGCTSRHRRLSVHLLVHHHHHHHHYHLGN 541

Db 450 RLAQVSRAGVGRAGLLSSPVARGQEQPQSGCTSRHRRLSVHLLVHHHHHHHHYHLGN 509

QY 542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTSPGGPPRGAESVHSFYHADCHLEPVRCQ 601

Db 510 GTLRVPRASPEIQDRDANGSRWLMLPPPSTPTSPGGPPRGAESVHSFYHADCHLEPVRCQ 569

QY 602 APPPRCPSEASGRTVSGKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTFSNIPPGPF 661

Db 570 APPPRSPSEASGRTVSGKVYPTVHTSPPEMLKDKALVEVAPSPGPPTLTFSNIPPGPF 629

QY 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPE SADVMPDSD 721

Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPE SADVMPDSD 689

QY 722 SEAVYEFTQDAQHSDLRDPHSRRRQRSGLPDAEPSSVLAFWRLICDTFERKIVDSKYFGRG 781

Db 690 SEAVYEFTQDAQHSDLRDPH-RRRRPSLGLPDAEPSSVLAFWRLICDTFERKIVDSKYFGRG 748

QY 782 IMIALLVNTLSMGIYHEQEPELTNALEISNIVFTSLPALEMLLKLVLVGPFGYIKNPYN 841

Db 749 IMIALLVNTLSMGIYHEQEPELTNALEISNIVFTSLPALEMLLKLVLVGPFGYIKNPYN 808

QY 842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDVATF 901

Db 809 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDVATF 868

QY 902 CMLLMFIFIFISILGMHLFGCKFASERDGDITLPRKNFDSLLWAIIVTVFQILTQEDWNKV 961
Db 869 CMLLMFIFIFISILGMHLFGCKFASERDGDITLPRKNFDSLLWAIIVTVFQILTQEDWNKV 928
QY 962 LYNGMASTSSWAALYFIALMTFNGVYVLFNLLVAILVEGFAE-----1003
Db 929 LYNGMASTSSWAALYFIALMTFNGVYVLFNLLVAILVEGFAEIGKREDTSGQLSCIQLP 988
QY 1004 -----GDATKSESEPDFFFSPVDGDRKKRLALVALGEHAELRKSLLPLIHTAATPM 1058
Db 989 VNSQGGDATKSESEPDFFFSPVDGDRKKRLALVALGEHSELKSLPLPLIHTAATPM 1048
QY 1059 SHEPKSSSTGVGEALGSGSRRTSSSGSAEPGAHHEMKCPPSARSSPHSPWSAASSWTSRR 1118
Db 1049 SLPKSSSTGVGEALGSGSRRTSSSGSAEPGTAHHEMKPPSARSSPHSPWSAASSWTSRR 1108
QY 1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEEDRASPGSDHHRGSLERE 1178
Db 1109 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEEDRASPGSDHHRGSLERE 1168
QY 1179 AKSSFDLPDTLOVPGHLHRTASGRSSASEHQDCNGKSGASGRLARTLRTDDPQDGGDDNDE 1238
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QY 1239 GNLSKGERIQAWRSRLPACCRERDSWSAYIFPQSRFRLLCHRIITHKMFHDHVVLIIF 1298
Db 1229 GNLSKGERLRAWVRARLPACCRERDSWSAYIFPQSRFRLLCHRIITHKMFHDHVVLIIF 1288
QY 1299 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1358
Db 1289 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1348
QY 1359 VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLTLRPLRVISRAQGLKLVVETLMS 1418
Db 1349 VLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLTLRPLRVISRAQGLKLVVETLMS 1408
QY 1419 SLKPIGNIVVICAPFIIIFGILGVQLFKGKFFVCQGEDTRNITNKSCEAEASYRWVRHKY 1478
Db 1409 SLKPIGNIVVICAPFIIIFGILGVQLFKGKFFVCQGEDTRNITNKSCEAEASYRWVRHKY 1468
QY 1479 NFDNLGQALMSLFLASKDGVVDIMYDGLDVGVDVQOQPMNHNPNMMLLYFISFLLIIVAFF 1538
Db 1469 NFDNLGQALMSLFLASKDGVVDIMYDGLDVGVDVQOQPMNHNPNMMLLYFISFLLIIVAFF 1528
QY 1539 VLNMFVGVVVENFHKCRHQHQBEEARRRERKRLRLEKRRSRKEKQMA-----1586
Db 1529 VLNMFVGVVVENFHKCRHQHQBEEARRRERKRLRLEKRRSRKEKQMA-----1586
QY 1587 -----EAQCKPYSDYSRFRLLVHLCTSHYDLDFITVIGLNVVTMAMEHYQQPQILD 1640
Db 1589 SASAASEAQCKPYSDYSRFRLLVHLCTSHYDLDFITVIGLNVVTMAMEHYQQPQILD 1648
QY 1641 EALKICNYIFTVIFVLESVFKLVAFARFRFFQDRWNQDLAIVLISIMGITLEEIEVNLS 1700
Db 1649 EALKICNYIFTVIFVLESVFKLVAFARFRFFQDRWNQDLAIVLISIMGITLEEIEVNLS 1708
QY 1701 LPINPTIIRIMRVLRIARVLKLLKMAVGRALLHTVMQALPQVGNLGLLFFLFFIFAAL 1760
Db 1709 LPINPTIIRIMRVLRIARVLKLLKMAVGRALLHTVMQALPQVGNLGLLFFLFFIFAAL 1768
QY 1761 GVELFGDLECDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSCRDCQEST 1820
Db 1769 GVELFGDLECDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPSCRDCQEST 1828
QY 1821 CYNVTISPIYFVSFVLTQAQFVLNVVIAVLMKHLEESNKEAEAELEAELEEMKTLSP 1880
Db 1829 CYNVTISPIYFVSFVLTQAQFVLNVVIAVLMKHLEESNKEAEAELEAELEEMKTLSP 1888
QY 1881 QPHSPLGSPFLWPGEVGNSTDSKPKGAPHTTAHIGAA-SGFSLEHPTMVPHPEEVPVPL 1939
Db 1889 QPHSPLGSPFLWPGEVGNSTDSKPKGAPHTTAHIGAA-SGFSLEHPTMVPHPEEVPVPL 1948

RESULT 5
Q6PFV8

ID Q6PFV8 PRELIMINARY; PRT; 2248 AA.
AC Q6PFV8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ccna1g protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057399; AAH57399.1; -;
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.


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QY 2090 RSGIQSKVSKHIRLPAPCPGLEPSPWAKDPDPETRSSLELDTLSWISGDLPLSPSQEBPLFP 2149
Db 2052 RSGSQSKVSKHIRLPAPCPGLEPSPWAKDPQETRSSLELDTLSWISGDLPLSPSQEBPLSP 2111
QY 2150 RDLKKCYSVETQSCRRRPPGFWLDEQRRHSIAVSCDSGSPRLCPSPSSSLGGQPLGPGS 2209
Db 2112 RDLKKCYVEAQSCRRRPPGSLWDEQRRHSIAVSCDSGSPRLCPSPSSSLGGQPLGPGS 2171
QY 2210 RPKKLSPPSISIDPPESQGRPPCPGVCCLRRRAPASDSKDPVSSPLDSTAASPKK 2269
Db 2172 RPKKLSPPSISIDPPESQGRPPCPGVCCLRRRAPASDSKDPVSSPLDSTAASPKK 2231
QY 2270 DTLSSGLSSDPTDMDP 2286
Db 2232 DALSSGLSSDPTDLDP 2248

RESULT 6
AAH57399
ID AAH57399 PRELIMINARY; PRT; 2248 AA.
AC AAH57399;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Caenalg protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057399; AAH57399.1; -
SQ SEQUENCE 2248 AA; 24888 MW; 332C5A8D9115A64F CRC64;
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Query Match 93.6%; Score 11263; DB 2; Length 2248;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 2155; Conservative 12; Mismatches 40; Indels 30; Gaps 4;

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QY 62 GAAGAGSTKDPGADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPFWRVSM 121
Db 30 GRQPGSTKDPGADSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPFWRVSM 89
QY 122 VILLNCVTGLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKWVALGIFGKKCVLG 181
Db 90 VILLNCVTGLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKWVALGIFGKKCVLG 149
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QY 242 MLGNVLLLCFFVFFIFIGIVGVQLWAGLLRNRCFLPENFSLPSVDLEPYQYQTEDESPF 301
Db 210 MLGNVLLLCFFVFFIFIGIVGVQLWAGLLRNRCFLPENFSLPSVDLEPYQYQTEDESPF 269
QY 302 ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLDYETNYSSTNTTCVNNQYTYNCSAGEHN 361
Db 270 ICSQPRENGMRSCRSVPTLRGEGGGPPCGLDYEAYNYSSTNTTCVNNQYTYNCSAGEHN 329
QY 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 421
Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINL 380
QY 422 CLVVIATQFSETKQRESQRLMREQVRFLSNASTLASFSEPGSCYEELLLKYLVLKKAAR 481
Db 381 -----FSETKQRESQRLMREQVRFLSNASTLASFSEPGSCYEELLLKYLVLKKAAR 432
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Db 433 RLAQVSRAGVRAGLLLSPVVRGGQEPQPSGSCSTRSHRRRLSVHLLVHHHHHHHHYHLGN 492
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QY 602 APPPRCPSEASGRTVGSGKYPTVHTSPPPPEILKDKALVEVAPSPGPTLTSTENIPPGPF 661
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QY 842 IFDGVIVISVWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDVATF 901
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Db 1212 RDSWSAYIFPPQSRFLLRCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFL 1271
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Db 1512 EARRREEKRLRLEKRRNMLDDVIAAGSASAAEAQCKPYYSYRFRLLLVHHLCTS 1571
QY 1611 HYLDLFIITGVLGNVVTMAMEHYQQPQILDEALKICNYIFTVIFVESVFKLVAFARFR 1670
Db 1572 HYLDLFIITGVLGNVVTMAMEHYQQPQILDEALKICNYIFTVIFVESVFKLVAFARFR 1631
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QY 1851 MKHLEESNKEAKEAELEAELEEMKTLSPQPHSPGSPFLWPVGVEGVNSTDSPKPGAPH 1910
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QY 1911 TTAHIGAA-SGFSLEHPTMVPHEVPVPLGPDLLTVKSGVSRTHSLPNDSYMCRNGST 1969
Db 1872 TTAHIGAASSGFSLEHPTMVPHEEGVPVPLGPDLLTVKSGVSRTHSLPNDSYMCRNGST 1931
QY 1970 AERSLHGRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPP 2029
Db 1932 AERSLHGRGWGLPKAQSGSILSVHSQPADTSCILQLPKDAHYLLQPHGAPTWGAIPKLPP 1991
QY 2030 PGRSPLAQRPLRQAARTDSDLVQGLGSREDLLSEVSGPSCPLTRSSSFWGSSIQVQQ 2089
Db 1992 PGRSPLAQRPLRQAARTDSDLVQGLGSREDLLSEVSGPSCPLTRSSSFWGSSIQVQQ 2051
QY 2090 RSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRRSSLELDTLSWISGDLPLPSSQEEPLFP 2149
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QY 2150 RDLKKCYSVETQSCRRRPPGFWLDEORRHIAVSCLDGSGQPRCLCPSPSSLGQPLGGPGS 2209
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QY 2210 RPKKLSPPSISIDPPESQSGRRPPCPGVCLRRRAPASDKDPVSSPLDSTAASPPKK 2269
Db 2172 RPKKLSPPSISIDPPESQSGRRPPCPGVCLRRRAPASDKDPVSSPLDSTAASPPKK 2231
QY 2270 DTLSLSGLSDDPTDMDP 2286
Db 2232 DALSLSGLSDDPTDLDP 2248

CCAG_HUMAN
ID _CCAG_HUMAN STANDARD; PRT; 2377 AA.
AC Q43497; Q43498; Q94770; Q9NYU4; Q9NYU5; Q9NYU6; Q9NYU7; Q9NYU8;
AC Q9NYU9; Q9NYV0; Q9NYV1; Q9UHN9; Q9UHP0; Q9ULU6; Q9UNG7; Q9Y5T2;
AC Q9Y5T3;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-gated calcium channel alpha subunit Cav3.1) (Cav3.1c) (NBR13).
DE gated calcium channel alpha subunit Cav3.1 (Cav3.1c) (NBR13).
GN Name=CACNA1G; Synonyms=KIAA1123;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 4 AND 5).
RC TISSUE=Brain;
RX MEDLINE=20014446; PubMed=10548410;
RA Mittman S., Guo J., Agnew W.S.;
RT "Structure and alternative splicing of the gene encoding alpha1G, a human brain T calcium channel alpha subunit.";
RL Neurosci. Lett. 274:143-146(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=20115462; PubMed=10648811;
RA Cribbs L.B., Gomora J.C., Daud A.N., Lee J.-H., Perez-Reyes E.;
RT "Molecular cloning and functional expression of ca(v)3.1c, a T-type calcium channel from human brain.";
RL FEBS Lett. 466:54-58(2000).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 1-2 AND 6-13).
RC TISSUE=Brain;
RX MEDLINE=20158909; PubMed=10692398;
RA Monteil A., Chemin J., Bourinet E., Mennessier G., Lory P., Nargeot J.;
RT "Molecular and functional properties of the human alpha1G subunit that forms T-type calcium channels.";
RL J. Biol. Chem. 275:6090-6100(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 14).
RA Kishi F.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 550-2377 FROM N.A. (ISOFORM 13).
RC TISSUE=Brain;
RX MEDLINE=22158633; PubMed=12168954;
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones.";
RL DNA Res. 9:99-106(2002).
RN [6]
RP SEQUENCE OF 750-2377 FROM N.A. (ISOFORM 13).
RC TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirose M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND GENE STRUCTURE.
RC TISSUE=Prostatic carcinoma;
RX MEDLINE=99421245; PubMed=10493502;
RA Toyota M., Ho C., Ohe-Toyota M., Baylin S.B., Issa J.-P.J.;
RT "Inactivation of CACNA1G, a T-type calcium channel gene, by aberrant methylation of its 5' CpG island in human tumors.";
RL Cancer Res. 59:4535-4541(1999).
RN [8]
RP SEQUENCE OF 1126-1444; 1778-1927 AND 2021-2312 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98154730; PubMed=9495342;

Db	210	MLGNVLLLCFFVFFIFIGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYYYQTENEDESPF	269	Db	1288	LNCITIAMERP	KIDPHSAERI	IFLTLSNYIFTAVFLAEMTVKVVALGWC	FGEQAYLRSSWN	1347																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
QY	302	ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSNTTCVNWNQYITNC	SAGEHN	361	1359	VLDGLLV	LIS	VID	ILVS	KVSDSGTKILGMLRVLRLLR	TLRPLRVISRAOGLKLVVETLMS	1418																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
Db	270	ICSQPRENGMRSCRSVPTLRGDDGGGPPCGLDYEAYNSSNTTCVNWNQYITNC	SAGEHN	329	1348	VLDGLLV	LIS	VID	ILVSMVSDSTKILGMLRVLRLLR	TLRPLRVISRAOGLKLVVETLMS	1407																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
QY	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNYFIYFILLIIVGSFFMINL	421	QY	1419	SLKPI	GN	IV	VICCAFFIIFGILGVQLFKGKFFVCQGED	TNITKSDCAEASyrwvrhky	1478																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNYFIYFILLIIVGSFFMINL	389	Db	1408	SLKPI	GN	IV	VICCAFFIIFGILGVQLFKGKFFVCQGED	TNITKSDCAEASyrwvrhky	1467																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
QY	422	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIYILRKAAR	481	QY	1479	NFDNL	G	O	ALMSLFLVASKDGWVDIMYDGLDAVGVD	QOQPINMHNFWMLLYFISFLLIVAFF	1538																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
Db	390	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIYILRKAAR	449	Db	1468	NFDNL	G	O	ALMSLFLVASKDGWVDIMYDGLDAVGVD	QOQPINMHNFWMLLYFISFLLIVAFF	1527																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
QY	482	RLAQV	SRAIGVRAGLLSSPVARSQEQPQSGSCTRSRRRLSVHLLVHHHHHHHHVHLGN	541	QY	1539	VLMFV	G	V	V	V	V	E	N	F	H	K	C	R	O	H	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E

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RESULT 8
Q6ZPX4
ID Q6ZPX4 PRELIMINARY; PRT; 1389 AA.
AC Q6ZPX4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIAA1123 protein (Fragment).
GN Name=mkIAA1123;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
DR EMBL; AK129294; BAC98104.1; -.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR002077; Ca_channel_alpha.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans; 2.
DR PRINTS; PR00167; CACHANNEL.
KW Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW Transmembrane; Transport; Voltage-gated channel.
FT NON TER 1
SQ SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;

Query Match 56.6%; Score 6809.5; DB 2; Length 1389;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 1317; Conservative 8; Mismatches 29; Indels 35; Gaps 3;

QY 933 LPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL 992
Db 1 LPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL 60

QY 993 VAILVEGFQAE-----GDATKSESEPDFFSPSVDGDGRKKR 1029
Db 61 VAILVEGFQAEIEGKREDTSGQLSCIQLPVNSQGGDATKSESEPDFFSPSVDGDGRKKR 120

QY 1030 LALVALGEHAELRKSLLPPLIIHTAATPMGHPKSSSTGVGEALGSGSRRTSSSGSAEPGA 1089
Db 121 LALVALGEHSELKSLPPLIIHTAATPMGHPKSSSTGVGEALGSGSRRTSSSGSAEPGT 180

QY 1090 AHHEMKPPSARSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGOE 1149
Db 181 AHHEMKPPSARSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGOE 240

QY 1150 SQDEEESSEEDRASPDGSHRHGSLERAKSSFDPDPTLQVPLGHLRTASGRSSASEHQD 1209
Db 241 SQDEEESSEEDRASPDGSHRHGSLERAKSSFDPDPTLQVPLGHLRTASGRSSASEHQD 300

QY 1210 CNGKSASGRRLARTLTDDPQLDGDNDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI 1269
Db 301 CNGKSASGRRLARTLTDDPQLDGDNDNDEGNLSKGERLRAWVRARLPACCRERDSWSAYI 360

QY 1270 FPPQSRFLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1329
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Db 361 FPPQSRFLLCHRIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 420

QY 1330 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLR 1389
Db 421 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLR 480

QY 1390 VLRLRLTLRLPLRVISRAOGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGF 1449
Db 481 VLRLRLTLRLPLRVISRAOGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGF 540

QY 1450 FVCQGEDTRNITNKSDCAEASYSRWVRHKYNFNDLQALMSLFLVASKDGVDMYDGLDA 1509
Db 541 FVCQGEDTRNITNKSDCAEASYSRWVRHKYNFNDLQALMSLFLVASKDGVDMYDGLDA 600

QY 1510 VGVDQQPINMHNPMWMLLYFISFLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREK 1569
Db 601 VGVDQQPINMHNPMWMLLYFISFLIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREK 660

QY 1570 RLRLLEKKRR-----SKEKQMAEAQCKPYYSRFRLLVHHLCTSHYLDLFI 1618
Db 661 RLRLLEKKRRNMLDDVIASSSSASAASEAQCKPYYSRFRLLVHHLCTSHYLDLFI 720

QY 1619 GVIGLVVVTMAMEHYQQPQILDEALKICNYIFTVIFVESVEKLVAFARFRFPQDRWNQL 1678
Db 721 GVIGLVVVTMAMEHYQQPQILDEALKICNYIFTVIFVESVEKLVAFARFRFPQDRWNQL 780

QY 1679 DLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRARVLKLLKMAVGMRAALLHTVMQ 1738
Db 781 DLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRARVLKLLKMAVGMRAALLHTVMQ 840

QY 1739 ALPQVGNLGLLFFLFFIPAALGVLEFGDLECDETHPCGLGRHATFRNFGMAFLTFRV 1798
Db 841 ALPQVGNLGLLFFLFFIPAALGVLEFGDLECDETHPCGLGRHATFRNFGMAFLTFRV 900

QY 1799 STGDNWNGIMKOPSRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVIAMKHLSESN 1858
Db 901 STGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVIAMKHLSESN 960

QY 1859 KEAKEAEAELEAELEEMKTLSPQHPSPGLSPFLWPVGVEGNSTDSKPGAPHTTAHIGAA 1918
Db 961 KEAKEAEAELEAELEEMKTLSPQHPSPGLSPFLWPVGVEGNSTDSKPGAPHTTAHIGAA 1020

QY 1919 -SGFSLEHPTMVPHEEVPVPLGPDLLTVRKSGVSRTHSLPNDSMCRNGSTAESLGH 1977
Db 1021 SSGFSLEHPTMVPHEEVPVPLGPDLLTVRKSGVSRTHSLPNDSMCRNGSTAESLGH 1080

QY 1978 GWGLPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPLPPGRSPLAQ 2037
Db 1081 GWGLPKAQSGSILSVHSQPADTSCILQPKDAHYLLQPHGAPTWGAIPKLPPLPPGRSPLAQ 1140

QY 2038 RPLRRQAAIRTDSDLVQGLGSRDILLSEVSGPSCPLTRSSSFVWGSSIQVQORSIGISKV 2097
Db 1141 RPLRRQAAIRTDSDLVQGLGSRDILLSEVSGPSCPLTRSSSFVWGSSIQVQORSIGISKV 1200

QY 2098 SKHIRLPAPCPGLEPSWAKDPPETRSLELDTLSWISGDLPLSSQEEPLFPRDLKKCVS 2157
Db 1201 SKHIRLPAPCPGLEPSWAKDPPETRSLELDTLSWISGDLPLSSQEEPLFPRDLKKCVS 1260

QY 2158 VETQSCRRRPGFWLDEQRRHSIAVSLDSDSGSQPRLCPSPSSLLGGQPLGGPSRPPKKLSP 2217
Db 1261 VEAQSCRRRPGFWLDEQRRHSIAVSLDSDSGSQPRLCPSPSSLLGGQPLGGPSRPPKKLSP 1320

QY 2218 PSISIDPPESQGSRRPPCPSPGVCLRRRAPASDKOPSVSSPLDSTAASPPKKOTLSLGL 2277
Db 1321 PSISIDPPESQGSRRPPCPSPGVCLRRRAPASDKOPSVSSPLDSTAASPPKKOTLSLGL 1380

QY 2278 SSDPTDMDP 2286
Db 1381 SSDPTDLDP 1389
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RESULT 9

BAC98104 PRELIMINARY; PRT; 1389 AA.
ID BAC98104;
AC BAC98104;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIAA1123 protein (Fragment).
GN MKIAA1123.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT III. The Complete Nucleotide Sequences of 500 Mouse KIAA-homologous
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-fractionated Libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129294; BAC98104.1; -.
FT NON TER 1
SQ SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;

Query Match 56.6%; Score 6809.5; DB 2; Length 1389;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 1317; Conservative 8; Mismatches 29; Indels 35; Gaps 3;

QY 933 LPDRKNFDSLWAIWTVFOILTQEDWNKVLNGWASTSSWAALYFIALMTFGNYVLFNLL 992
DB 1 LPDRKNFDSLWAIWTVFOILTQEDWNKVLNGWASTSSWAALYFIALMTFGNYVLFNLL 60
QY 993 VAILVEGFQAE-----GDATKSESEPDFFSPVDGDGRKKR 1029
DB 61 VAILVEGFQAEIIGKREDTSGQLPVSQGGDATKSESEPDFFSPVDGDGRKKR 120
QY 1030 LALVALGEHAELRKSLLPPLIHTAATPMHPSKSSSTGVGEALGSGRRRTSSSGSAEPGA 1089
DB 121 LALVALGEHSELKSLPPLIHTAATPMSLPKSSSTGVGEALGSGRRRTSSSGSAEPGT 180
QY 1090 AHHEMKPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEQE 1149
DB 181 AHHEMKPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEQE 240
QY 1150 SQDEEESSEEDRASPGSDHRRHRSGLERAKSSFDLPTLQVPLHRTASGRSSASEHQD 1209
DB 241 SQDEEESSEEDRASPGSDHRRHRSGLERAKSSFDLPTLQVPLHRTASGRSSASEHQD 300
QY 1210 CNGKSASGLARTLRDDPPLDGDGDEGNLSKGERLQAVWRSLRPAACCRERDSWSAYI 1269
DB 301 CNGKSASGLARTLRDDPPLDGDGDEGNLSKGERLQAVWRSLRPAACCRERDSWSAYI 360
QY 1270 FPPQSRFRLLCHRIITHKMFHVVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1329
DB 361 FPPQSRFRLLCHRIITHKMFHVVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 420
QY 1330 AVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLR 1389
DB 421 AVFLAEMTVKVVVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLR 480
QY 1390 VLRLRLTRPLRVLISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILGVQFKGKF 1449
DB 481 VLRLRLTRPLRVLISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILGVQFKGKF 540
QY 1450 FVCQGEDTRNITNKSDCAEASRWVRHKYNFNDLQALMSLFLVASKDGVVDIMYDGLDA 1509
DB 541 FVCQGEDTRNITNKSDCAEASRWVRHKYNFNDLQALMSLFLVASKDGVVDIMYDGLDA 600
QY 1510 VGVDQQPIMHNPNWMLLYFISFLLIIVAFFVLNMVGVVVENFHKCRQHOOEERREK 1569
DB 601 VGVDQQPIMHNPNWMLLYFISFLLIIVAFFVLNMVGVVVENFHKCRQHOOEERREK 660

QY 1570 RLRRLEKRR-----SKEKQMAEAQCKPYYSRFRLLVHHLCTSHYDLDFIT 1618
DB 661 RLKRLEKRRNLMLDDVIASGSSASAASEAQCKPYYSRFRLLVHHLCTSHYDLDFIT 720
QY 1619 GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVESVKLVAFARFRFFQDRWNQL 1678
DB 721 GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVESVKLVAFARFRFFQDRWNQL 780
QY 1679 DLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRLHHTVMQ 1738
DB 781 DLAIVLLSIMGITLEEIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRLHHTVMQ 840
QY 1739 ALPQVGNLGLLFFMLLFFIFAALGVLEFGDLECDETHPCGEGLRHATFRNFGMAFLTLFRV 1798
DB 841 ALPQVGNLGLLFFMLLFFIFAALGVLEFGDLECDETHPCGEGLRHATFRNFGMAFLTLFRV 900
QY 1799 STGDNWNGIMKDPESRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLSEEN 1858
DB 901 STGDNWNGIMKDLTRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLSEEN 960
QY 1859 KEAKEEALEAELEEMKTLSPQPHSPGLSPFLMPGVEGVNSTDPKPGAPHTTAHIGAA 1918
DB 961 KEAKEEALEAELEEMKTLSPQPHSPGLSPFLMPGVEGVNSTDPKPGAPHTTAHIGAA 1020
QY 1919 -SGFSLEHPTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH 1977
DB 1021 SSGFSLEHPTMVPHTEEGVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGH 1080
QY 1978 GWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTGWAIPLKPPGRSPLAQ 2037
DB 1081 GWGLPKAQSGSILSVHSQPADTSCILQLPKDAHYLLQPHGAPTGWAIPLKPPGRSPLAQ 1140
QY 2038 RPLRRQAAIRTDSDVQGLGSRDILLSEVSGPCLTRSSSFWSGSSIQVQQRSGIQSKV 2097
DB 1141 RPLRRQAAIRTDSDVQGLGSRDILLSEVSGPCLTRSSSFWSGSSIQVQQRSGIQSKV 1200
QY 2098 SKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLPSSQEEPLFPRDLKKCYS 2157
DB 1201 SKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLPSSQEEPLFPRDLKKCYS 1260
QY 2158 VETQSCRRRPGFWLDEORRHSIAVSCLDGSGPRLCPSPSSLGQPLGGPSRPPKKLSP 2217
DB 1261 VEAQSCRRRPGFWLDEORRHSIAVSCLDGSGPRLCPSPSSLGQPLGGPSRPPKKLSP 1320
QY 2218 PSISIDPPESQSGRRPPCPGVCLRRRAPASDSDKPSVSSPLDSTAASPSPKDTLSLSGL 2277
DB 1321 PSISIDPPESQSGRRPPCPGVCLRRRAPASDSDKPSVSSPLDSTAASPSPKDTLSLSGL 1380
QY 2278 SSDPTMDP 2286
DB 1381 SSDPTDLD 1389

RESULT 10

CCAH RAT STANDARD; PRT; 2359 AA.
ID CCAH RAT
AC Q9EQ60;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2).
GN Name=Cacnalh;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
RX PubMed=11073957; DOI=10.1074/jbc.M008215200;
RA McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,

QY	368	NFDNIGAWIAIQVITILEGWVDIMYFVMDAHSFYNFYIFILLIIVGSEFFMINCLVIVIA	427	1392	RLRLRLRLRVISRAOGLKLVVETLMSSLKPIGNIVIVICCAFFIIFGILGVQLFKGKFFV	1451
Db	360	NFDNIGAWIAIQVITILEGWVDIMYVMDAHSFYNFYIFILLIIMSGSEFFMINCLVIVIA	419	1410	RLRLRLRLRVISRAPGLKLVVETLISSLRPIGNIVILICCAFFIIFGILGVQLFKGKFFY	1469
QY	428	TOFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIYLKRAARLAQVS	487	1452	CQGEDTRNITKSDCAEASYSRWVRHKYNFDNLGOALMSLFLVASKDQGWVDMYDGLDVG	1511
Db	420	TOFSETKQRENQLMREQARYLSDNSTLASFSEPGSCYEELLKVVGHI FRKVRRSLRLY	479	1470	CEGTDTRNITTKAECHAAHYRWVRKYNFDNLGOALMSLFLVSSKDGWVNMIDGLDVG	1529
QY	488	RAIGVRAGLLSSPVAR-----SGQEPQPSGSTRSHRRLSVHHLV-HHHHHHHHHYHLGN	541	1512	VDQQPIMNHPWMLLYFISFLLIIVAFVVLNMFVGVVVENFHKRQHQQEAEARRRREKRL	1571
Db	480	ARQSRWRKKVDPSTVHGQGPGRRRPRAG-----RRTASVHHLVYHHHHHHHHYHFSH	534	1530	IDQQPVQNHNPWMLLYFISFLLIIVSFFVLNMFVGVVVENFHKRQHQQEAEARRRREKRL	1589
QY	542	GTLRVPRASPEIQDRDANGSRRLM--LPPSTPTPSGGPRGAEVSVHSFYHADCHLEPVR	599	1572	RRLEKKRRSKEQMAEAQCKPYYSYSRFRLLVHHLCTSHYLDLFTIGVIGLNVVTMAME	1631
Db	535	GGPR--RPSPE-----PGAGDNRLVRACAPSPSPGHGPP-DSESVHSIYHADCHVEGQP	587	1590	RRLERRR-----KAQRRPYADYSHTRRSIHSLCTSHYLDLFTIICLNVTMSME	1642
QY	600	CQAPPPRCPSEASGRTVGSG--KVYPTV-----HTSPPPHILKDKALVEVAPSP	646	1632	HYQPOILDEALKICNYIFTVIFVFESVFKLVAFARFRFFQDRWNQDLAIIVLLSIMGIT	1691
Db	588	ERARVAHSIATAASLKLASGLTMYPTILPSTGVNSKGGTSRRPKLGR-----AGAP	641	1643	HYNPKSLDEALKYCNVFTIVFVFEAALKLVAFGFRFFKDRWNQDLAIIVLLSIMGIA	1702
QY	647	GPPTLTSENI-PPGPFSSMHKLLTQSTGACHSSCK-ISSPC-----SKADSGACGPDSCP	700	1692	LEEIEVNLSPINPTIIRIMRVLRIARVLKLLKMAVGMALLHTVMQALPQVGNLGLLFM	1751
Db	642	GAAVHSPSLGSPRPYKIQDVVGEQGLGRASHLSGLSVPCPLPSPOAGTLTCELKSCP	701	1703	LEEIEMNAALPINPTIIRIMRVLRIARVLKLLKMATGMALLDTTVQALPQVGNLGLLFM	1762
QY	701	YCARGTAGEP--ESADHVMPDSDSEAVYEFTQDAQHSDLRDP-----HSRRRQR	747	1752	LLFFIFAALGVLEFGLDECTHPCCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKOP	1811
Db	702	YCA-SALEDPFEFSGSESDSADHGVYEFTQDVHRGDCRDPVQQPHEVGTGPHSNERR	760	1763	LLFFIYAALGVLEFGRLECEDNCPCEGLSRHATFTNFGMAFLTFRVSTGDNWNGIMKDT	1822
QY	748	S-LGPDAAEPSSVLAFWRLICDTFRKIIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTN	806	1812	SRDC--DQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAELE	1868
Db	761	TPLRKASQGGIGHLWASFSGKLRRIVDSKYFNRGIMAAILLVNTLSMGVEYHEQPEELTN	820	1823	LRETRREDKHCLSYLPALSPVYFVTMLVAQFVLVNVVAVLMKHLEESNKEAREDAEMD	1882
QY	807	ALEISNIVFTSLFALEMLLKLIVGPFYIKNPYINFDGVIIVISVWEIVGQGGGLSVL	866	1869	AELLEEMKTLSPOHSPGLSPFLWPVGVEGVNSTDTPKPGAPHTTAHIGAASGFSLEHPTM	1928
Db	821	ALEISNIVFTSMFALEMLLKLACGLGIYRNPYINFDGVIIVISVWEIVGQADGGQSVL	880	1883	AEIELEM-----AQGSTAQPPPTAQES-----	1904
QY	867	RTFRLMVLKLVFLPALQRLVLMKMTMDNVATFCMLMLLFI FIFSIILGMHLFGCKFAS	926	1929	VPHPPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGRWGGLP-----	1982
Db	881	RTFRLRLVLKLVFLPALRRQLVVLMTMDNVATFCMLMLLFI FIFSIILGMHLFGCKFSL	940	1905	-----QGTQPDTPNLLVVRKVSVRMLSLPNDSYMFRPVAPAAAPHSH-----	1954
QY	927	ERD-GDTLPDRKNFDSLLWAIIVTVFQILTQEDWNKVLNMGMASTSSWAALYFIALMTFGN	985	1983	KAQSGSILSVHSQPADTSCILQLP-----KDVHYLLQPHGAPTWGAIPKLPPPPGRS	2033
Db	941	KTDGDIIVDRKNFDSLLWAIIVTVFQILTQEDWNVVLNMGMASTSSWAALYFVALMTFGN	1000	1955	ETYTGPTVTSAHSPPLEPRASFQVPSAASSPARVSDPLCALSPRGTP-----RS	2002
QY	986	YVFNLLVAILVEGFOAEGDATKSESEPDFSPSDGDRKKRL-----ALVALG	1036	2034	PLAQRPLRQAAIRTDSD--VQGLGSREDLLSEVSGPSCPLTRSSSFWGG-----	2082
Db	1001	YVFNLLVAILVEGFOAEGDATRSDDTKSTQLEGDFDKLDRLATKMYSLAVTPN	1060	2003	LSLSRILCRQEAHMHSESGKVDVGG--DSIPDYTEPAENMSTSQASTGAPRSPCSPR	2060
QY	1037	EHAELRKSLLPPLIHTAATPMHSHPKSS-STGVGEALGSGSRRTSSSGSAEPGAHHMK	1095	2083	-SSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLIPS	2141
Db	1061	GHLEGRGSLPPLIHTAATPMPTPKSSPNLDVAHAL-LDSRR-SSSGSVDPQLG--DQK	1116	2061	PASVTRKHTFGQRCISSR-----PPTLGGDEAAADP-----ADEEVSHITSSAHPW	2108
QY	1096	CPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEE-	1154	2142	SQEEPLFP-----RDLKKCYSVETQSCRRRPPGFWLDEQRHSHIAV-----	2181
Db	1117	SLASLRSSPCTPWGPNAGSAGSRRSRNSLGRAPSLKRRNQCGERRSLLSGEGKGTDEA	1176	2109	PATEPHSPEASPTASPVKGTMGSGRDPRRFCSDAQSFLDKPG-RPDAQRWSSVELDNGE	2167
QY	1155	ESSEEDRASPGSDHRHRGSLEREAKSSFDLPDTLQVPLHRTASGRSSA---SEHQDCN	1211	2182	SLDSDGS-----QPRLCPSSSLGQPLGGPGSRPKKLSPPSISIDPP--ESQSGSR	2231
Db	1177	EDSRPSTGTHPGASPGPRATPLRAE-SLDHRSTLDL-----CPRPAALLPTKFHDCN	1229	2168	SHLESGEVGRASELEPAL-----GSRKKKMSPPCISIEPPTKDEGSSR	2212
QY	1212	GKSASGRLARLTRDDPQLDGGDDNDEGNLSKGERIQAWVRSLPACCRERDSWSAYIFP	1271	2232	PPCSPG--VCLRRAPASDS--KDPSSVSSPLDSTAASP-----SPKDTLSLSG	2276
Db	1230	GQMVALPSEFFLRIDSHKEDAAEFDDDIEDSCCFRLHKVLEPYAPQWCRSRRESWALYLF	1289	2213	PAAEGGNTTLRRRTPSCAAALHRDCPEPTEPGTGGDPVAKGERWGQASCRAEHLTVPN	2272
QY	1272	PQSEFRLCHRITTHKMFHDVVLVIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTAV	1331	2277	LSSDPTDM	2284
Db	1290	PQNRUVSCQKVI AHKMFHDVVLVIFLNCITIALERPDI DPGSTERAFLSVSNYIFTAI	1349	2273	FAFEPLDM	2280
QY	1332	FLAEMTVKVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1391			
Db	1350	FVVENMVKVALGLLWGEHAYLOSSWNVLDGLLVLSLVDIIVAMASAGGAKILGLRVV	1409			

RESULT 11
CCAH HUMAN
ID CCAH HUMAN STANDARD; PRT; 2353 AA.
AC O95180; O95802; Q8WWI6; Q96Q16; Q96RZ9; Q9NY4; Q9NY5;

DT 15-JUL-1999 (Rel. 38, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2) (Low-voltage-activated calcium channel alpha 3.2 subunit).

DE Name=CACNA1H;

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Heart;

RX MEDLINE=98333998; PubMed=9670923;

RA Cribbs L.L., Lee J.-H., Yang J., Satin J., Zhang Y., Daud A.N., Barclay J., Williamson M.P., Fox M., Rees M., Perez-Reyes E.;

RT "Cloning and characterization of alpha1H from human heart, a member of the T-type Ca2+ channel gene family.";

RL Circ. Res. 83:103-109(1998).

RN [2]

RP REVISIONS.

RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Thyroid carcinoma;

RX MEDLINE=99127945; PubMed=9930755;

RA Williams M.E., Washburn M.S., Hans M., Urrutia A., Brust P.F., Prodanovich P., Harpold M.M., Stauderman K.A.;

RT "Structure and functional characterization of a novel human low-voltage activated calcium channel.";

RL J. Neurochem. 72:791-799(1999).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=21096910; PubMed=1157797;

RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K., Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J., Higgs D.R.;

RT "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";

RL Hum. Mol. Genet. 10:339-352(2001).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Testis;

RX MEDLINE=21864207; PubMed=11751928; DOI=10.1074/jbc.M105345200;

RA Jagannathan S., Punt E.L., Gu Y., Arnoult C., Sakas D., Barratt C.L., Publicover S.J.;

RT "Identification and localization of T-type voltage-operated calcium channel subunits in human male germ cells. Expression of multiple isoforms.";

RL J. Biol. Chem. 277:8449-8456(2002).

RN [6]

RP SEQUENCE OF 86-817 FROM N.A.

RA Cobley V.E.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [7]

RP SEQUENCE OF 424-661 AND 838-2373 FROM N.A. (ISOFORM 1).

RA Mittman S., Agnew W.S.;

RT "Organization and alternative splicing of CACNA1H.";

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth

CC muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1; Synonyms=AlH-a;

CC IsoId=O95180-1; Sequence=Displayed;

CC Name=2; Synonyms=AlH-b;

CC IsoId=O95180-2; Sequence=VSP_000949;

CC -!- TISSUE SPECIFICITY: Expressed in kidney, liver, heart, brain.

CC Isoform 2 seems to be testis-specific.

CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.

CC -!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.

CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

CC -!- CAUTION: AT-AC pre mRNA splicing gives rise to the isoform 1 shown in this entry. The additional 20 amino acids found in the Ref.4 and Ref.6 sequences are due to a misunderstanding of the real type of splicing mechanism involved.

CC -----

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CC -----

DR EMBL; AF051946; AAC67239.3; -.

DR EMBL; AF073931; AAD17668.1; -.

DR EMBL; AE006466; AAK61268.1; ALT_SEQ.

DR EMBL; AJ420779; CAD12646.1; -.

DR EMBL; AL031703; CAC42094.1; ALT_SEQ.

DR EMBL; AF223562; AAF60162.1; -.

DR EMBL; AF223563; AAF60163.1; -.

DR Genew; HGNC:1395; CACNA1H.

DR MIM; 607904; -.

DR GO; GO:0005891; C:voltage-gated calcium channel complex; TAS.

DR GO; GO:0008332; F:low voltage-gated calcium channel activity; TAS.

DR GO; GO:0006936; P:muscle contraction; TAS.

DR GO; GO:0007520; P:myoblast fusion; TAS.

DR GO; GO:0008016; P:regulation of heart rate; TAS.

DR GO; GO:0006810; P:transport; TAS.

DR InterPro; IPR001682; Ca/Na_pore.

DR InterPro; IPR002111; Cat_channel_TrpL.

DR InterPro; IPR005821; Ion_trans.

DR InterPro; IPR005820; M+channel_nlg.

DR Pfam; PF00520; Ion_trans; 4.

DR PRINTS; PR01629; TVDCCALPHA1.

KW Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein; Ion transport; Ionic channel; Multigene family; Phosphorylation; Repeat; Transmembrane; Voltage-gated channel.

FT REPEAT 87 422 I.

FT REPEAT 779 1018 II.

FT REPEAT 1281 1558 III.

FT REPEAT 1602 1863 IV.

FT DOMAIN 1 100 Cytoplasmic (Potential).

FT TRANSMEM 101 119 S1 of repeat I (Potential).

FT DOMAIN 120 139 Extracellular (Potential).

FT TRANSMEM 140 160 S2 of repeat I (Potential).

FT DOMAIN 161 169 Cytoplasmic (Potential).

FT TRANSMEM 170 184 S3 of repeat I (Potential).

FT DOMAIN 185 193 Extracellular (Potential).

FT TRANSMEM 194 212 S4 of repeat I (Potential).

FT DOMAIN 213 232 Cytoplasmic (Potential).

FT TRANSMEM 233 253 S5 of repeat I (Potential).

FT	DOMAIN	254	394	Extracellular (Potential).	263	QY	QLWAGLLNRNRCFLPENFSLPLSVD-LEPYQTENEDESPFICSQPRENGMRSCRSVPTLR	321
FT	TRANSMEM	395	419	S6 of repeat I (Potential).				
FT	DOMAIN	420	793	Cytoplasmic (Potential).	250	Db	QLWAGLLNRNRCFLDSAFVRNNLTLFRLPYQTEBGEENFICSSRRDNGMOKSHIP---	306
FT	TRANSMEM	794	814	S1 of repeat II (Potential).				
FT	DOMAIN	815	827	Extracellular (Potential).				
FT	TRANSMEM	828	849	S2 of repeat II (Potential).	322	QY	GEAGGGPPCSLDYETYN-----SSNTTCVNNQYITNCAGEHNPFKGAINDFNIGY	374
FT	DOMAIN	850	855	Cytoplasmic (Potential).	307	Db	GRRELMPCTLGWEAYTQPAEGVGAARNACINWNQYINVCERSGDSNPHNGAINFNIGY	366
FT	TRANSMEM	856	874	S3 of repeat II (Potential).				
FT	DOMAIN	875	882	Extracellular (Potential).	375	QY	AWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETK	434
FT	TRANSMEM	883	906	S4 of repeat II (Potential).	367	Db	AWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETK	426
FT	DOMAIN	907	917	Cytoplasmic (Potential).				
FT	TRANSMEM	918	938	S5 of repeat II (Potential).	435	QY	QRESQLMREQVRFLSNASTLASFSEPGSCYEELLYLVYILRKAARRLAQVSRRAIGVRA	494
FT	DOMAIN	939	990	Extracellular (Potential).	427	Db	QRESQLMREQVRFLSNASTLASFSEPGSCYEELLYLVYILRKAARRLAQVSRRAIGVRA	486
FT	TRANSMEM	991	1015	Cytoplasmic (Potential).				
FT	DOMAIN	1016	1290	S1 of repeat III (Potential).	495	QY	GLSSPVARSGQPPQPSGSCSTRSHR-----LSVHHLV-HHHHHHHHHYHLNGTILRV	546
FT	TRANSMEM	1291	1313	Extracellular (Potential).	487	Db	RKKVDPSAVQGGP-----GHRQRRAGRHTASVHHLVYHHHHHHHHYHSHGSPRR	538
FT	TRANSMEM	1314	1331	S2 of repeat III (Potential).				
FT	TRANSMEM	1332	1352	Cytoplasmic (Potential).	547	QY	PRASPEIQDRDANGSRRLML--PPSTPTPSGGPPRGAESVHSFYHADCHLE--FVRCQA	602
FT	TRANSMEM	1353	1362	S3 of repeat III (Potential).	539	Db	PGPEPGACD-----TRLVRAGAPPPSPGPGPP-DAESVHSIYHADCHIEGPQERARV	591
FT	TRANSMEM	1363	1382	Extracellular (Potential).				
FT	TRANSMEM	1383	1396	S4 of repeat III (Potential).	603	QY	PPRCPSEASGR-TVSGKV-YPTV-----HTSPPEILKDKALVEVAPSP----	646
FT	TRANSMEM	1397	1418	Cytoplasmic (Potential).	592	Db	AHAAATAAASRLATGLTMNYPTILPSGVSGSGKSTSPGPK-----GKWAGGPPGTG	644
FT	TRANSMEM	1419	1428	Extracellular (Potential).				
FT	TRANSMEM	1429	1452	S5 of repeat III (Potential).	647	QY	--GPPTLTSTFNIPPGPFSSMHKLLTQSTGAC--HSS-----CKISSPCSKADSGACPD	697
FT	TRANSMEM	1453	1529	S6 of repeat III (Potential).	645	Db	GHGPLSLNS---PDPYEKIPHVVGHEHGLGQAPGHLGSLVPCPLPSP--PAGTLTCELK	698
FT	TRANSMEM	1530	1555	Cytoplasmic (Potential).				
FT	TRANSMEM	1556	1616	Extracellular (Potential).	698	QY	SCPYCART-GAGEPESADHVPDSDSEAVYEFTQDAQHSDLRDP-----	740
FT	TRANSMEM	1617	1637	S1 of repeat IV (Potential).	699	Db	SCPYCTRALEDPEGELSGESGSDSGRGVYEFTQDVRHGDRWDTPRPPRATDTPGPGPGS	758
FT	TRANSMEM	1638	1651	Extracellular (Potential).				
FT	TRANSMEM	1652	1673	S2 of repeat IV (Potential).	741	QY	HSRRQRSLGPDAPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQ	800
FT	TRANSMEM	1674	1680	Cytoplasmic (Potential).	759	Db	PORRAQORAAP-GEPCWGMRLWVTFSGKLRRIVDSKYFSRGIMMAILVNTLSMGIEYHEQ	817
FT	TRANSMEM	1681	1699	S3 of repeat IV (Potential).				
FT	TRANSMEM	1700	1713	Extracellular (Potential).	801	QY	PEELTNALAEISNIVFTSLFALEMLKLLVYGPFGYIKPNPYNIFDGVIVVISVMEIVGQOG	860
FT	TRANSMEM	1714	1737	S4 of repeat IV (Potential).	818	Db	PEELTNALAEISNIVFTSMFALEMLKLLACGPLGIYRNPNYNIFDGIIVVISVMEIVGQAD	877
FT	TRANSMEM	1738	1751	Cytoplasmic (Potential).				
FT	TRANSMEM	1752	1772	S5 of repeat IV (Potential).	861	QY	GGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDVATECMLLMFLFIFISILGMHLF	920
FT	TRANSMEM	1773	1835	Extracellular (Potential).	878	Db	GGLSVLRTFRLMRVLKLVRLPALQRLVLMKTMNDVATECMLLMFLFIFISILGMHLF	937
FT	TRANSMEM	1836	1863	S6 of repeat IV (Potential).				
FT	TRANSMEM	1864	2353	Cytoplasmic (Potential).	921	QY	GCKFASEED-GDTLPDRKNFDSLLWAIIVTFQILTOEDWNKVLYNGMASTSSWAALYFIA	979
FT	DOMAIN	520	530	Poly-His.	938	Db	GCKFSLKTDGTVDPDRKNFDSLLWAIIVTFQILTOEDWNKVLYNGMASTSSWAALYFVA	997
FT	DOMAIN	530	530	Poly-Ser.				
FT	DOMAIN	1107	1110	Poly-Arg.	980	QY	LMTFGNYVLFNLLVAILVEGFOAEGDATKSESEPDFSPSDGDDRKRLALVAL----	1035
FT	DOMAIN	1583	1586	Calcium ion selectivity and permeability	998	Db	LMTFGNYVLFNLLVAILVEGFOAEGDANRSDTDEKTSVHFEEDFHKLRELQTTTELKMS	1057
FT	SITE	378	378	(By similarity).				
FT	SITE	974	974	Calcium ion selectivity and permeability	1036	QY	-----GEHAELRKSLPLPLIHTAATPMSPKSSS-TGVGFAIGSGSRRTSSSGSAEPGA	1089
FT	SITE	1504	1504	(By similarity).	1058	Db	LAVTPNGHLEGRGSLSPPLIMCTAATPMPTKSSPFLDAAPSLDPSRRSGSSGDPPLG-	1116
FT	SITE	1808	1808	Calcium ion selectivity and permeability				
FT	SITE	1808	1808	(By similarity).	1090	QY	AHEMKCPPSPSPSPSPSAASSWTSSRRSSRNISGRAPSLKRRSPSGERRSLLSGEQE	1149
FT	CARBOHYD	192	192	Calcium ion selectivity and permeability	1117	Db	---DQKPPASLRSSPCAPWGPSPGAMSSRRSSWSLGRAPSLKRRSQCGERESLLSGEKG	1173
FT	CARBOHYD	271	271	N-linked (GlcNAc. .) (Potential).	1150	QY	SQDEEESSEEDRASPA--GSDHRRHGRSLEREAKSSFDLPDIL-----QVPLH-----R	1196
FT	CARBOHYD	271	271	N-linked (GlcNAc. .) (Potential).	1174	Db	STDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPPTCKDRDQGVVALPSDFLRL	1231
FT	CARBOHYD	271	271	N-linked (GlcNAc. .) (Potential).	1197	QY	TASGRSSASEHQDCNGKKSASGRRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSRLP	1256
FT	CARBOHYD	271	271	N-linked (GlcNAc. .) (Potential).	1232	Db	IDSHREDAAEALDDDDSEDSCCCLRLHLKVLPEYKPO-----W-----	1265
FT	CARBOHYD	271	271	N-linked (GlcNAc. .) (Potential).	1257	QY	ACCRERDSWSAYIFPPQSRRLCHRIITHKHFHDHVLVLIIFLNCITIAMERPDKIDPHSA	1316

Query Match	51.7%;	Score	6222;	DB	1;	Length	2353;
Best Local Similarity	56.7%;	Pred.	No.	7.1e-303;			
Matches	1370;	Conservative	208;	Mismatches	529;	Indels	310;
Gaps	62;						
QY	25	PPGRLARGWTRRRMERAPRSRDSPP--VASRSSTTCPPGGAAGAGSTEKDPGSADSEAE	82				
Db	19	PPGPAALVG-----ASPESPGAGREARSGELGVSPSPSPAERGAELGA--DEEQR	69				
QY	83	LPYPALAPVVFYLSQDSRPSRWCLRTVCNPWFERSVLMVLNLCVTLMGFRPCEDIACD	142				
Db	70	VYPALAAATVFFCLGQTTTPRSRWCLRVNPNWFHVSMLVIMLNCVTLMGFRPCEDVECG	129				
QY	143	SQCRILQAFDDFIFAFAFVEMVVKMVALGIFGKKCYLGDWNRLLDFFIAGMLEYSLD	202				
Db	130	SERCNILEAFDAFIFAFVEMVVKMVALGIFGKKCYLGDWNRLLDFFIAGMLEYSLD	189				
QY	203	LQNVFSAVRTVRVLRPLRINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGV	262				
Db	190	GHNVSLSAIRTVRVLRLRINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGV	249				

Db 934 FGCKFSLKTDSDGTVDPDRKNFDSLLWAIWTVFQILTQEDNNVLYNGMASTSSWAALYFV 993

QY 979 ALMTFGNYVLNLLVAILVEGFOAEGDATKSESEPDFFSPSVDGDGRKK----- 1028

Db 994 ALMTFGNYVLNLLVAILVEGFOAEGDATRSDTDEKSTHLEBEDFKLRDVRATEMKMY 1053

QY 1029 RLALVALGHAELRKSLLPPLIITHAATPMHPKSS-STGVGEALGSGRRRTSSGSAEP 1087

Db 1054 SLAVTPNG-HLEGRGSLPPLITHAATPMPTPKSSPHLDMHTL-LDSRR-SSSGSDVP 1110

QY 1088 GAAHEMKPPSARSSPHSPWASAASWTSRRSSNLSGRAPSLKRRSPSGERRSLLSGEG 1147

Db 1111 QLG--DOKSLASLRSSPCAPWGPNSAGSSRRSSWNSLGRAPSLKRRSQCGERESLLSGEG 1168

QY 1148 QESQDEE-ESSEEDRASPGSDHRRHGSLEA-----KSSFDL-----PDTLQVPGLHRT 1197

Db 1169 KGSTDDAEADSRPNSGTHPGASPGPRATPLRRAESLGRHSRSTMDLCPRPATL-LP----- 1222

QY 1198 ASGRSSASEHQDCNGKSASGRRLARTLRTDDPQLDGGDDNDEGNLSKGERIQAWVRSLPA 1257

Db 1223 -----TKFRDCNGQMVLPSEFFLRIDSHKEDAAEFDDIEDSCCFRLHKVLEPYAPQ 1275

QY 1258 CCBERSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVVLVIFLNCITIAMERKIDPHSAE 1317

Db 1276 WCSRESWALYLFPPQNRRLRVSCQKVIHAKMFDHVVVLVIFLNCITIALERPDIIDPGSTE 1335

QY 1318 RIFLTLNYSIYFTAVFLAEMTVKVALGWCFOGQAYLRSSWNVLDGLLVLSVIDILVSMV 1377

Db 1336 RAFLSVSNYIFTAIFVVMVMKVVALGLLWGEHAYLQSSWNVLDGLLVLSLVDIIVAVA 1395

QY 1378 SDSGTKILMLRVLRLRLTLRLPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIF 1437

Db 1396 SAGGAKILGVLRLRLTLRLPLRVISRAPGLKLVVETLISSLRPIGNIVVICCAFFIIF 1455

QY 1438 GILGVQLFKGKFFVCGEDTRNITNKSDCAEASYRWRHKKYNFNDLQALMSFLVLASKD 1497

Db 1456 GILGVQLFKGKFYCEGTDTRNITTKAECHAAHYRWRKKYNFNDLQALMSFLVLSSKD 1515

QY 1498 GWVDIMYDGLDAVGVDQOQIMHNHPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQH 1557

Db 1516 GWVNIMYDGLDAVGIDQOPVQNHNPWMLLYFISFLLIIVFFVLNMFVGVVVENFHKCRQH 1575

QY 1558 QEEEEARRRREKKLRLEKRRSKEKQMAQAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFI 1617

Db 1576 QEAEAEARRRREKKLRRLERRRRSTFPN-PEAQRPPYADYSHTRRSIHSLSCTSHYLDLFI 1634

QY 1618 TGVLGNVVTMAEHYQOQILDEALKICNYIFTVIFVESVFVKLVAFAFRFFQDRNQ 1677

Db 1635 TFIICLVITSMEHYNQPKSLDEALKYCNVFTIVFVFEALKLVAFGFRFFQDRNQ 1694

QY 1678 LDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALHTVM 1737

Db 1695 LDLAIVLLSIMGIALEEIEMNAALPINPTIIRIMRVLRIARVLKLLKMATGMRALDVTV 1754

QY 1738 QALPQVGNLGLLFFLFFIFAALGVFLFGDLECDETHPCGELGRHATFRNFGMAFLTFR 1797

Db 1755 QALPQVGNLGLLFFLFFIYAALGVLEFGRLECSNPNCEGLSRHATFTNFGMAFLTFR 1814

QY 1798 VSTGDNWNGIMKDPDRDC---DQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHL 1854

Db 1815 VSTGDNWNGIMKDTLRECTREDKHCLSYLPALSPVYFVFLVAQFVLNVVIAVLMKHL 1874

QY 1855 EESNKEAEBAEAELEEMKTLSPQPHSPGLSPFLWPGVEGVNSTDSPKPGAPHTTAH 1914

Db 1875 EESNKEAREDAEMDAEIELEI----- 1895

QY 1915 IGAAGSFSLHPTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSL 1974

Db 1896 ---AQGSTAQPPSTAQESQGTD-PDTPNLLVVRKVSVRMLSLPNDSYMFRPVAPAAAPH 1951

QY 1975 GHRGWGLP-----KAQSGSILSVHSQPADTSCILQLP-----KDVHYLLQPHGAP 2019

Db 1952 SH-----PLQEVEMETYTGPVTSAHSPSLPRTSTFQVPSAASSPARASDPLCALSPRDT 2006

RESULT 13

CCAI_HUMAN

ID_CCAI_HUMAN STANDARD; PRT; 2223 AA.

AC Q9P0X4; Q95504; Q7Z6S9; Q8NFX6; Q9NZC8; Q9UH15; Q9UH30; Q9ULU9;

AC Q9UNE6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage-gated calcium channel alpha subunit Cav3.3) (Ca(v)3.3).

DE Name=CACN1I; Synonyms=KIAA1120;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Brain;

RX MEDLINE=99381950; PubMed=10454147;

RA Mittman S., Guo J., Emerick M.C., Agnew W.S.;

RT "Structure and alternative splicing of the gene encoding alpha1, a human brain T calcium channel alpha1 subunit.";

RL Neurosci. Lett. 269:121-124 (1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RC TISSUE=Brain;

RX MEDLINE=20287513; PubMed=10749850; DOI=10.1074/jbc.C000090200;

RA Monteil A., Chemin J., Leuranguer V., Altier C., Mennessier G., Bourinet E., Lory P., Nargeot J.;

RT "Specific properties of T-type calcium channels generated by the human alpha1 subunit.";

RL J. Biol. Chem. 275:16530-16535 (2000).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT VAL-1040.

RC TISSUE=Brain;

RX MEDLINE=22074770; PubMed=12080115;

RA Gomora J.C., Murbartian J., Arias J.M., Lee J.-H., Perez-Reyes E.;

RT "Cloning and expression of the human T-type channel Ca(v)3.3: insights into prepulse facilitation.";

RL Biophys. J. 83:229-241 (2002).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M., Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Copley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.,
RT "The DNA sequence of human chromosome 22."
RL Nature 402:489-495(1999).
RN [5]
RP SEQUENCE OF 1200-2223 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirosewa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA Ohara O.;
RT "Characterization of cDNA clones selected by the GeneMark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC entry of calcium ions into excitable cells and are also involved
CC in a variety of calcium-dependent processes, including muscle
CC contraction, hormone or neurotransmitter release, gene expression,
CC cell motility, cell division and cell death. Isoform alpha-11
CC gives rise to T-type calcium currents. T-type calcium channels
CC belong to the "low-voltage activated (LVA)" group and are strongly
CC blocked by nickel and mibefradil. A particularity of this type of
CC channels is an opening at quite negative potentials, and a
CC voltage-dependent inactivation. T-type channels serve pacemaking
CC functions in both central neurons and cardiac nodal cells and
CC support calcium signaling in secretory cells and vascular smooth
CC muscle. They may also be involved in the modulation of firing
CC patterns of neurons which is important for information processing
CC as well as in cell growth processes. Gates in voltage ranges
CC similar to, but higher than alpha 1G or alpha 1H (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=Delta36b;
CC IsoId=Q9P0X4-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9P0X4-2; Sequence=VSP_000951;
CC Name=3; Synonyms=Alphall-1;
CC IsoId=Q9P0X4-3; Sequence=VSP_000950, VSP_000951;
CC

CC Name=4;
CC IsoId=Q9P0X4-4; Sequence=VSP_000950;
CC -!- TISSUE SPECIFICITY: Brain specific.
CC -!- DOMAIN: Each of the four internal repeats contains five
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC positively charged transmembrane segment (S4). S4 segments
CC probably represent the voltage-sensor and are characterized by a
CC series of positively charged amino acids at every third position.
CC -!- PTM: In response to raising of intracellular calcium, the T-type
CC channels are activated by Cam-kinase II (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
CC -!- CAUTION: Ref.4 (CAB62996) sequence differs from that shown due to
CC erroneous gene model prediction.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF129133; AAD45251.1; -;
CC EMBL; AF142567; AAF25722.1; -;
CC EMBL; AF211189; AAF44626.1; -;
CC EMBL; AF393329; AAM67414.1; -;
CC EMBL; AL008716; CAA15494.1; -;
CC EMBL; AL022312; CAB62988.1; -;
CC EMBL; AL022319; CAB62996.1; ALT_SEQ.
CC EMBL; AL022319; CAD92536.1; -;
CC EMBL; AB032946; BAA86434.1; -;
CC Genew; HGNC:1396; CACNAL1.
CC MIM; 608230; -;
CC GO; GO:0005891; C:voltage-gated calcium channel complex; NAS.
CC GO; GO:0008332; F:low voltage-gated calcium channel activity; NAS.
CC GO; GO:0006816; P:calcium ion transport; NAS.
CC InterPro; IPR001682; Ca/Na_pore.
CC InterPro; IPR002111; Ca_channel_TripL.
CC InterPro; IPR002077; Ca_channel_alpha.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR005820; M+channel_nlg.
CC InterPro; IPR005445; TVDCCAlphal.
CC Pfam; PF00520; Ion_trans; 4.
CC PRINTS; PR00167; CCHANNEL.
CC PRINTS; PR01629; TVDCCALPHAL.
CC KW Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;
KW Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW Polymorphism; Repeat; Transmembrane; Voltage-gated channel.
FT REPEAT 66 401 I.
FT REPEAT 626 865 II.
FT REPEAT 1157 1434 III.
FT REPEAT 1472 1733 IV.
FT DOMAIN 1 78 Cytoplasmic (Potential).
FT TRANSMEM 79 99 S1 of repeat I (Potential).
FT DOMAIN 100 120 Extracellular (Potential).
FT TRANSMEM 121 141 S2 of repeat I (Potential).
FT DOMAIN 142 148 Cytoplasmic (Potential).
FT TRANSMEM 149 168 S3 of repeat I (Potential).
FT DOMAIN 169 173 Extracellular (Potential).
FT TRANSMEM 174 191 S4 of repeat I (Potential).
FT DOMAIN 192 211 Cytoplasmic (Potential).
FT TRANSMEM 212 232 S5 of repeat I (Potential).
FT DOMAIN 233 377 Extracellular (Potential).
FT TRANSMEM 378 398 S6 of repeat I (Potential).
FT DOMAIN 399 640 Cytoplasmic (Potential).
FT TRANSMEM 641 661 S1 of repeat II (Potential).
FT DOMAIN 662 676 Extracellular (Potential).
FT TRANSMEM 677 697 S2 of repeat II (Potential).
FT DOMAIN 698 702 Cytoplasmic (Potential).
FT TRANSMEM 703 721 S3 of repeat II (Potential).
FT DOMAIN 722 729 Extracellular (Potential).
FT TRANSMEM 730 753 S4 of repeat II (Potential).

FT	DOMAIN	754	764	Cytoplasmic (Potential).
FT	TRANSMEM	765	785	S5 of repeat II (Potential).
FT	DOMAIN	786	841	Extracellular (Potential).
FT	TRANSMEM	842	862	S6 of repeat II (Potential).
FT	DOMAIN	863	1166	Cytoplasmic (Potential).
FT	TRANSMEM	1167	1187	S1 of repeat III (Potential).
FT	DOMAIN	1188	1209	Extracellular (Potential).
FT	TRANSMEM	1210	1230	S2 of repeat III (Potential).
FT	DOMAIN	1231	1244	Cytoplasmic (Potential).

Query Match

Best Local Similarity

Matches 1235; Conservative 243; Mismatches 533; Indels 462; Gaps 68;

12

TPPLRGSRPSSDP

-----PGPRLARGWTRRRMERAPRSDSPVASRSTTCPPGGAAG

65

6

SPPSSAAAPAAEPGVTEQPGPR

-----SPPSSPPGLEEPLDGA--

45

66

AGSTEKDPGSADSEAGLPYPALAPVVFYLSQDSRPRSCWLRVTCNPNWFERVSMVLVILL

125

46

-----DP-----HVPHPDLAPIAFAFLRQTTSRPNWCIMKVCNPNWFECVSMVLVILL

91

126

NCVTLMFRPCEDIACDSQRCRILQAFDDFIAPFAVEMVVMKVALGIFGKKCYLGDTWN

185

92

NCVTLMYQPCDDMDCLSDRCKILQVFDFFIFFAMEMVLKVALGIFGKKCYLGDTWN

151

186

RLDFFIVIAGMLEYSLDLQNVSPSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGN

245

152

RLDFFIVMAGMVEYSLDLQNLNSAIRTVRVLRLPLKAINRVPSMRILVNLLDTPMLGN

211

246

VLLLCFFVFFIFGIVGVQLWAGLLNRCLPENFSLPLSDVLEPYQOTENEDSPFICSQ

305

212

VLLLCFFVFFIFGIQVQLWAGLLNRCLFLENFTIQGDVALPPYQPEEDDEMPFICSL

271

306

PRENGMRSCRSVPTLRGEGGGPPCSL-----DYETVNSSNTT--CVNNQYYTNCSA

357

272

SGDNGIMGCHEIPLPKEQ---GRECLSKDDVYDFGAGRQDLNASGLCVNWNRYNVCRT

328

358

GEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFF

417

329

GSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYVMDAHSFYNFYIFILLIIVGSFF

388

418

MINCLVVIATQFSETKQRESQLMREQRVRFSLNASTLASFSEPGSCYEELLKYLVIILR

477

389

MINCLVVIATQFSETKQREHRLMLEQRQYLS--SSTVASYAEPGDCYEEIFQYVCHILR

447

478

KAARRLAQVSRAGIVRAGLLSSPVARSQEQPQSGSCSTRSHRRLSVHHLVHHHHHHHY

537

448

KAKRRALGLYQALQSRQAL--GPEAPAPAKPGP-----HAKEPRHY

487

538

H---LGNGTLRVPRASPEIQDRDAN--GSRRLM--LPPSPSTPTSPGGPRGAESVHSFYHAD

592

488

HGKTGQG-----DEGRHLGSRHCQTLHGPAASP---GNDHSGRE-----

523

593

CHLEPVRCQAPPPRCPEASGRTVSGSKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLT

652

524

-----LC---PQHSPLDA-----TPHT-----LVQ---PIPATLA

547

653

SENIPPGPFSSMHKLELTQSTGAC--HSSCKISSPCSKADSGACGPDSCPYCARTGAGEPE

711

548

S-----DPASCPCQCHEDRRRPSGLGSTDGQSGS---GSSAGGEDE

588

712

SADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQSLGPDABPSSVLA--FWRLICDTF

769

589

A-----DGDGA---RSESDGASSELGKEEEEQ-----ADGAVWLCDGVWRETRAKL

633

770

RKIVDSKYFGRGIMAILVNTLSMGIEYHQPEELTNALEISNIVFTSLFALEMILKLLV

829

634

RGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNILEICNVVFTSMFALEMILKLA

693

830

YGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRLPALQRLV

889

694

FGLFDYLRPNYNIFDSIIIVISWEIVGQADGGLSVLRTFRLRLVLKLVRFMPALRRQLV

753

QY	890	VLMKTMNDNVATFCMLLMLEFIFISILGMHLFGCKFASERD--GDTLPDRKNFDSLLWAIVT	948
Db	754	VLMKTMNDNVATFCMLLMLEFIFISILGMHLFGCKFSLRTDGTGTVDRKNFDSLLWAIVT	813
QY	949	VFOILTQEDMNKVLNGMASTSSWAALYPIALMTFGNYVLFNLVAILVEGFOAEGDATK	1008
Db	814	VFOILTQEDWNVLYNGMASTSPWASLYFVALMTFGNYVLFNLVAILVEGFOAEGDANR	873
QY	1009	SESEPDFFPSV-----DGDGRKKRLALVALGEHAELKSLPLLIHT-----A	1054
Db	874	SYSEDEQSSSNIIEFDFKLQEGLDSSGDPK--LCPIWTPNGHLDPSL--PLGGHLGPAGA	929
QY	1055	ATPMShPKSSSTGVGEALGSGRRRTSSSGSAEPGAHHHEMKCPPSARSSPHSPWSAASSW	1114
Db	930	AGPA--PRLSLQPDPMVALGSRKSSVMSL---GRMSYDQRSLSRSSSYYPGWGRSAAW	984
QY	1115	TSRRSRNSLGRAPSLKRRSPSGERRSLLSGE--GOESQDEHESSEE--DRASPAGSDH--	1169
Db	985	ASRRSSWN-----SLKHKPPSAEHESLLSAERGGGARVCVAADGPPRAAPLHTPHAH	1038
QY	1170	-----RHGSLEREAKSSFDLPDTLQVPLGHLRTASGRSS--ASEHQCNGKS	1214
Db	1039	HIHGHPLAHRHRHRTLSLNRDSVDLAELVPAGVAHPRAAWRAAGPAGHEDCNGRM	1098
QY	1215	ASGRLLARTLTD--DPQLDGGDDNDENGLSKGERIQAWVRSLPACCRERDSWSAYIFPPQ	1273
Db	1099	PS--IAKDVFTKMGDRGRGEDEEIDYTLCFVRKIMIDVYKPDCEVREDWSVYLFSP	1156
QY	1274	SRFLLCHRIITHKMFHVVLVIFLNCITIAMERPKIDPHSAERIFLTLNSYIFTAVEL	1333
Db	1157	NRFVLCQTIIAHKLFDYVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIV	1216
QY	1334	AEMTVKVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVLR	1393
Db	1217	GEMTLKWSLGLYFGEQAYLRSSWNVLDGFLVFVSIIDIVVSLASAGAKILGVLRLR	1276
QY	1394	LRTLRLRVISRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQ	1453
Db	1277	LRTLRLRVISRAPGLKLVVETLISLKPIGNIVLICCAFFIIFGILGVQLFKGKFFHCL	1336
QY	1454	GEDTRNITNKSDCAEASRYRWRHKYNFDFNLGQALMSLFLVASKDQWVDIMYDGLDAVGD	1513
Db	1337	GVDTRNITNRSDCMAANYRWHHKYNFDFNLGQALMSLFLVASKDQWVNIMYNGLDAVAD	1396
QY	1514	QOPIMHNPMWLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQHQBEEARRRREKRLRR	1573
Db	1397	QOPVTNHNPMWLLYFISFLLIIVSFFVLMFVGVVVENFHKCRHQHQBEEARRRREKRLRR	1456
QY	1574	LEKKRRSKEKQMAEAAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLNVVTMAMEHY	1633
Db	1457	LEKKRR-----KAQRLPYATYCHTRLLIHSMTCTSHYLDIFTITFIICLVNVTMSLEHY	1509
QY	1634	QOQIILDEALKICNYIFTVIFVFESVFKLVAFARFRFFQDRWNQDLDAIVLLSIMGITLE	1693
Db	1510	NQPTSLETALKYCNMFTTVFVLEAVLKLVAFLRRFFKDRWNQDLDAIVLLSIMGITLE	1569
QY	1694	EIEVNLSPINPTIIRIMRVLRIRARVLKLLKMAVGMRLHVTVMQALPQVGNLGLLFMLL	1753
Db	1570	EIEINAALPINPTIIRIMRVLRIRARVLKLLKMATGMRLLDVTVQALPQVGNLGLLFMLL	1629
QY	1754	FFIFAALGVELFGDLECEDETHPCBGLGRHATFRNFGMAFLTRFVSTGDNWNGIMKDPSSR	1813
Db	1630	FFIYAALGVELFGKLVNDENPCBGRHATFENFGMAFLTRFQVSTGDNWNGIMKDTLR	1689
QY	1814	DC--QOESTCYNTV--ISPIYFVSFVLTAQFVLNVVIAVIMKHLSESNKEAKEEAELEAE	1870
Db	1690	DCTHDERSCSLSLQFVSPLYFVSFVLTAQFVLNVVIAVIMKHLDDSNKEAQEDAEMDAE	1749
QY	1871	LELEM-KTSLSPQSPHSPGSP-----FLW-----	1892
Db	1750	LELEMAHGLGPGPRLPTGSPGAPGRPGGAGGGGTGGGLCRRCYSPAQENLWLDVSLI	1809

RL RL

FT	TRANSMEM	688	711	S4 of repeat II (Potential).
FT	DOMAIN	712	722	Cytoplasmic (Potential).
FT	TRANSMEM	723	743	S5 of repeat II (Potential).
FT	DOMAIN	744	795	Extracellular (Potential).
FT	TRANSMEM	796	820	S6 of repeat II (Potential).
FT	DOMAIN	821	1125	Cytoplasmic (Potential).
FT	TRANSMEM	1126	1148	S1 of repeat III (Potential).
FT	DOMAIN	1149	1166	Extracellular (Potential).
FT	TRANSMEM	1167	1187	S2 of repeat III (Potential).
FT	DOMAIN	1188	1197	Cytoplasmic (Potential).
FT	TRANSMEM	1198	1217	S3 of repeat III (Potential).
FT	DOMAIN	1218	1231	Extracellular (Potential).
FT	TRANSMEM	1232	1253	S4 of repeat III (Potential).
FT	DOMAIN	1254	1263	Cytoplasmic (Potential).
FT	TRANSMEM	1264	1287	S5 of repeat III (Potential).
FT	DOMAIN	1288	1364	Extracellular (Potential).
FT	TRANSMEM	1365	1390	S6 of repeat III (Potential).
FT	DOMAIN	1391	1445	Cytoplasmic (Potential).
FT	TRANSMEM	1446	1466	S1 of repeat IV (Potential).
FT	DOMAIN	1467	1480	Extracellular (Potential).
FT	TRANSMEM	1481	1502	S2 of repeat IV (Potential).
FT	DOMAIN	1503	1509	Cytoplasmic (Potential).
FT	TRANSMEM	1510	1528	S3 of repeat IV (Potential).
FT	DOMAIN	1529	1542	Extracellular (Potential).
FT	TRANSMEM	1543	1566	S4 of repeat IV (Potential).
FT	DOMAIN	1567	1580	Cytoplasmic (Potential).
FT	TRANSMEM	1581	1601	S5 of repeat IV (Potential).
FT	DOMAIN	1602	1664	Extracellular (Potential).
FT	TRANSMEM	1665	1692	S6 of repeat IV (Potential).
FT	DOMAIN	1693	1835	Cytoplasmic (Potential).
FT	SITE	355	355	Calcium ion selectivity and permeability (By similarity).
FT	SITE	779	779	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1339	1339	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1637	1637	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	171	171	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	242	242	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	309	309	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	1301	1301	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	1304	1304	N-linked (GlcNAc. .) (Potential).
FT	CONFLICT	193	193	M -> L (in Ref. 3).
FT	CONFLICT	291	291	C -> V (in Ref. 3).
FT	CONFLICT	394	394	V -> L (in Ref. 3).
FT	CONFLICT	406	406	E -> N (in Ref. 3).
FT	CONFLICT	485	485	C -> S (in Ref. 3).
FT	CONFLICT	512	512	D -> Y (in Ref. 3).
FT	CONFLICT	558	558	S -> R (in Ref. 3).
FT	CONFLICT	683	683	G -> S (in Ref. 3).
FT	CONFLICT	691	691	F -> S (in Ref. 3).
FT	CONFLICT	739	740	MH -> ID (in Ref. 3).
FT	CONFLICT	833	833	C -> Y (in Ref. 3).
FT	CONFLICT	846	846	F -> L (in Ref. 3).
FT	CONFLICT	856	856	S -> R (in Ref. 3).
FT	CONFLICT	905	905	L -> R (in Ref. 3).
FT	CONFLICT	913	913	M -> YW (in Ref. 3).
FT	CONFLICT	936	936	W -> G (in Ref. 3).
FT	CONFLICT	996	996	A -> R (in Ref. 3).
FT	CONFLICT	1060	1060	I -> M (in Ref. 3).
FT	CONFLICT	1094	1094	D -> CC (in Ref. 3).
FT	CONFLICT	1197	1198	SS -> TD (in Ref. 3).
FT	CONFLICT	1229	1231	Missing (in Ref. 3).
FT	CONFLICT	1422	1422	K -> Y (in Ref. 3).
FT	CONFLICT	1623	1625	FGM -> SAR (in Ref. 3).
FT	CONFLICT	1656	1656	S -> T (in Ref. 3).
FT	CONFLICT	1737	1737	P -> A (in Ref. 3).
SQ	SEQUENCE	1835	AA; 205348 MW; E6025E0F1BE80CCA CRC64;	

Query Match 44.5%; Score 5354; DB 1; Length 1835;
Best Local Similarity 55.4%; Pred. No. 1.6e-259;
Matches 1138; Conservative 217; Mismatches 374; Indels 324; Gaps 45;

QY	43	PRSRDSPVASRSSTCPGGAAGAGSTKDPGSADSEAG-----LPYPALAPVVFYLSQ	98
Db	8	PSSAAAPAPPEGITEQGP-----RSPPPSPGLEPLEGINPDVPHDLPAPVAFCLRQ	62
QY	99	DSRPRSCLRTVCNPFERVSMLVLLNCVTLGMFPCEDTACDSQRCRILQAFDDTIFA	158
Db	63	TTSRPNWCIMVCNPFECVSMVLVLLNCVTLGMYQPCDDMECLSDRCKILQVFDFTFI	122
QY	159	FFAVEMVVMVALGIFGKKCYLGDWTNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLR	218
Db	123	FFAMEMVLKVALGIFGKKCYLGDWTNRLDFFIVMAGMVEYSLDLQNLNSAIRTVRVL	182
QY	219	PLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIGVGVQLWAGLLRNRCLPEN	278
Db	183	PLKAINRVPSMRILVNLDDTLMLGNVLLLCFFVFFIGVGVQLWAGLLRNRCLFLEN	242
QY	279	FSLPLSVLDLEPYQTENEDESPFICSQPRENGMRSCRVPVTLRGGGGPPCSL-----	332
Db	243	FTIQGDVALPPYQPEEDDEMPFICSLTGDNGIMGCHIPPPLKEQ---GRECCLSKDDVY	299
QY	333	DYETYNSSNTT--CVNMNOYTNCSAGEHNPKGAINFDNIGYAWIAIFQVITLEGWVD	390
Db	300	DFGAGRQDLNAGSLCVNMNRYNVVCRGTGNANPKGAINFDNIGYAWIVIFQVITLEGWVE	359
QY	391	IMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLS	450
Db	360	IMYVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS	419
QY	451	NASTLASFSEPGSCYEELLKYLVIILRKAARLAQVSRAGLSSPVARSQEQPQ	510
Db	420	-SSTVASYAEPGDCYEELFYQVCHILRKAKR-----RALGLYQAL-----	458
QY	511	SGSCTRSRRRLSVHLLVHHHHHHHHYHLNGTGLRVPRASPEIQDRDANGSRRLMLPPPS	570
Db	459	-----QNRQA-----MGPST-----PAPA	473
QY	571	TPTPSGGPPRGAESVHSFYHADCHLEPVRCOAPPPRCPSEASGRVTGSGKVYPTVHTSPP	630
Db	474	KPGP-----HAK---EPHCKLCPRHSPLD-----PTPHT-----	500
QY	631	PEILKDKALVEVAPSPGPTLTSTFNIPPGPFSSMHKLLTQSTGACHSSCKISSPCSKAD	690
Db	501	-----LVQ-----PISAIL-----	509
QY	691	SGACGPDSCPYC-----ARTGAGEPESADHVHVDSDSEAVYEFTQDAQH	734
Db	510	--ASDPSSCPHCQHEAGRRPSGLGSTSGQEGSGSGSAE---AEANGDGL-QSSEDDGVS	563
QY	735	SDLRDPHSRRRQSRSLGPDAPSSVLA-----FWRLICDTERKIVDSKYFGRGIMAILVN	789
Db	564	SD-----LGKEEEQEDGAARLCGDVWRETRKKLRGIVDSKYFNRGIMMAILVN	611
QY	790	TLSMGIEYHQPEELTNALEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNI FDGVIV	849
Db	612	TVSMGIEHHEQEPEELTNILEICNVVFTSMFALEMILKLAAGFLDYLRNPYNIFDSIIVI	671
QY	850	ISVWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRLVLMKTMNDVATFCMLLMFLI	909
Db	672	ISIWEIVGQADGGLSVLRTFRLRLVLKLVRFMPALRRQLVLMKTMNDVATFCMLLMFLI	731
QY	910	FIFSILGMHLFGCKFASERD-GDTLPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMAS	968
Db	732	FIFSILGMHIFGCKFSLRTDGTVPDRKNFDSLLWAIIVTFQILTQEDWNVVLNGMAS	791
QY	969	TSSWAALYFIALMTFGNVYLENLLVAILVEGFAEQAGKATKSESEPDFFSPSVDG-----	1022
Db	792	TPWASLYFVALMTFGNVYLENLLVAILVEGFAEQAGDANRSCDEDEQSSSNLEEFDKLPE	851
QY	1023	--DGRKKRLALVALGEHAELRKSLLPPLIIH--TAATPMSHPKSSSTGVGEALGSGSRR	1078
Db	852	GLDNRDLKLCPIPMTPNGHLDPSL--PLGAHLGFAGTMTGAPRLSLQDPVLVALDSRK	909

QY	1079	TSSGSAEPGAAHHEMKCPPSARRSPHSPWSAASWTGRRSSRNSLGRAPSLKRSPSGE	1138
Db	910	SSVMSL---GRMSYDQRLSSRSSSYYPGWGRSGTWASRRSWN-----SLKHPPSAE	960
QY	1139	RRSLSGEGQES--QDEESSEE--DRASPAGSDH-----RHRSGLEREA	1179
Db	961	HESLLSGEGGSCVRACEGAREEAPTRTAPLHAPHAHAHGHPLAHRHRHRTLSLDT	1020
QY	1180	KSSFDLPDLTQVPLHRTAS--GRSSASEHQDCNGKSASGRUARTLRTD-DPQLDGDND	1236
Db	1021	RDSVDLGELVPVVGAAHRAAWRGAGQAPGHEDCNGRMPN--IAKDVFTKMDRRDRGEDE	1078
QY	1237	DEGNLSKGERIQAWVRSLRPACCRERDSWYAYIFPPQSRFRLLCHRIITHKMFHDHVLVI	1296
Db	1079	EEIDYTLCFVRVKMIDVYKPDWCEVREDWSVYLFSPENKFRILCQTIIAHKLFDYVVLAF	1138
QY	1297	IFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSS	1356
Db	1139	IFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVSGLGYFGEQAYLRSS	1198
QY	1357	WNVLDGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLRLRLRLRLRLRLRLRLRLRLRL	1416
Db	1199	WNVLDGFLVFSIIDIVSVASAGGAKILGVLRLVRLRLRLRLRLRLRLRLRLRLRLRLRL	1258
QY	1417	MSSLKPIGNIVVICCAFEIIFGILGVQLFKGKFPVCQGEDTRNITNKSDCAEASRWVRH	1476
Db	1259	ISSLKPIGNIVLICCAFEIIFGILGVQLFKGKFKYHCLGVDTNRNITNRSDCVAANYRWVH	1318
QY	1477	KYNFDNLGOALMSLFVLASKDGMVDIMYDGLDAVGVDQOPIMHNPNMMLLYFISFLLIYA	1536
Db	1319	KYNFDNLGOALMSLFVLASKDGMVIMYNGLDVAVADQOPVTNHNPNMMLLYFISFLLIYS	1378
QY	1537	FFVLNMFVGVVVENFHKCRHQHEEEARRREEKRLRRLEKRRSKEKQMAEAQCKPYYS	1596
Db	1379	FFVLNMFVGVVVENFHKCRHQHEAAEARRREEKRLRRLEKRR-----KAQRLPYAT	1431
QY	1597	YSRFRLLVHHLCTSHYLDLFTIGVIGLVNVTMAMEHYQOPQILDEALKICNYIFTVIFV	1656
Db	1432	YCPTRLLIHSMTCTSHYLDIFITFIICLVNVTMSLEHYNQPTSLTALKYCNYMFTVFL	1491
QY	1657	ESVFKLVAFARFRFFQDRWNQLDLAIVLLSIMGITLIEIEVNLSLPINPTIIRIMVRLI	1716
Db	1492	EAVLKLVAFLGLRRFFKDRWNQLDLAIVLLSVMGITLIEIEINAALPINPTIIRIMVRLI	1551
QY	1717	ARVLKLLKMAVGMRAALLHTVMQALPQVGNLGLLFFLFFIFAALGVELFGDLECDTHPC	1776
Db	1552	ARVLKLLKMATGMRAALLDTVVQALPQVGNLGLLFFLFFIYAALGVELFGKLVCDENPC	1611
QY	1777	EGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDPNRDC-DQESTCYNTV--ISPIYFVS	1833
Db	1612	EGMSRHATFRNFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCSLSLQFVSPLYFVS	1671
QY	1834	FVLTAQFVLNVVVIAMKHLSEESNKEAEAELEAELEEMKTLSPQHPSPGLSPFLWP	1893
Db	1672	FVLTAQFVLNVVVAIVLMKHLDDSNKEAQEDAEMDAEIELEM-----	1713
QY	1894	GVEGVNSTDKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVVPL-GPDLLTV-----	1946
Db	1714	AHGLGPCPGPCPG-----PCPCPCPCPGPRLPSTSSPGAPG	1750
QY	1947	RKSGVSRTHSLPNDSYMCRN-GSTAERSLGHGWLPLKAQSGSILSVHSQPADTSCILQL	2005
Db	1751	RSGGGAGAGG-DTSHLCRHCYSPAQETL-----W----LDSVSLIKDSLEGELTIIDNL	1801
QY	2006	PKDV-HYLLQPHG	2017
Db	1802	SGSVFHHYASPDG	1814
RESULT 15			
Q7Z6S8			
ID	Q7Z6S8	PRELIMINARY;	PRT; 1994 AA.
AC	Q7Z6S8;		

DT	01-OCT-2003	(TrEMBLrel. 25, Created)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	DJ172B20.1	(Calcium channel, voltage-dependent, alpha 1I subunit)	
DE	(Fragment).		
GN	Name=CACNA1I;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Phillips S.;		
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AL022319; CAD92537.1; --		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0005261; F:cation channel activity; IEA.		
DR	GO; GO:0006812; P:cation transport; IEA.		
DR	InterPro; IPR001682; Ca/Na_pore.		
DR	InterPro; IPR002111; Cat channel TrpL.		
DR	InterPro; IPR000345; CytC_heme_B5.		
DR	InterPro; IPR005821; Ion_trans.		
DR	InterPro; IPR005820; M+channel_nlg.		
DR	Pfam; PF00520; Ion_trans; 4.		
DR	PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.		
KW	Ion transport; Ionic channel; Transmembrane; Transport.		
FT	NON TER 1		
SQ	SEQUENCE 1994 AA; 220004 MW; ASEFAESP32DCF76 CRC64;		
Query Match	39.5%;	Score 4750.5;	DB 2; Length 1994;
Best Local Similarity	49.0%;	Pred. No. 3e-229;	
Matches 1099;	Conservative 214;	Mismatches 485;	Indels 447; Gaps 61;
QY	229	MRILVTLLDITLPMGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPSVDLE	288
Db	1	MRILVNLLDITLPMGNVLLLCFFVFFIFGIIIGVQLWAGLLRNRCFLEENFTIQGDVALP	60
QY	289	PVYQTEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCSL-----DYETYNSSN	342
Db	61	PVYQPEEDDEMPFICSLSGDNGIMGCHEIPLKEQ---GRECCLSKDDVDFGAGRQDLN	117
QY	343	TT--CVNWNQYTYNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHS	400
Db	118	ASGLCVNWNRYNVCRTGTSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYVMDAHS	177
QY	401	FYNFIYFILLIIVGSFFFMINCLVVIATQFSETKQRESQLMRQVRFLSNASTLASFE	460
Db	178	FYNFIYFILLIIVGSFFFMINCLVVIATQFSETKQREHRLMLEQRQYLS--SSTVASYAE	236
QY	461	PGSCYEELLKYLVIILRKAAARLAQVSRAGIVRAGILSSPVARSGEQPQSGSCTSRHR	520
Db	237	PGDCYEEIFQYVCHILRKAKR-----RALGLYQALQS-----RR	270
QY	521	LSVHHLVHHHHHHHHYHLNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPR	580
Db	271	QAL-----GPE-----APAPAKPGP-----	285
QY	581	GAESVHSFYHADCHLEPVRCQAPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALV	640
Db	286	-----HAK---EPRHYQLCPQHSPLDA-----TPHT-----LV	310
QY	641	EVAPSPGPPTLTSTFNIPPGPFSSMHKILLETQSTGAC-HSSCKISSPCSKADSGACGDSC	699
Db	311	Q-----PIPATLAS-----DPASCPCQCHEDGRRPSGLGSTDGSGSGS-	350
QY	700	PYCARTGAGEPEESADHVPDSDSEAVYFTQDAQHSLDRDPHRRRRQSLGPDAEFSSVL	759
Db	351	---GSSAGGEDEA-----DGDGA---RSSEDGASSELGKEEBEEQ-----ADGAVML	392
QY	760	A--FWRLICDTFRKIVDSKYFGRGIMTIALVNTLSMGIEYHEQPELTNALEISNIVFTS	817
Db	393	CGDVWRETRAKLRGIVDSKYFNFRGIMMAILVNTVSMGIEHHEQPELTNILEICNVVFTS	452

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:06:00 ; Search time 186.635 Seconds
(without alignments)
4355.452 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEDGAGAEESGQPRSFM.....PKDVLSLSLSDPADLDP 2266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11862.5	99.7	2273	4	AAE01019 Human T-t
2	11758.5	98.8	2243	2	AAY14589 Human T-t
3	11758.5	98.8	2243	7	ADJ68819 Human hea
4	11741	98.6	2250	2	AAY14586 Human T-t
5	11735.5	98.6	2261	2	AAY14587 Human T-t
6	11727	98.5	2268	2	AAY14588 Human T-t
7	11653	97.9	2266	4	AAB66481 Human alp
8	11111	93.3	2428	3	AAY70720 Rat pancr
9	10962.5	92.1	2247	2	AAY14593 Rat T-typ
10	10945	91.9	2254	2	AAY14590 Rat T-typ
11	10939.5	91.9	2265	2	AAY14591 Rat T-typ
12	10925	91.8	2272	2	AAY14592 Rat T-typ
13	10774	90.5	2287	4	AAB66475 Rat T-typ
14	6315.5	53.1	1207	4	AAU00474 Human T-t
15	6218	52.2	2359	4	AAB66476 Rat alpha
16	6212	52.2	2353	2	AAY06299 Human act
17	6212	52.2	2353	6	ABP72254 Human T-t
18	6212	52.2	2353	7	ADJ69322 Human hea
19	6211	52.2	2353	2	AAY06298 Human act
20	6178	51.9	2353	5	ABG30840 Human vol
21	5855.5	49.2	2038	2	AAY14595 Human T-t
22	5845.5	49.1	2044	2	AAY14594 Human T-t
23	5709.5	48.0	2034	2	AAY06300 Human act
24	5492.5	46.1	2175	5	AAU10535 Human T-t
25	5492.5	46.1	2175	6	ABU08511 Human T-t

26	5492.5	46.1	2175	8	ADH69265 Human TCC
27	5484	46.1	2188	5	AAU10536 Human T-t
28	5484	46.1	2188	6	ABU08512 Human T-t
29	5484	46.1	2188	8	ADH69267 Human TCC
30	5366	45.1	1835	2	AAY14597 Rat T-typ
31	5366	45.1	1835	8	ADH69268 Rat T-typ
32	5361.5	45.0	1823	2	AAY14596 Human T-t
33	5198.5	43.7	1792	4	AAB66477 Rat brain
34	5043.5	42.4	982	4	AAM23743 Human EST
35	3959.5	33.3	1854	2	AAW79161 Human cal
36	3959.5	33.3	1854	4	AAB66472 Protein e
37	3442	28.9	2435	4	ABB60448 Drosophil
38	3427	28.8	644	4	AAB66478 Human alp
39	3020.5	25.4	1859	4	ABG10954 Novel hum
40	1960	16.5	853	4	AAM93437 Human pol
41	1960	16.5	853	8	ADL31041 Human pro
42	1753	14.7	2264	8	ADM31026 Human cal
43	1752.5	14.7	2339	2	AAR33549 Sequence
44	1750.5	14.7	2343	2	AAY31809 N-type ca
45	1749	14.7	2337	2	AAW37878 Human cal

ALIGNMENTS

RESULT 1
AAE01019
ID AAE01019 standard; protein; 2273 AA.
XX
AC AAE01019;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human T-type low voltage activated calcium channel alphasG-c protein.
XX
KW Human T-type low voltage activated calcium channel alphasG-c; stress;
KW epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;
KW endocrine disorder; respiratory disorder; peripheral muscle disorder;
KW muscle excitability; fertilisation; contraception; hypertension;
KW neuronal firing regulation; cardiovascular disorder; gene therapy;
KW forensic analysis; epidemiological study; neuroleptic.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
FT Misc-difference 1138 /note= "Encoded by GAG"
FT Misc-difference 1142 /note= "Encoded by GAA"
FT Misc-difference 1680 /note= "Encoded by ACG"
FT Misc-difference 1683 /note= "Encoded by GAA"
PN WO200130844-A1.
XX
PD 03-MAY-2001.
XX
PF 06-OCT-2000; 2000WO-US027761.
XX
PR 26-OCT-1999; 99US-00426998.
XX
(ORTH) ORTHO-MCNEIL PHARM INC.
PI Dubin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;
XX
DR WPI; 2001-300486/31.
XX
DR N-PSDB; AAD04756.
XX
PT New nucleic acid encoding human calcium channel protein, useful for
PT identifying specific modulators and potential pharmaceuticals for
PT treating e.g. epilepsy.

PS Claim 11; Page 81-99; 115pp; English.

XX The invention relates to isoform of human T-type low voltage activated calcium channel (alpha1G-c) cDNA and protein. Cells transformed with calcium channel DNA to express calcium alpha1G-c channel protein are used to identify specific modulators (antagonists or agonists). These modulators are useful as therapeutic agents and are used for treating wide range of calcium alpha1G-c channel-mediated disorders, e.g. stress epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease, endocrine disorders, respiratory disorder, peripheral muscle disorder, muscle excitability, fertilisation, contraception, disorders involving hypertension, neuronal firing regulation, potentiation of synaptic signals and cardiovascular disorders (e.g. atherosclerosis, cardiac hypertrophy, angina pectoris). Calcium alpha1G-c channel DNA is useful for isolating and identifying related molecule mutations. It is also optionally used as antisense sequences, in gene therapy. Calcium channel alpha1G-c DNA, protein and antibodies are useful for forensic analysis, diagnosis and epidemiological studies, by standard hybridisation or immunological assays. The present sequence is T-type low voltage activated calcium channel alpha1G-c protein

SQ Sequence 2273 AA;

Query Match 99.7%; Score 11862.5; DB 4; Length 2273;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 2260; Conservative 4; Mismatches 2; Indels 7; Gaps 1;

Qy	1	MDEEDGAGAEESGQPSFMRNLDSGAGRPGPSAEKDPGSADSAEGLPYPALAPVV	60
Db	1	MDEEDGAGAEESGQPSFMRNLDSGAGRPGPSAEKDPGSADSAEGLPYPALAPVV	60
Qy	61	FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLMGFRPCEDIACDSQRCRILQAF	120
Db	61	FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLMGFRPCEDIACDSQRCRILQAF	120
Qy	121	DDFIFAFFAVEMVVKMVALGIFGKKCYLGDWNRLDFFIVIAGMLEYSLDLQNVSFSAVR	180
Db	121	DDFIFAFFAVEMVVKMVALGIFGKKCYLGDWNRLDFFIVIAGMLEYSLDLQNVSFSAVR	180
Qy	181	TVRVLRLPRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240
Db	181	TVRVLRLPRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240
Qy	241	CFLEPNFSLPLSDLERYVQYOTENEDESPFICSPRENGMRSCRSVPTLRGDDGGPPCCGL	300
Db	241	CFLEPNFSLPLSDLERYVQYOTENEDESPFICSPRENGMRSCRSVPTLRGDDGGPPCCGL	300
Qy	301	DYEAYNSSNTTCVWNQYYTNCAGAHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM	360
Db	301	DYEAYNSSNTTCVWNQYYTNCAGAHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM	360
Qy	361	YFVMDAHSFYNFYIFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420
Db	361	YFVMDAHSFYNFYIFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420
Qy	421	STLASFSEPGSCYEELLYVILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPSS	480
Db	421	STLASFSEPGSCYEELLYVILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPSS	480
Qy	481	SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPASPEIQDRDANGSRRLMLPPPSTP	540
Db	481	SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPASPEIQDRDANGSRRLMLPPPSTP	540
Qy	541	ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE	600
Db	541	ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE	600
Qy	601	TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG	660
Db	601	TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG	660
Qy	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA	720
Db			

Db	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDA	720
Qy	721	EPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI	780
Db	721	EPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI	780
Qy	781	VFTSLFALEMLLKVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR	840
Db	781	VFTSLFALEMLLKVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR	840
Qy	841	VKLVRFLPALQRLVLMKTMNDNVATFCMLLMLFIFIFSLGMHLFGCKFASERDGTDL	900
Db	841	VKLVRFLPALQRLVLMKTMNDNVATFCMLLMLFIFIFSLGMHLFGCKFASERDGTDL	900
Qy	901	PDRKNFDSLLWAIIVTVFQILTQEDWNKVLVNGMASTSSWAALYFIALMTFGNYVFLNLLV	960
Db	901	PDRKNFDSLLWAIIVTVFQILTQEDWNKVLVNGMASTSSWAALYFIALMTFGNYVFLNLLV	960
Qy	961	AILVEGFOAEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDGRKKCL	1020
Db	961	AILVEGFOAEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDGRKKCL	1020
Qy	1021	ALVSLGEHPELKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA	1080
Db	1021	ALVSLGEHPELKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA	1080
Qy	1081	HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140
Db	1081	HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140
Qy	1141	DEESSEERASPAQSDHHRGSLEREAQSSFDLPDTLQVPLHRTASGRGSASEHQDCN	1200
Db	1141	DEESSEERASPAQSDHHRGSLEREAQSSFDLPDTLQVPLHRTASGRGSASEHQDCN	1200
Qy	1201	GKSASGRALARALRPPDPLDGGDDADDEGNLSKGERVRAWIRARLPACLERDSWSAYIFP	1260
Db	1201	GKSASGRALARALRPPDPLDGGDDADDEGNLSKGERVRAWIRARLPACLERDSWSAYIFP	1260
Qy	1261	POSRRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320
Db	1261	POSRRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320
Qy	1321	FLAEMTVKVALGWCQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1380
Db	1321	FLAEMTVKVALGWCQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1380
Qy	1381	RLRLTLRPLRVISRAQGLKLVVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGKFFV	1440
Db	1381	RLRLTLRPLRVISRAQGLKLVVETLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGKFFV	1440
Qy	1441	CQGEDTRNITNKSDCAEASRVWRVHKYNFDNLGQALMSLFLVASKDGWVDIMYDGLDAVG	1500
Db	1441	CQGEDTRNITNKSDCAEASRVWRVHKYNFDNLGQALMSLFLVASKDGWVDIMYDGLDAVG	1500
Qy	1501	VDQQPIMNHNPMWLLYFISFILLIVAFFVLNMFVGVVVENFHKCRHQHEEEARRRREKRL	1560
Db	1501	VDQQPIMNHNPMWLLYFISFILLIVAFFVLNMFVGVVVENFHKCRHQHEEEARRRREKRL	1560
Qy	1561	RRLEKRRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLDFITGVIGLNVVTWAME	1613
Db	1561	RRLEKRRSKEKQMAEAQCKPYSDYSRFRLLVHHLCTSHYLDLDFITGVIGLNVVTWAME	1620
Qy	1614	HYQQPQILDEALKICNYIFTVIFVLESVKLVAFGFRFFQDRWNQDLDAIVLLSIMGIT	1673
Db	1621	HYQQPQILDEALKICNYIFTVIFVLESVKLVAFGFRFFQDRWNQDLDAIVLLSIMGIP	1680
Qy	1674	LEEIEVNASLPINPTIIRIMRVLRARVLKLLKMAVGMRAALLDTVMQALPQVGNLGLLFM	1733
Db	1681	LEQIEVNASLPINPTIIRIMRVLRARVLKLLKMAVGMRAALLDTVMQALPQVGNLGLLFM	1740
Qy	1734	LLFFIFAALGVLFGLDLECDETHPCGELGRHATFRNFGMAFLTFLFRVSTGDNNGIMKDT	1793
Db	1741	LLFFIFAALGVLFGLDLECDETHPCGELGRHATFRNFGMAFLTFLFRVSTGDNNGIMKDT	1800

QY 1794 LRDCDQESTCVNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAELEAEL 1853
Db |||||||
QY 1801 LRDCDQESTCVNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAELEAEL 1860
Db |||||||
QY 1854 ELEMKTLSPOHSPGLSPFLWPVGEGDPSPDPKPGALHPAAHARSASHFSLEHPTMQPH 1913
Db |||||||
QY 1861 ELEMKTLSPOHSPGLSPFLWPVGEGDPSPDPKPGALHPAAHARSASHFSLEHPTMQPH 1920
Db |||||||
QY 1914 PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHS 1973
Db |||||||
QY 1921 PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHS 1980
Db |||||||
QY 1974 QPADTSYIILQPKDAPHLLQPHSAPTWTGTPKLPDPGRSPLAQRPLRRQAAIRTDSDVQ 2033
Db |||||||
QY 1981 QPADTSYIILQPKDAPHLLQPHSAPTWTGTPKLPDPGRSPLAQRPLRRQAAIRTDSDVQ 2040
Db |||||||
QY 2034 GLGSREDLLAEVSGSPPLARAYFWGQSSSTQAQQHRSRSHSKISKHMTTPAPCPGPEPNW 2093
Db |||||||
QY 2041 GLGSREDLLAEVSGSPPLARAYFWGQSSSTQAQQHRSRSHSKISKHMTTPAPCPGPEPNW 2100
Db |||||||
QY 2094 GKGPPETRSSLELDTLSWISGDLPLPPGGQEEPPSPRDLKKCYSEVAQSCORRPTSWLDE 2153
Db |||||||
QY 2101 GKGPPETRSSLELDTLSWISGDLPLPPGGQEEPPSPRDLKKCYSEVAQSCORRPTSWLDE 2160
Db |||||||
QY 2154 QRRHSIAVSCLDGSGQPHLGTDPNSLGGQPLGGPSRPPKKLSPPSITIDPPESQGRTP 2213
Db |||||||
QY 2161 QRRHSIAVSCLDGSGQPHLGTDPNSLGGQPLGGPSRPPKKLSPPSITIDPPESQGRTP 2220
Db |||||||
QY 2214 PSPGICLRRRAPSSDSKDPPLASGPPDMSAASPSPKKDVLSSLGLSSDPADLDP 2266
Db |||||||
QY 2221 PSPGICLRRRAPSSDSKDPPLASGPPDMSAASPSPKKDVLSSLGLSSDPADLDP 2273
Db |||||||

RESULT 2
AAY14589

XX AAY14589 standard; protein; 2243 AA.
AC AAY14589;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human T-type voltage-gated Ca channel alpha-1-G (hCavT1d).
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
OS Homo sapiens.

XX WO9929847-A1.
XX
PD 17-JUN-1999.
XX
XX 30-OCT-1998; 98WO-US023161.
PF
XX
PR 05-DEC-1997; 97US-00985809.
XX
XX (LOYO) UNIV LOYOLA CHICAGO.
PA
XX
PI Perez-Reyes E, Cribbs LL;
XX

DR WPI; 1999-394972/33.
XX
DR N-PSDB; AAX83484.
XX

PT New T-type voltage-gated calcium channels.
XX
XX Disclosure; Page 58-67; 138pp; English.
PS
XX

CC This sequence represents a human T-type voltage-gated calcium (Ca)
CC channel alpha-1-G designated hCavT1d. Voltage gated channels are membrane
CC bound glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and

CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC -channels contains a putative IVS4 region comprising the amino acid
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium
CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel nucleic
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX

SQ Sequence 2243 AA;

Query Match 98.8%; Score 11758.5; DB 2; Length 2243;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 1; Indels 23; Gaps 1;

QY 1 MDEEDGAGAEESGQPRSEFMRINDLSGAGRPGGSAEKDPGSADSEAEGLYPALAPVV 60
Db |||||||
QY 1 MDEEDGAGAEESGQPRSEFMRINDLSGAGRPGGSAEKDPGSADSEAEGLYPALAPVV 60
Db |||||||
QY 61 FFYLSQDSRPSRWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIAQSCRCRILQAF 120
Db |||||||
QY 61 FFYLSQDSRPSRWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIAQSCRCRILQAF 120
Db |||||||
QY 121 DDFIFAFFAVEMVMVALGIFGKKCYLGDWTNRLLDFFIAGMLEYSLDLQNVSFSAVR 180
Db |||||||
QY 121 DDFIFAFFAVEMVMVALGIFGKKCYLGDWTNRLLDFFIAGMLEYSLDLQNVSFSAVR 180
Db |||||||
QY 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLCFFVFFIFGIVGVQLWAGLLNR 240
Db |||||||
QY 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLCFFVFFIFGIVGVQLWAGLLNR 240
Db |||||||
QY 241 CFLPENFSLPLSVDLERYYTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300
Db |||||||
QY 241 CFLPENFSLPLSVDLERYYTENEDESPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL 300
Db |||||||
QY 301 DYEAYNSSNTTCVNMNQYTYNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM 360
Db |||||||
QY 301 DYEAYNSSNTTCVNMNQYTYNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM 360
Db |||||||
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQESQLMREQVRFLSNA 420
Db |||||||
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQESQLMREQVRFLSNA 420
Db |||||||
QY 421 STLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAAGVRVGLLSSPAPLGQETQPSS 480
Db |||||||
QY 421 STLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAAGVRVGLLSSPAPLGQETQPSS 480
Db |||||||
QY 481 SCSRSRRRLSVHHLVHHHHHHHHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db |||||||
QY 481 SCSRSRRRLSVHHLVHHHHHHHHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db |||||||
QY 541 ALSGAPPGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
Db |||||||
QY 541 ALSGAPPGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPE 600
Db |||||||
QY 601 TLKEKALVEVAASSGPPPTLSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
Db |||||||
QY 601 TLKEKALVEVAASSGPPPTLSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
Db |||||||
QY 661 ACGPDCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSILGPD 720
Db |||||||
QY 661 ACGPDCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSILGPD 720
Db |||||||
QY 721 EPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780
Db |||||||
QY 721 EPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780
Db |||||||
QY 781 VFTSLFALEMLLKLIVYGPFGYIKNPYINFDGVIIVISVWEIVGQGGGLSVLRTFLMR 840
Db |||||||

Db	781	VFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR	840
Qy	841	VLKLVRFPLPALORQLVLMKTMNDNVATFCMLLMLFIFIFISILGMHLFGCKFASERDGTTL	900
Db	841	VLKLVRFPLPALORQLVLMKTMNDNVATFCMLLMLFIFIFISILGMHLFGCKFASERDGTTL	900
Qy	901	PDRKNFDSLLWAIVTVFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV	960
Db	901	PDRKNFDSLLWAIVTVFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV	960
Qy	961	AILVEGFQAEHISKREDASGQLSCIQLPVDSQGGDANKSPSEPDFSPSLDGDGRKKCL	1020
Db	961	AILVEGFQAE-----GDANKSEGEPDFSPSLDGDGRKKCL	997
Qy	1021	ALVSLGEHPELRKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA	1080
Db	998	ALVSLGEHPELRKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA	1057
Qy	1081	HEMKSPPSARSHPSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140
Db	1058	HEMKSPPSARSHPSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1117
Qy	1141	DEESSEEEERASPAGSDHRRGSLEREAKSSFDPDPTLQVPLGHLRTASGRGSASEHQDCN	1200
Db	1118	DEESSEEEERASPAGSDHRRGSLEREAKSSFDPDPTLQVPLGHLRTASGRGSASEHQDCN	1177
Qy	1201	GKSASGRLARALPDPPPLDGGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP	1260
Db	1178	GKSASGRLARALPDPPPLDGGDDADDEGNLSKGERVRAWIRARLPACCLERDSWSAYIFP	1237
Qy	1261	QOSRFRLLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320
Db	1238	QOSRFRLLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1297
Qy	1321	FLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1380
Db	1298	FLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1357
Qy	1381	RLRLTLRPLRVISRAQGLKVVETLMSLLKPIGNIIVVICCAFFIIFGILGVQLFKGKFFV	1440
Db	1358	RLRLTLRPLRVISRAQGLKVVETLMSLLKPIGNIIVVICCAFFIIFGILGVQLFKGKFFV	1417
Qy	1441	COGEDTRNITNKSDCAEASVYRVRHKYNFNDLGOALMSLFLVASKDGVVDIMYDGLDVG	1500
Db	1418	COGEDTRNITNKSDCAEASVYRVRHKYNFNDLGOALMSLFLVASKDGVVDIMYDGLDVG	1477
Qy	1501	VDQQPMNHNPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREKRL	1560
Db	1478	VDQQPMNHNPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREKRL	1537
Qy	1561	RRLEKKRKAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTVGIVGLNVVTMAMEHYQQPQI	1620
Db	1538	RRLEKKRKAQCKPYYSYDSYRFRLLVHHLCTSHYLDLFTVGIVGLNVVTMAMEHYQQPQI	1597
Qy	1621	LDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDLAIIVLLSIMGITLLEEIEVN	1680
Db	1598	LDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQDLAIIVLLSIMGITLLEEIEVN	1657
Qy	1681	ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRRALDVTVMQALPQVGNLGLLFFLFFIFA	1740
Db	1658	ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRRALDVTVMQALPQVGNLGLLFFLFFIFA	1717
Qy	1741	ALGVELFGDLECDETHPC EGLGRHATERNFGMAFLTFLRVSTGDNWNGIMKDTLRDCDQE	1800
Db	1718	ALGVELFGDLECDETHPC EGLGRHATERNFGMAFLTFLRVSTGDNWNGIMKDTLRDCDQE	1777
Qy	1801	STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMMKHLEESNKEAKEAELEAEELEMKTL	1860
Db	1778	STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMMKHLEESNKEAKEAELEAEELEMKTL	1837
Qy	1861	SPQHPSPGSPFLWPGEVGPDSPPSPKPGALHPAAHARSASHFSLEHPTMQPHTELPGP	1920
Db	1838	SPQHPSPGSPFLWPGEVGPDSPPSPKPGALHPAAHARSASHFSLEHPTMQPHTELPGP	1897
Qy	1921	DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSY	1980
Db	1898	DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSY	1957
Qy	1981	ILQLPKDAPHLLLOPHSAPTWTGTFPKLPPPGRSPLAQRLRRQAAIRTDLSLVQGLGSRED	2040
Db	1958	ILQLPKDAPHLLLOPHSAPTWTGTFPKLPPPGRSPLAQRLRRQAAIRTDLSLVQGLGSRED	2017
Qy	2041	LLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPET	2100
Db	2018	LLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPET	2077
Qy	2101	RSSLELDTLSWISGDLPLPPGGQEEPPSPRDLKKCYSEVAQSCORRPTSWLDEQRRHSIA	2160
Db	2078	RSSLELDTLSWISGDLPLPPGGQEEPPSPRDLKKCYSEVAQSCORRPTSWLDEQRRHSIA	2137
Qy	2161	VSCLDSGSQPHLGTDPNLGGQPLGGPGSRPKKLSPPSITIDPPESQGPRTTPPSPGICL	2220
Db	2138	VSCLDSGSQPHLGTDPNLGGQPLGGPGSRPKKLSPPSITIDPPESQGPRTTPPSPGICL	2197
Qy	2221	RRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP	2266
Db	2198	RRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGLSSDPADLDP	2243
RESULT 3			
ADJ68819			
ID	ADJ68819 standard; protein; 2243 AA.		
XX			
AC	ADJ68819;		
XX			
DT	06-MAY-2004 (first entry)		
XX			
DE	Human heat mitochondrial protein as a therapeutic target SeqID625.		
XX			
KW	mitochondrial; human; screening assay; diabetes mellitus;		
KW	Huntington's disease; osteoarthritis;		
KW	Leber's hereditary optic neuropathy; LHON;		
KW	mitochondrial encephalopathy lactic acidosis and stroke; MELAS;		
KW	myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;		
KW	neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;		
KW	osteopathic; ophthalmological; cytostatic.		
XX	Homo sapiens.		
OS	WO2003087768-A2.		
XX			
PN	23-OCT-2003.		
XX			
PF	04-APR-2003; 2003WO-US010870.		
XX			
PR	12-APR-2002; 2002US-0372843P.		
PR	17-JUN-2002; 2002US-0389987P.		
PR	20-SEP-2002; 2002US-0412418P.		
XX			
PA	(MITO-) MITOKOR.		
PA	(BUCK-) BUCK INST AGE RES.		
XX			
PI	Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;		
PI	Warnock DE;		
XX			
DR	WPI; 2003-845369/78.		
XX			
PT	Identifying a mitochondrial target for drug screening assays and for		
PT	treating diseases associated with altered mitochondrial function,		
PT	comprises detecting a modified polypeptide in a sample and correlating		
PT	with the disease.		
XX			
PS	Claim 1; SEQ ID NO 625; 180pp; English.		
XX			
CC	This invention relates to novel mitochondrial targets that can be used		
CC	for therapeutic intervention in treating a disease associated with		

CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 2243 AA;

Query Match		98.8%;	Score 11758.5;	DB 7;	Length 2243;
Best Local Similarity		98.9%;	Pred. No. 0;		
Matches 2242;		Conservative	0;	Mismatches	1;
				Indels	23;
				Gaps	1;
QY	1	MDEEEDGAGAEESGQPRSFMRNLDSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV	60		
Db	1	MDEEEDGAGAEESGQPRSFMRNLDSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV	60		
QY	61	FFYLSQSRPRSWCLRTVCNPFERISMLVILLNCVTLGMFRPCEDIAQDSQRCRILQAF	120		
Db	61	FFYLSQSRPRSWCLRTVCNPFERISMLVILLNCVTLGMFRPCEDIAQDSQRCRILQAF	120		
QY	121	DDFTAPFAVEMVVKMVALGIFGKKCYLGDWTNRLLDFFIAGMLEYSLDLQNVSFSAVR	180		
Db	121	DDFTAPFAVEMVVKMVALGIFGKKCYLGDWTNRLLDFFIAGMLEYSLDLQNVSFSAVR	180		
QY	181	TVRVLRLPRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFIGIVGVQLWAGLLNR	240		
Db	181	TVRVLRLPRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFIGIVGVQLWAGLLNR	240		
QY	241	CFLPENFSLPLSVDLERYQTENEDESPFICQPRENGMRSCRSVPTLRGDDGGGPPCGL	300		
Db	241	CFLPENFSLPLSVDLERYQTENEDESPFICQPRENGMRSCRSVPTLRGDDGGGPPCGL	300		
QY	301	DYEAYNSSNTTCVWNQYTYNCESAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM	360		
Db	301	DYEAYNSSNTTCVWNQYTYNCESAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM	360		
QY	361	YFVMDAHSFYNFIFILLIIVGSSFFMINCLVVIATQFSETKQRESQRLMREQVRFLSNA	420		
Db	361	YFVMDAHSFYNFIFILLIIVGSSFFMINCLVVIATQFSETKQRESQRLMREQVRFLSNA	420		
QY	421	STLASFSEPGSCYBELLKYLVIYILRKAARLAQVSRAAGVRVGLLSSPAPLGQETQPS	480		
Db	421	STLASFSEPGSCYBELLKYLVIYILRKAARLAQVSRAAGVRVGLLSSPAPLGQETQPS	480		
QY	481	SCSRSHRRLSVHLLVHHHHHHHHYHLNGNGLRAPRASPEIQDRDANGSRRLMLPPSTP	540		
Db	481	SCSRSHRRLSVHLLVHHHHHHHHYHLNGNGLRAPRASPEIQDRDANGSRRLMLPPSTP	540		
QY	541	ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE	600		
Db	541	ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE	600		
QY	601	TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTOSTGACQSSCKISSPCLKADSG	660		
Db	601	TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTOSTGACQSSCKISSPCLKADSG	660		
QY	661	ACGPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS	720		
Db	661	ACGPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS	720		
QY	721	EPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILLVNTLSMGIEYHEQPEELTNALEISNI	780		
Db	721	EPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILLVNTLSMGIEYHEQPEELTNALEISNI	780		
QY	781	VFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISWWEIVGQGGGLSVLRTFLMR	840		

Db	781	VFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISWWEIVGQGGGLSVLRTFLMR	840		
QY	841	VKLVRFLPALQRLVLMKTMNDVATFCMLLMLEFIFISILGMHLFGCKFASERDGT	900		
Db	841	VKLVRFLPALQRLVLMKTMNDVATFCMLLMLEFIFISILGMHLFGCKFASERDGT	900		
QY	901	PDRKNFDSLLWAIIVTFQILTQEDWNKVLYNGMASTSSWAAALFYIALMTFGNYVLFN	960		
Db	901	PDRKNFDSLLWAIIVTFQILTQEDWNKVLYNGMASTSSWAAALFYIALMTFGNYVLFN	960		
QY	961	AILVEGFOAEIISKREDASGQLSCIQLPVDSQGGDANKSESEPFFSPSLDGDGRKKCL	1020		
Db	961	AILVEGFOAEIISKREDASGQLSCIQLPVDSQGGDANKSESEPFFSPSLDGDGRKKCL	997		
QY	1021	ALVSLGHEPRLKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA	1080		
Db	998	ALVSLGHEPRLKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA	1057		
QY	1081	HEMKSPPSARSSPHSPWSAASWTSSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140		
Db	1058	HEMKSPPSARSSPHSPWSAASWTSSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1117		
QY	1141	DEESSEERASAPAGSDHRHRSGLEREAASSFDLPDQLVQPLGHRHTASGRSASEHQDCN	1200		
Db	1118	DEESSEERASAPAGSDHRHRSGLEREAASSFDLPDQLVQPLGHRHTASGRSASEHQDCN	1177		
QY	1201	GKSASGRLARALRPDPPLDGDADDDEGNLSKGERVRAWIRARLPACVLERDSWSAYIFP	1260		
Db	1178	GKSASGRLARALRPDPPLDGDADDDEGNLSKGERVRAWIRARLPACVLERDSWSAYIFP	1237		
QY	1261	POSRRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1320		
Db	1238	POSRRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV	1297		
QY	1321	FLAEMTVKVVVALGWCFCGEQAYLRSSNNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1380		
Db	1298	FLAEMTVKVVVALGWCFCGEQAYLRSSNNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVL	1357		
QY	1381	RLRLTLRLPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIFIGILGVQLFKGKFFV	1440		
Db	1358	RLRLTLRLPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIFIGILGVQLFKGKFFV	1417		
QY	1441	COGEDTRNITNKSDCAEASVYRVRHKYNFNDLQALMSLFVLASKDGVWDIMYDGLDVG	1500		
Db	1418	COGEDTRNITNKSDCAEASVYRVRHKYNFNDLQALMSLFVLASKDGVWDIMYDGLDVG	1477		
QY	1501	VDQOPIMNHNPMWLLYFISFLLIVAFVFLNMVGVVVENFHKRQHQRREERREKRL	1560		
Db	1478	VDQOPIMNHNPMWLLYFISFLLIVAFVFLNMVGVVVENFHKRQHQRREERREKRL	1537		
QY	1561	RRLEKKRKAQCKPYYSYDSRFRLLVHHLCTSHYLDLFTITVIGLVNVTMAMEHYQQPQI	1620		
Db	1538	RRLEKKRKAQCKPYYSYDSRFRLLVHHLCTSHYLDLFTITVIGLVNVTMAMEHYQQPQI	1597		
QY	1621	LDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLDAIVLLSIMGITLEEIEVN	1680		
Db	1598	LDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLDAIVLLSIMGITLEEIEVN	1657		
QY	1681	ASLPINPTIIRIMRVLRIRVLLKLMVGMRALDVTVMQALPQVGNLGLLFFIFA	1740		
Db	1658	ASLPINPTIIRIMRVLRIRVLLKLMVGMRALDVTVMQALPQVGNLGLLFFIFA	1717		
QY	1741	ALGVLEFGDLECEDETHPCCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDCQE	1800		
Db	1718	ALGVLEFGDLECEDETHPCCEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDCQE	1777		
QY	1801	STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMKHEESNKEAKEAEAELELEMKTL	1860		
Db	1778	STCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMKHEESNKEAKEAEAELELEMKTL	1837		
QY	1861	SPOPHSPLGSPFLWPGVEGPDSPDPSKPGALHPAAHARSASHFSLEHPTMQPHPTLPGP	1920		

Db 1838 SPOHSPGLSPFLWPGEVGPDPSPKPGALHPAAHARSASHFSLEHPTMQHPTELPGP 1897

QY 1921 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGLSVHSPADTSY 1980

Db 1898 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGLSVHSPADTSY 1957

QY 1981 ILQLPKDAPHLLOPHSAPTWTGTPKLPPPPGRSPLAQRPLRQAARTDSDLVQGLSRED 2040

Db 1958 ILQLPKDAPHLLOPHSAPTWTGTPKLPPPPGRSPLAQRPLRQAARTDSDLVQGLSRED 2017

QY 2041 LLAEVSGPSPPLARAYSFWGQSSSTAQQHRSRSHSKISKHMTTPAPCPGPEPNWGKGPET 2100

Db 2018 LLAEVSGPSPPLARAYSFWGQSSSTAQQHRSRSHSKISKHMTTPAPCPGPEPNWGKGPET 2077

QY 2101 RSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSEVAQSCORRPTSWLDEQRRHSIA 2160

Db 2078 RSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSEVAQSCORRPTSWLDEQRRHSIA 2137

QY 2161 VSCLDSGSQPHLGTDPNSLGGQPLGGPSRPPKKLSPPSITIDPPESQGPRTPPSPGICL 2220

Db 2138 VSCLDSGSQPHLGTDPNSLGGQPLGGPSRPPKKLSPPSITIDPPESQGPRTPPSPGICL 2197

QY 2221 RRRAPSSDSKDPLASGPPDSMAASPSPKDVLSLGLSSDPADLDP 2266

Db 2198 RRRAPSSDSKDPLASGPPDSMAASPSPKDVLSLGLSSDPADLDP 2243

RESULT 4

AAAY14586

ID AAY14586 standard; protein; 2250 AA.

XX

AC AAY14586;

XX

DT 07-DEC-1999 (first entry)

XX

DE Human T-type voltage-gated Ca channel alpha-1-G (hCavT1a).

XX

KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;

KV activation; current; rat; screen; drug; cardiomyopathy; epilepsy.

XX

OS Homo sapiens.

XX

PN WO9929847-A1.

XX

PD 17-JUN-1999.

XX

PF 30-OCT-1998; 98WO-US023161.

XX

PR 05-DEC-1997; 97US-00985809.

XX

PA (LOYO) UNIV LOYOLA CHICAGO.

XX

PI Perez-Reyes E, Cribbs LL;

XX

DR WPI; 1999-394972/33.

XX

DR N-PSDB; AAX83481.

XX

PT New T-type voltage-gated calcium channels.

XX

PS Disclosure; Page 31-40; 138pp; English.

XX

CC This sequence represents a human T-type voltage-gated calcium (Ca)

CC channel alpha-1-G designated hCavT1a. Voltage gated channels are membrane

CC bound glycosylated proteins formed of several subunits. The large alpha

CC subunits form a pore in the membrane that is selective for a given ionic

CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and

CC each domain contains 6 putative transmembrane helical segments (S1-S6). T

CC -type Ca channels are activated at a lower voltage than L- or N-type

CC channels. Characteristics of T-type channels include short current time,

CC slow activation kinetics near threshold, fast inactivation kinetics and

CC slow tail current. The sequences AAX83481-X83492 represent novel T-type

CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca

CC -channels contains a putative IVS4 region comprising the amino acid

CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium

CC channel proteins can be used to screen for drugs which affect calcium

CC channels. Methods are also disclosed for treating a disease or disorder

CC associated with a deficiency in a native T-type calcium channel nucleic

CC acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX

SQ Sequence 2250 AA;

Query Match 98.6%; Score 11741; DB 2; Length 2250;

Best Local Similarity 98.6%; Pred. No. 0;

Matches 2241; Conservative 1; Mismatches 1; Indels 30; Gaps 2;

QY 1 MDEEEDGAGAEESGQPRSFMRNLDSLGGAGRPGPSAEKDPGSAEGLPYPALAPVV 60

Db 1 MDEEEDGAGAEESGQPRSFMRNLDSLGGAGRPGPSAEKDPGSAEGLPYPALAPVV 60

QY 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF 120

Db 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF 120

QY 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDWTNRLLDFFIVIAAGMLEYSLDLQNVFSFAVR 180

Db 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDWTNRLLDFFIVIAAGMLEYSLDLQNVFSFAVR 180

QY 181 TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

Db 181 TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR 240

QY 241 CFLPENFSLPLSVDLERYYTENEDESPFICSQPRENMRSCRSVPTLRGDDGGGPPCGGL 300

Db 241 CFLPENFSLPLSVDLERYYTENEDESPFICSQPRENMRSCRSVPTLRGDDGGGPPCGGL 300

QY 301 DYEAYNSSNTTCVNNWQYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360

Db 301 DYEAYNSSNTTCVNNWQYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360

QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420

Db 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420

QY 421 STLASFSEPGSCYEELLKYLVIILKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPSS 480

Db 421 STLASFSEPGSCYEELLKYLVIILKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPSS 480

QY 481 SCSRSHRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

Db 481 SCSRSHRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVSGKVYPTVHTSPPE 600

Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPRSPSEASGRTVSGKVYPTVHTSPPE 600

QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTETQSTGACQSSCKISSPCLKADSG 660

Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTETQSTGACQSSCKISSPCLKADSG 660

QY 661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQSLGPD 720

Db 661 ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQSLGPD 720

QY 721 EPSSVLAFWRLLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780

Db 721 EPSSVLAFWRLLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780

QY 781 VFTSLFALEMLLKLJVYGPFGYIKNPYNIFDGVIVISVWEIVGQGGGLSVLRTFRLMR 840

Db 781 VFTSLFALEMLLKLJVYGPFGYIKNPYNIFDGVIVISVWEIVGQGGGLSVLRTFRLMR 840

QY 841 VLKLVRFPLALQRLVLMKTMNDVATFCMLLMLFIFIFSLGMHLFGCKFASERDGDITL 900

Db 841 VLKLVRFPLALQRLVLMKTMNDVATFCMLLMLFIFIFSLGMHLFGCKFASERDGDITL 900

QY 901 PDRKNFDSLLWAIIVTFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLV 960

Db 901 PDRKNFDSLLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLIV 960
QY 961 AILVEGFQAEIISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDGDRKKCL 1020
Db 961 AILVEGFQAEIISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDGDRKKCL 997
QY 1021 ALVSLGEHPPELRSKLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
Db 998 ALVSLGEHPPELRSKLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1057
QY 1081 HEMKSPSARSPPHSPWSAASSWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1140
Db 1058 HEMKSPSARSPPHSPWSAASSWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ 1117
QY 1141 DEEESSEERASPDGDRHRRGSLEREAKSSFDLPTLQVPGHLRTASGRGSAEHQDCN 1200
Db 1118 DEEESSEERASPDGDRHRRGSLEREAKSSFDLPTLQVPGHLRTASGRGSAEHQDCN 1177
QY 1201 GKSASGRLARALRPPDPLDGDADDEGNLSKGERVRAWRARLPACYLERDSWSAYIFP 1260
Db 1178 GKSASGRLARALRPPDPLDGDADDEGNLSKGERVRAWRARLPACYLERDSWSAYIFP 1237
QY 1261 PQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
Db 1238 PQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1297
QY 1321 FLAEMTVKVVVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLRVL 1380
Db 1298 FLAEMTVKVVVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLRVL 1357
QY 1381 RLLRTLRLPLRVISRAOGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGFFV 1440
Db 1358 RLLRTLRLPLRVISRAOGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGFFV 1417
QY 1441 CQGEDTRNITNKSDCAEASRVWRHKYNFNDLGOALMSLFVLASKDGVVIMYDGLDAVG 1500
Db 1418 CQGEDTRNITNKSDCAEASRVWRHKYNFNDLGOALMSLFVLASKDGVVIMYDGLDAVG 1477
QY 1501 VDQQPIMNHNPMMLLYFISFLLIIVAFVFLNMFVGVVVENFHKRQHQBEEHARRREKRL 1560
Db 1478 VDQQPIMNHNPMMLLYFISFLLIIVAFVFLNMFVGVVVENFHKRQHQBEEHARRREKRL 1537
QY 1561 RRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLNVVTMAME 1613
Db 1538 RRLEKKRRSKEKQMAFAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLNVVTMAME 1597
QY 1614 HYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLAIVLLSIMGIT 1673
Db 1598 HYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLAIVLLSIMGIT 1657
QY 1674 LEEIEVNASLPINPTIIRIMRVLRIRARVLKLMKMAVGMRALDITVMQALPQVGNLGLLFM 1733
Db 1658 LEEIEVNASLPINPTIIRIMRVLRIRARVLKLMKMAVGMRALDITVMQALPQVGNLGLLFM 1717
QY 1734 LLEFFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1793
Db 1718 LLEFFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1777
QY 1794 LRCDQESTCYNTVISPIYFVSFVLTAQVFLVNVVIAVLMKHLEESNKEAEAELEAEL 1853
Db 1778 LRCDQESTCYNTVISPIYFVSFVLTAQVFLVNVVIAVLMKHLEESNKEAEAELEAEL 1837
QY 1854 ELEMKTLSPOHSPPLGSPFLWPVGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPH 1913
Db 1838 ELEMKTLSPOHSPPLGSPFLWPVGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPH 1897
QY 1914 PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGLGHRGWGLPKAQSGSVLSVHS 1973
Db 1898 PTELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGLGHRGWGLPKAQSGSVLSVHS 1957
QY 1974 QPADTSYILQPKDAPHLLOPHSAPTWTGTPKLPGRSPLAQRPLRQAIRTDSDLVQ 2033

Db 1958 QPADTSYILQPKDAPHLLOPHSAPTWTGTPKLPGRSPLAQRPLRQAIRTDSDLVQ 2017
QY 2034 GLGSREDLLAEVSGSPPLARAYSFWGQSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNW 2093
Db 2018 GLGSREDLLAEVSGSPPLARAYSFWGQSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNW 2077
QY 2094 GKGPPESTRSSLELDTLSWISGDLPLPGQEEPPSPRDLKCYVSAEQSCORRPTSWLDE 2153
Db 2078 GKGPPESTRSSLELDTLSWISGDLPLPGQEEPPSPRDLKCYVSAEQSCORRPTSWLDE 2137
QY 2154 QRRHSIAVSCLDSCSQPHLGTDPNSNLGGQPLGGPSRPPKKLSPPSITIDPPESQGRTP 2213
Db 2138 QRRHSIAVSCLDSCSQPHLGTDPNSNLGGQPLGGPSRPPKKLSPPSITIDPPESQGRTP 2197
QY 2214 PSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKDVLSSGLSSDPADLDP 2266
Db 2198 PSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKDVLSSGLSSDPADLDP 2250

RESULT 5
AAY14587

ID AAY14587 standard; protein; 2261 AA.
XX AAY14587;
AC AAY14587;
XX 07-DEC-1999 (first entry)
DT Human T-type voltage-gated Cc channel alpha-1-G (hCavT1b).
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
DE activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX Homo sapiens.
OS WO9929847-A1.
XX 17-JUN-1999.
PD 30-OCT-1998; 98WO-US023161.
XX 05-DEC-1997; 97US-00985809.
XX (LOYO) UNIV LOYOLA CHICAGO.
PA Perez-Reyes E, Cribbs LL;
PI WPI; 1999-394972/33.
XX N-PSDB; AAX83482.
XX New T-type voltage-gated calcium channels.
XX Disclosure; Page 40-49; 138pp; English.

This sequence represents a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCavT1b. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

Sequence 2261 AA;

Query Match	98.6%;	Score 11735.5;	DB 2;	Length 22261;
Best Local Similarity	98.1%;	Pred. No. 0;		
Matches 2241;	Conservative	1;	Mismatches	1;
			Indels	41;
			Gaps	2;
QY	1	MDEEDGAGAEESGQPRSFMRNLDSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV	60	
Db	1	MDEEDGAGAEESGQPRSFMRNLDSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV	60	
QY	61	FFYLSQDSRPRSWCLRTVCNPPWFERISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF	120	
Db	61	FFYLSQDSRPRSWCLRTVCNPPWFERISMLVILLNCVTLMFRPCEDIAQDSQRCRILQAF	120	
QY	121	DDFIFAFFAVEMVVKVALGIFGKKCYLGDTWNRLDFFIVIAQMLEYSLDLQNVFSFSAVR	180	
Db	121	DDFIFAFFAVEMVVKVALGIFGKKCYLGDTWNRLDFFIVIAQMLEYSLDLQNVFSFSAVR	180	
QY	181	TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR	240	
Db	181	TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR	240	
QY	241	CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDCGGPPCGL	300	
Db	241	CFLPENFSLPLSVDLERYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDCGGPPCGL	300	
QY	301	DYEAYNSSNTTCVNNQYYTNCAGEHNPFKGAINFNDIGNYAWIAIFQVITILEGWVDIM	360	
Db	301	DYEAYNSSNTTCVNNQYYTNCAGEHNPFKGAINFNDIGNYAWIAIFQVITILEGWVDIM	360	
QY	361	YFVMDAHSFYNFIFYILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420	
Db	361	YFVMDAHSFYNFIFYILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420	
QY	421	STLASFSFSGCYEELLKYLVIILRKAARRLAQVSRAAGVRVGLLSSPAPLGQETQPSS	480	
Db	421	STLASFSFSGCYEELLKYLVIILRKAARRLAQVSRAAGVRVGLLSSPAPLGQETQPSS	480	
QY	481	SCSRSHRRLSVVHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP	540	
Db	481	SCSRSHRRLSVVHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP	540	
QY	541	ALSGAPPGGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRITVSGKVYPTVHTSPPE	600	
Db	541	ALSGAPPGGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRITVSGKVYPTVHTSPPE	600	
QY	601	TLKEKALVEVAASSGPPPLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG	660	
Db	601	TLKEKALVEVAASSGPPPLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG	660	
QY	661	ACGPDSCPYPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQRLGPDA	720	
Db	661	ACGPDSCPYPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQRLGPDA	720	
QY	721	EPSSVLAFWRLLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALEISNI	780	
Db	721	EPSSVLAFWRLLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALEISNI	780	
QY	781	VFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMR	840	
Db	781	VFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMR	840	
QY	841	VLKLVRFPLALQRLVLMKTMNDNVATFCMLLMFLIFPSILGMHLFGCKFASERDGDTL	900	
Db	841	VLKLVRFPLALQRLVLMKTMNDNVATFCMLLMFLIFPSILGMHLFGCKFASERDGDTL	900	
QY	901	PDRKNFDSLILWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLV	960	
Db	901	PDRKNFDSLILWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLV	960	
QY	961	AILVEGFQAEELISKREDASGQLSCIQLPVDVSGQDANKSESEPDPFSPSLDGDGRKKCL	1020	
Db	961	AILVEGFQAEELISKREDASGQLSCIQLPVDVSGQDANKSESEPDPFSPSLDGDGRKKCL	997	
QY	1021	ALVSLGEHPELRKSLPLIITHAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEFGAA	1080	

1021 ALVSLGEHPRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080

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Db 2078 PAPCPGPEPNWKGPPETRSSLLELDTELSWISGDLPLPPGGQEEPPSPRDLKKCYSEVAQS 2137
QY 2143 CORRPTSWLDEQRHSHIAVSCLDSCSQPHLGTDPNSLGGQPLGGPSRPPKKLSPPSITI 2202
Db 2138 CORRPTSWLDEQRHSHIAVSCLDSCSQPHLGTDPNSLGGQPLGGPSRPPKKLSPPSITI 2197
QY 2203 DPESQGPRTPPSPGICLRRRAPSSDSKDFLASGPPDSMAASPSPKKDVLSLSGLSSDPA 2262
Db 2198 DPESQGPRTPPSPGICLRRRAPSSDSKDFLASGPPDSMAASPSPKKDVLSLSGLSSDPA 2257
QY 2263 DLDP 2266
Db 2258 DLDP 2261

RESULT 6
AAY14588
ID AAY14588 standard; protein; 2268 AA.
XX AC AAY14588;
XX

DT 07-DEC-1999 (first entry)
XX
DE Human T-type voltage-gated Ca channel alpha-1-G (hCavT1c).
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX

OS Homo sapiens.
XX
XX WO9929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX

PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
DR N-PSDB; AAX83483.
XX

PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 49-58; 138pp; English.
XX

CC This sequence represents a human T-type voltage-gated calcium (Ca)
CC channel alpha-1-G designated hCavT1c. Voltage gated channels are membrane
CC bound glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC -channels contains a putative IVS4 region comprising the amino acid
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium
CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel nucleic
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX

SQ Sequence 2268 AA;

Query Match 98.5%; Score 11727; DB 2; Length 2268;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 2240; Conservative 1; Mismatches 2; Indels 48; Gaps 2;

QY 1 MDEEDGAGAEESQPRSRFMRNLNLSGAGRPGPGSAEKOPGSADSAEGLPYPALAPVV 60
Db 1 MDEEDGAGAEESQPRSRFMRNLNLSGAGRPGPGSAEKOPGSADSAEGLPYPALAPVV 60
QY 61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIAQDSQRCRILQAF 120
Db 61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLGMFRPCEDIAQDSQRCRILQAF 120
QY 121 DDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAAGMLEYSLDLQNVSPSAVR 180
Db 121 DDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAAGMLEYSLDLQNVSPSAVR 180
QY 181 TVRVLRLRAINRVPSMRILVTLLDLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Db 181 TVRVLRLRAINRVPSMRILVTLLDLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
QY 241 CFLPENFSLPLSVDLERYQYOTENEDESPFICSQPRENMRSCRSVPTLRGDDGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYQYOTENEDESPFICSQPRENMRSCRSVPTLRGDDGGGPPCGL 300
QY 301 DYEAYNSSNTTCVWNQYYTNCAGEHNPFKGAINFONIGYAWIAIFQVITLBEWVDIM 360
Db 301 DYEAYNSSNTTCVWNQYYTNCAGEHNPFKGAINFONIGYAWIAIFQVITLBEWVDIM 360
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQESQLMREQVRFLSNA 420
Db 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQESQLMREQVRFLSNA 420
QY 421 STLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAGVRVGLLSPPAPLGGQETQPS 480
Db 421 STLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAGVRVGLLSPPAPLGGQETQPS 480
QY 481 SCSRSHRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db 481 SCSRSHRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRVCOAPPRSPSEASGRTVSGKVYPTVHTSPPE 600
Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRVCOAPPRSPSEASGRTVSGKVYPTVHTSPPE 600
QY 601 TLKEKALVEVAASSGPTLTSLNIPPGPYSSMHKLETSQSTGACQSSCKISSPCLKADSG 660
Db 601 TLKEKALVEVAASSGPTLTSLNIPPGPYSSMHKLETSQSTGACQSSCKISSPCLKADSG 660
QY 661 ACPDSCPCYCARAGAGEVELADREMPDSSEAVYEFTQDAHQSDLRDPHSRRQSLGPD 720
Db 661 ACPDSCPCYCARAGAGEVELADREMPDSSEAVYEFTQDAHQSDLRDPHSRRQSLGPD 720
QY 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
Db 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
QY 781 VFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVIVISVWEIVGQGGGLSVLRTFLMR 840
Db 781 VFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVIVISVWEIVGQGGGLSVLRTFLMR 840
QY 841 VLKLVRFPLALQRLVLMKTMNDVATFCMLLLMFIFISILGMHLFGCKFASERDGTDL 900
Db 841 VLKLVRFPLALQRLVLMKTMNDVATFCMLLLMFIFISILGMHLFGCKFASERDGTDL 900
QY 901 PDRKNFDSLWAIIVTFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLIV 960
Db 901 PDRKNFDSLWAIIVTFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLIV 960
QY 961 AILVEGFOAEIISKREDASGQLSCIQLPVDSSQGDANKSESEPDFFSPSLDGDGRKKCL 1020
Db 961 AILVEGFOAEIISKREDASGQLSCIQLPVDSSQGDANKSESEPDFFSPSLDGDGRKKCL 997
QY 1021 ALVSLGEHPRLKSLLPPLIHTAATPMSLTPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1080
Db 998 ALVSLGEHPRLKSLLPPLIHTAATPMSLTPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1057
QY 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGLRAPSLKRRSPSGERRSLLSGEGESQ 1140

Db	2138	YSVEAQSCQRRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDPNSLGGQPLGGSPRPKKLL	2197
QY	2196	SPPSITIDPPESQGPRTTSPGICLRRRAPSSDSKDPPLASGPPDSMAASPSPKDVL	2255
Db	2198	SPPSITIDPPESQGPRTTSPGICLRRRAPSSDSKDPPLASGPPDSMAASPSPKDVL	2257
QY	2256	GLSSDPADLDP	2266
Db	2258	GLSSDPADLDP	2268
RESULT 7			
ID	AAB66481	standard; protein; 2266 AA.	
XX	AAB66481;		
AC	AAB66481;		
XX	09-APR-2001	(first entry)	
DT			
XX		Human alpha-IG T-type calcium channel protein.	
DE			
XX		Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;	
KW		T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;	
KW		hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel.	
XX			
OS		Homo sapiens.	
XX		WO200102561-A2.	
PN		11-JAN-2001.	
XX			
PD			
XX		04-JUL-2000; 2000WO-CA0000794.	
PF			
XX		02-JUL-1999; 99US-00346794.	
PR		(NEUR-) NEUROMED TECHNOLOGIES INC.	
XX			
PA		Snutch TP, Baillie DL;	
XX			
PI			
XX			
DR		WPI; 2001-123111/13.	
DR		N-PSDB; AAF31684.	
XX		Novel T-type calcium channel alpha-1 subunit gene useful for treating	
PT		cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and	
PT		epilepsy.	
XX			
PS		Example 3; Fig 6; 103pp; English.	
XX			
CC		The present sequence is given in a specification providing sequences and	
CC		partial sequences for three types of mammalian (human and rat) T-type	
CC		calcium channel subunits. An expression cassette has been generated which	
CC		comprises a nucleotide sequence encoding a T-type calcium channel alpha_1	
CC		subunit operably linked to control sequences to effect its expression.	
CC		The novel calcium channel nucleic acids and proteins are useful for	
CC		treating conditions characterised by undesirable levels of T-type calcium	
CC		channel activity such as cardiac hypertrophy, cardiac arrhythmia,	
CC		hypertension, sleep disorder and epilepsy	
XX		Sequence 2266 AA;	
SQ			
Query Match 97.9%; Score 11653; DB 4; Length 2266;			
Best Local Similarity 98.8%; Pred. No. 0;			
Matches 2239; Conservative 7; Mismatches 20; Indels 0; Gaps 0;			
QY	1	MDEEDGAGAEESQPRSFMRNLDSGAGRPGPSAEKDPGSADSEAGLPYPALAPVV	60
Db	1	MDEEDGAGAEESQPRSFMRNLDSGAGRPGPSAEKDPGSADSEAGLPYPALAPVV	60
QY	61	FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTGLMFRPCEDIACDSQRCRILQAF	120
Db	61	FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTGLMFRPCEDIACDSQRCRILQAF	120
QY	121	DDFIFAFFAVEMVVKMVALGIFGKKCYLGTWNRLDFFIVIAGMLEYSLDLQNVFSAVR	180

Db 121 DDFIAFAVEMVKNVALGIFGKCYLGDNNRLDFFIVIAAGMLEYSLDLQNVSPSAVR 180
QY 181 TVRVLRLPLRAINRVPSMRILVTLLLDTLPMGNVLLLCFFVFFIFIGIVGVQWAGLLNR 240
Db 181 TVRVLRLPLRAINRVPSMRILVTLLLDTLPMGNVLLLCFFVFFIFIGIVGVQWAGLLNR 240
QY 241 CFLPENFSLPLSDLERYYYQTENEDESPFICSQPRENGMRCRSVPTLRGDGGGPPCGL 300
Db 241 CFLPENFSLPLSDLERYYYQTENEDESPFICSQPRENGMRCRSVPTLRGDGGGPPCGL 300
QY 301 DYEAYNSSNTTCVNNQYYTNC SAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360
Db 301 DYEAYNSSNTTCVNNQYYTNC SAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
Db 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
QY 421 STLASFSEPGSCYEBELLKYLVIILKAARRLAQVSRAGVRVGLLSSPAPLGGOETQPSS 480
Db 421 STLASFSEPGSCYEBELLKYLVIILKAARRLAQVSRAGVRVGLLSSPAPLGGOETQPSS 480
QY 481 SCSRSRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRMLMPPSTP 540
Db 481 SCSRSRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRMLMPPSTP 540
QY 541 ALSGAPPGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600
Db 541 ALSGAPPGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
QY 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQRS LGPDA 720
Db 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQRS LGPDA 720
QY 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQBELTNALEISNI 780
Db 721 EPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQBELTNALEISNI 780
QY 781 VFTSLFALEMLLKLVLVGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMR 840
Db 781 VFTSLFALEMLLKLVLVGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMR 840
QY 841 VLKLVRFALPALQRLVVLMTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900
Db 841 VLKLVRFALPALQRLVVLMTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGDTL 900
QY 901 PDRKNFDSLWLWAIWTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLIV 960
Db 901 PDRKNFDSLWLWAIWTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLIV 960
QY 961 AILVEGFOAEEISKREDASQGLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKCL 1020
Db 961 AILVEGFOAEEISKREDASQGLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKCL 1020
QY 1021 ALVSLGEHPELRKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
Db 1021 ALVSLGEHPELRKSLPLPIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
QY 1081 HEMKSPPSARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLSGEGQESQ 1140
Db 1081 HEMKSPPSARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLSGEGQESQ 1140
QY 1141 DEEESSEERASPGDHRHRGSLERBAKSSFDLPTTLQVPLHRTASGRGSASEHQDCN 1200
Db 1141 DEEESSEERASPGDHRHRGSLERBAKSSFDLPTTLQVPLHRTASGRGSASEHQDCN 1200
QY 1201 GKSASGRLARALRPDDPLDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260

Db 1201 GKSASGRLARALRPDDPLDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260
QY 1261 PQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
Db 1261 PQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
QY 1321 FLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSIVIDILVSMVSDSGTKILGMLRVL 1380
Db 1321 FLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSIVIDILVSMVSDSGTKILGMLRVL 1380
QY 1381 RLLRTLRLPLRVISRAQGLKLVVETLMSSLKPIGNIIVVICCAFFIIFGILGVQLFKGKFFV 1440
Db 1381 RLLRTLRLPLRVISRAQGLKLVVETLMSSLKPIGNIIVVICCAFFIIFGILGVQLFKGKFFV 1440
QY 1441 COGEDTRNITNKSDCAEASRWRHKNYFNDNLGOALMSLFLVASKDGVIMYDGLDAVG 1500
Db 1441 COGEDTRNITNKSDCAEASRWRHKNYFNDNLGOALMSLFLVASKDGVIMYDGLDAVG 1500
QY 1501 VDQOQIMNHNPMWMLLYFISFLLIVAFVFLNMFVGVVVVENFHKCRHQHEEEAARREKRL 1560
Db 1501 VDQOQIMNHNPMWMLLYFISFLLIVAFVFLNMFVGVVVVENFHKCRHQHEEEAARREKRL 1560
QY 1561 RRLEKKRKAQCKPYSDYSRFRLLVHHLCTSHYLDLFIITGVIGLVNVTMAMBYQQPQI 1620
Db 1561 RRLEKKRKAQCKPYSDYSRFRLLVHHLCTSHYLDLFIITGVIGLVNVTMAMBYQQPQI 1620
QY 1621 LDEALKICNYIFTVIFVLESVFKLAVAFGRFRFFQDRWNQDLAIIVLLSIMGITLEEIEVN 1680
Db 1621 LDEALKICNYIFTVIFVLESVFKLAVAFGRFRFFQDRWNQDLAIIVLLSIMGITLEEIEVN 1680
QY 1681 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRAALLDTVMQALPOVGNLGLLFMLLFFIFA 1740
Db 1681 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRAALLDTVMQALPOVGNLGLLFMLLFFIFA 1740
QY 1741 ALGVLEFGDLECEDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOTLRDCDQE 1800
Db 1741 ALGVLEFGDLECEDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKOTLRDCDQE 1800
QY 1801 STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAEMTKL 1860
Db 1801 STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAEMTKL 1860
QY 1861 SPQPHSPLGSPFLWPGEVGPDSPPSPKPGALHPAAHARSASHFSLEHPTMQPHTELPGP 1920
Db 1861 SPQPHSPLGSPFLWPGEVGPDSPPSPKPGALHPAAHARSASHFSLEHPTMQPHTELPGP 1920
QY 1921 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTYS 1980
Db 1921 DLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTYS 1980
QY 1981 ILQLPKDAPHLLOPHSAPTWTGTIPKLPPGRSPLAQRPLRQAAIRTDSDLDVQGLGSRED 2040
Db 1981 ILQLPKDAPHLLOPHSAPTWTGTIPKLPPGRSPLAQRPLRQAAIRTDSDLDVQGLGSRED 2040
QY 2041 LLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKI SKHMTTPAPCPGPEPNWKGPPET 2100
Db 2041 LLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKI SKHMTTPAPCPGPEPNWKGPPET 2100
QY 2101 RSSLELDTLSWISGDLPLPPGQEEPPSPRDLKKCYSVBAQSCQRRPTSWLDEQRHSIA 2160
Db 2101 RSSLELDTLSWISGDLPLPPGQEEPPSPRDLKKCYSVBAQSCQRRPTSWLDEQRHSIA 2160
QY 2161 VSCLDGSGQPHLGTDPNSNLGGPLGGPSRPPKKSPPSITIDPPESQGPRTPPSPGICL 2220
Db 2161 VSCLDGSGQPHLGTDPNSNLGGPLGGPSRPPKKSPPSITIDPPESQGPRTPPSPGICL 2220
QY 2221 RRRAPSSDSKDPLASGPPDSSMAASPPKKDVLSSLGSSDPAADLDP 2266
Db 2221 RRRAPSSDSKDPLASGPPDSSMAASPPKKDVLSSLGSSDPAADLDP 2266

QY 900 LPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLENNL 959
Db 953 LPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLENNL 1012
QY 960 VAILVEGFQAEIISKREDASQGLSCIQLPVDSQGGDANKSESEPDEFPSLDGDKRKKC 1019
Db 1013 VAILVEGFQAEIISKREDASQGLSCIQLPVNSQGGDATKSESEPDEFPSVVDGDKRKR 1072
QY 1020 LALVSLGEHPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA 1079
Db 1073 LALVALGEHAELRKSLLPLLIHTAATPMSLPKSSSTGVGEALGSGRRTSSSGSAEPGA 1132
QY 1080 A-HEMKSPPSARSSPHSPWSAASSWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1138
Db 1133 AHHEMKSPPSARSSPHSPWSAASSWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1192
QY 1139 SQDEEESSEERASPDGSDHRHGRGSLEREAKSSFDLPDTLQVPGHLRTASGRGSAEHQD 1198
Db 1193 SQDEEESSEEDRASPDGSDHRHGRGSLEREAKSSFDLPDTLQVPGHLRTASGRSSAHEQD 1252
QY 1199 CNGKSASGRALARALRPDDPPLDGGDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258
Db 1253 CNGKSASGRALARLTDDPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI 1312
QY 1259 FPPQSRFRLLCHRIITHKMFHVVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
Db 1313 FPPQSRFRLLCHRIITHKMFHVVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1372
QY 1319 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSIVIDILVSMVSDSGTKILGMLR 1432
Db 1373 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSIVIDILVSMVSDSGTKILGMLR 1432
QY 1379 VLRLRLTLRPLRVISRAOGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGF 1438
Db 1433 VLRLRLTLRPLRVISRAOGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGF 1492
QY 1439 FVCOGEDTRNITNKSDCAEASVRWVRHKYNFDNLGQALMSLFVLASKDGVWDIMYDGLDA 1498
Db 1493 FVCOGEDTRNITNKSDCAEASVRWVRHKYNFDNLGQALMSLFVLASKDGVWDIMYDGLDA 1552
QY 1499 VGVDOQPIMNHNPMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHQBEEARRREK 1558
Db 1553 VGVDOQPIMNHNPMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHQBEEARRREK 1612
QY 1559 RLRRLEKKRR-----KAQCKPYSDYSRFRLLVHLCCTSHYLDLFI 1600
Db 1613 RLRRLEKKRRNMLDDVIAAGSSASAASEAQCKPYSDYSRFRLLVHLCCTSHYLDLFI 1672
QY 1601 GVIGLNVVTMAMEHYQQQIILDEALKICNYIIFTVFVLESVKLVAFGFRFRFFQDRWNQL 1660
Db 1673 GVIGLNVVTMAMEHYQQQIILDEALKICNYIIFTVFVLESVKLVAFGFRFRFFQDRWNQL 1732
QY 1661 DLAIIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDVTMQ 1720
Db 1733 DLAIIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDVTMQ 1792
QY 1721 ALPOVGNLGLLFFLFFIFAALGVELFGDLECDETHPCEGLRHATFRNFGMAFLTFRV 1780
Db 1793 ALPOVGNLGLLFFLFFIFAALGVELFGDLECDETHPCEGLRHATFRNFGMAFLTFRV 1852
QY 1781 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEEN 1840
Db 1853 STGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEEN 1912
QY 1841 KEAKEEALEAELEEMKTLSPQPHSPPLCPFLWPVGVEGPDSPDKPGALHPAAHARSA 1900
Db 1913 KEAKEEALEAELEEMKTLSPQPHSPPLCPFLWPVGVEGPDSPDKPGAPHTTAHIGAA 1972
QY 1901 SHFSLEHPTMQHPTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957
Db 1973 SGFSLEHPTMVPHEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAERSLGHG 2032

QY 1958 WGLPKAQSGSVLSVHSQPADTSYIILQLPKDAPHLLQPHSAPTWTGTIPKLPBPPGRSPLAQ 2017
Db 2033 WGLPKAQSGSVLSVHSQPADTSYIILQLPKDAPHLLQPHSAPTWTGTIPKLPBPPGRSPLAQ 2092
QY 2018 PLRRQAAIRTDSDLVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKIS 2077
Db 2093 PLRRQAAIRTDSDLVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKIS 2152
QY 2078 KHMTTPAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLPLPGQBEPPSPRDLKKCYS 2137
Db 2153 KHIRLPAPCPGLEPSWAKDPPETRSLSLELDTLSWISGDLPLPGQBEPPSPRDLKKCYS 2211
QY 2138 VEAQSCQRRPTSWLDEQRRHSIAVSCLDSCSQPHLGTDPNSNLGGQPLGGPSRPPKKLSP 2197
Db 2212 VETQSCRRRPGSWLDEQRRHSIAVSCLDSCSQPHLGTDPNSNLGGQPLGGPSRPPKKLSP 2271
QY 2198 PSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDMSMAASPPKKDVLSLSG 2257
Db 2272 PSISIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDMSMAASPPKKDVLSLSG 2331
QY 2258 SSDPADLDP 2266
Db 2332 SSDPTDMDP 2340

RESULT 9

AA14593

ID AA14593 standard; protein; 2247 AA.

XX AA14593;

AC AA14593;

XX 07-DEC-1999 (first entry)

XX Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1d).

DE Human; T-type voltage-gated calcium channel; membrane; pore; ion;

XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy.

OS Rattus sp.

XX WO9929847-A1.

XX 17-JUN-1999.

PF 30-OCT-1998; 98WO-US023161.

PR 05-DEC-1997; 97US-00985809.

XX (LOYO) UNIV LOYOLA CHICAGO.

PI Perez-Reyes E, Cribbs LL;

XX WPI; 1999-394972/33.

DR N-PSDB; AAX83488.

PT New T-type voltage-gated calcium channels.

XX Disclosure; Page 94-103; 138pp; English.

CC This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC alpha-1-G designated rCavT1d. Voltage gated channels are membrane bound
CC glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than I- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC -channels contains a putative IVS4 region comprising the amino acid
CC sequence AA14598. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium

CC	channels. Methods are also disclosed for treating a disease or disorder									
CC	associated with a deficiency in a native T-type calcium channel nucleic									
CC	acid, e.g. to treat cardiomyopathy, epilepsy, etc									
XX										
SQ	Sequence 2247 AA;									
	Query Match	92.1%;	Score	10962.5;	DB	2;	Length	2247;		
	Best Local Similarity	92.8%;	Pred. No.	0;						
	Matches	2108;	Conservative	33;	Mismatches	101;	Indels	29;	Gaps	5;
QY	1	MDEEDGAGAEESQPRSFMRINDLSGAGRPGPSAEKDPGSADSEAEGLYPALAPVV	60							
DB	1	MDEEDGAGAEESQPRSFQTNLDSGAGRGQPGSTKDPGSADSEAEGLYPALAPVV	60							
QY	61	FFYLSQDSRPSWCLRTVCNPFERISMLVILLNCVTLMGERPCEDIACDSQRCRILQAF	120							
DB	61	FFYLSQDSRPSWCLRTVCNPFERVSMVLVILLNCVTLMGERPCEDIACDSQRCRILQAF	120							
QY	121	DDFIFAFAFVEMVMVVALGIFGKKCYLGDWNRDLDFVIAGMLEYSLDLQNVSFSAVR	180							
DB	121	DDFIFAFAFVEMVMVVALGIFGKKCYLGDWNRDLDFVIAGMLEYSLDLQNVSFSAVR	180							
QY	181	TVRVLRPLRAINRVPSMRILVTLTLLDPLMGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240							
DB	181	TVRVLRPLRAINRVPSMRILVTLTLLDPLMGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240							
QY	241	CFLPENFSLPLSDLEYYQTENEDESPFICSPRENGMRSCRSVPTLRDGGGGPPCGL	300							
DB	241	CFLPENFSLPLSDLEYYQTENEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCSL	300							
QY	301	DYEAYNSSNTTCVNNQYVYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM	360							
DB	301	DYETYNSSNTTCVNNQYVYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM	360							
QY	361	YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420							
DB	361	YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420							
QY	421	STLASFSEPGSCYEELLYVILRKAARRLAQVSRAGVRVGLLSSPAPLGQETQPSS	480							
DB	421	STLASFSEPGSCYEELLYVILRKAARRLAQVSRAGVRVGLLSSPVARSGQEPQPSG	480							
QY	481	SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP	540							
DB	481	SCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTP	540							
QY	541	ALSGAPPGABSVHSFYHADCHLEPVRCQAPPRSPSEASGRVTGSGKVYPTVHTSPPE	600							
DB	541	TPSGGPPRGABSVHSFYHADCHLEPVRCQAPPRCPSEASGRVTGSGKVYPTVHTSPPE	600							
QY	601	TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG	660							
DB	601	ILKDKALVEVAPSPGPTLTSTFNIPGPFSSMHKLLETQSTGACHSSCKISSPCKADSG	660							
QY	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRS LGPD	719							
DB	661	ACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS LGPD	720							
QY	720	AEPSSVLAFWRLICDTRFKIVDSKYFGRGIMTALLVNTLSMGIEYHEQPEELTNALEISN	779							
DB	721	AEPSSVLAFWRLICDTRFKIVDSKYFGRGIMTALLVNTLSMGIEYHEQPEELTNALEISN	780							
QY	780	IVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFRM	839							
DB	781	IVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFRM	840							
QY	840	RVLKLVRFPLPALQRLVVLMTMDNVATFCMLMLFIFIPFISILGMHLFGCKFASERDGT	899							
DB	841	RVLKLVRFPLPALQRLVVLMTMDNVATFCMLMLFIFIPFISILGMHLFGCKFASERDGT	900							
QY	900	LPDRKNFDSLLWAIIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL	959							
DB	901	LPDRKNFDSLLWAIIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL	960							

Qy	960	VAILVEGFOAEISKREDASGQLSCIQLPVDSQGDANKSESEPDFFSPSLDGDGRKKC	1019
Db	961	VAILVEGFOAE-----GDATAKSESEPDFFSPSVDDGDGRKKR	997
Qy	1020	LALVSLGHEPRLKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA	1079
Db	998	LALVALGEHAE LRKSLLPPLIIHTAATPM SHPKSSSTGVGEALGSGRRTSSSGSAEPGA	1057
Qy	1080	A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEQE	1138
Db	1058	AHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEQE	1117
Qy	1139	SQDEEESSEERASPA GSDHRRHRSLE REAKSSFDLPDTLQVPCGLHRTASGRGSASEHQD	1198
Db	1118	SQDEEESSEEDRASPA GSDHRRHRSLE REAKSSFDLPDTLQVPCGLHRTASGRSSASEHQD	1177
Qy	1199	CNGKSASGRLARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYI	1258
Db	1178	CNGKSASGRLARLTFTDDPQLDGD DDDNDDEGNLSKGERIQAWVRSRLPACCRERDSWSAYI	1237
Qy	1259	FPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1318
Db	1238	FPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1297
Qy	1319	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVL DGLLVLSVIDILVMSVSDSGTKILGMLR	1378
Db	1298	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVL DGLLVLSVIDILVMSVSDSGTKILGMLR	1357
Qy	1379	VLRLRLTLRPLRVISRAQGLKV VETLMSLSLKPIGNIVVICAFFIIFGILGVQLFKGF	1438
Db	1358	VLRLRLTLRPLRVISRAQGLKV VETLMSLSLKPIGNIVVICAFFIIFGILGVQLFKGF	1417
Qy	1439	FVCGEDTRNITNKSDCAEAS YRVRHKYNFDFNLGQALMSLFVLASKDGV DMYDGLDA	1498
Db	1418	FVCGEDTRNITNKSDCAEAS YRVRHKYNFDFNLGQALMSLFVLASKDGV DMYDGLDA	1477
Qy	1499	VGVDQOQIMNHNPM LLYFTSFLLI VAFVLMFVGVVVENFHKCRHQHEEERREK	1558
Db	1478	VGVDQOQIMNHNPM LLYFTSFLLI VAFVLMFVGVVVENFHKCRHQHEEERREK	1537
Qy	1559	RLRLEKKRRKAQCKPYYS DYSRFRLLVHHLCTSHYLDLFI TGVIGLVNVTMAMEHYQOP	1618
Db	1538	RLRLEKKRRKAQCKPYYS DYSRFRLLVHHLCTSHYLDLFI TGVIGLVNVTMAMEHYQOP	1597
Qy	1619	QILDEALKICNYIFTVIFVLES VFVKLVAFGRFRFFQDRWNQLDLAIVLLSIMGITLEEIE	1678
Db	1598	QILDEALKICNYIFTVIFVLES VFVKLVAFGRFRFFQDRWNQLDLAIVLLSIMGITLEEIE	1657
Qy	1679	VNASLPINPTIIRIMRVLR IARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFLM LFFI	1738
Db	1658	VNLSLPINPTIIRIMRVLR IARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFLM LFFI	1717
Qy	1739	FAALGVELFGDLECDETHPC EGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKOTLRDCD	1798
Db	1718	FAALGVELFGDLECDETHPC EGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKOTLRDCD	1777
Qy	1799	QESTCYNTVISPIYFVSFV LTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAEMK	1858
Db	1778	QESTCYNTVISPIYFVSFV LTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAEMK	1837
Qy	1859	TLSPQSPHSPGLSPFLWP GVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTLP	1918
Db	1838	TLSPQSPHSPGLSPFLWP GVEGVNSTDSPKPGAPHTTAHIGAASGFSL EHTMTVPHPPEVP	1897
Qy	1919	--GPDLLTVRKSGVSRTHSLPND SYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQP	1975
Db	1898	VPLGPDLLTVRKSGVSRTHSLPND SYMCRNGSTAERSLGHARGWGLPKAQSGSILSVHSQP	1957
Qy	1976	ADTSYIILQPKDAPHL LQPHSAPTWGTIPKLPPPGSRPLAQRPLRQAARTDSL DVQGL	2035
Db	1958	ADTSYIILQPKDVHYLLQPHGAPTWGAIPKLPPPGSRPLAQRPLRQAARTDSL DVQGL	2017

QY	2149	SWLDEQRHRSIAVSCLDGSGQPHLGTDPNSLGGQPLGGPSRPPKKLSPPSITIDPPESQ	2208
Db	2137	FWLDEQRHRSIAVSCLDGSGQPRLCPSPPSSLLGGQPLGGPSRPPKKLSPPSISIDPPESQ	2196
QY	2209	GPRTPPSPGICLRRRAPSSDSKDPLASGPPDMSAASPSPKDVLSGLSSDPADLDP	2266
Db	2197	GSRPPCSPGVCLRRRAPASDSKDPVSSPLDSTAASPSPKDTLSLGLSSDPTDMDP	2254
RESULT 11			
AAAY14591			
ID	AAAY14591	standard; protein; 2265 AA.	
XX	AAAY14591;		
AC			
DT	07-DEC-1999	(first entry)	
XX		Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1b).	
DE			
XX		Human; T-type voltage-gated calcium channel; membrane; pore; ion;	
KW		activation; current; rat; screen; drug; cardiomyopathy; epilepsy.	
KW			
XX			
OS		Rattus sp.	
XX			
PN	WO9929847-A1.		
XX			
PD	17-JUN-1999.		
XX			
PF	30-OCT-1998;	98WO-US023161.	
XX			
PR	05-DEC-1997;	97US-00985809.	
XX			
XX	(LOYO)	UNIV LOYOLA CHICAGO.	
PA			
XX			
PI	Perez-Reyes E,	Cribbs LL;	
XX			
DR	WPI; 1999-394972/33.		
DR	N-PSDB; AAX83486.		
XX			
PT		New T-type voltage-gated calcium channels.	
XX			
PS	Disclosure; Page 76-85;	138pp; English.	
XX			
CC	This sequence represents a rat T-type voltage-gated calcium (Ca) channel		
CC	alpha-1-G designated rCavT1b. Voltage gated channels are membrane bound		
CC	glycosylated proteins formed of several subunits. The large alpha		
CC	subunits form a pore in the membrane that is selective for a given ionic		
CC	species. Each alpha subunit contains 4 domains (I, II, III and IV) and		
CC	each domain contains 6 putative transmembrane helical segments (S1-S6). T		
CC	-type Ca channels are activated at a lower voltage than L- or N-type		
CC	channels. Characteristics of T-type channels include short current time,		
CC	slow activation kinetics near threshold, fast inactivation kinetics and		
CC	slow tail current. The sequences AAX83481-X83492 represent novel T-type		
CC	voltage-gated Ca channel genes from humans and rats. Each of the novel Ca		
CC	-channels contains a putative IVS4 region comprising the amino acid		
CC	sequence AAAY14598. Cells expressing the T-type voltage-gated calcium		
CC	channel proteins can be used to screen for drugs which affect calcium		
CC	channels. Methods are also disclosed for treating a disease or disorder		
CC	associated with a deficiency in a native T-type calcium channel nucleic		
CC	acid, e.g. to treat cardiomyopathy, epilepsy, etc		
XX			
SQ	Sequence 2265 AA;		
Query Match			
Best Local Similarity 91.9%; Score 10939.5; DB 2; Length 2265;			
Matches 2107; Conservative 34; Mismatches 101; Indels 47; Gaps 6;			
QY	1	MDEEDGAGAEESGQPRSFMRNLNDLSGAGRGPGSAEKDPGSADSAGLPPALAPVV	60
Db	1	MDEEDGAGAEESGQPRSFMRNLNDLSGAGRGPGSAEKDPGSADSAGLPPALAPVV	60
QY	61	FFYLSQDSRPRSWCLRTVCNPPWFERISMLVILLNCVTLMFRPCEDIACDSQRCLIQAF	120

QY	1080	A-HEMKSPSARSPHSPWSAASWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE	1138
Db	1058	AHEMKCPSPARSPHSPWSAASWTSSRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE	1117
QY	1139	SQDEESSEERASPDGHRHRSGLERAKSSFDLPDTLQVPGIHRGTASGRGSASEHQD	1198
Db	1118	SQDEESSEEDRASPDGHRHRSGLERAKSSFDLPDTLQVPGIHRGTASGRSSASEHQD	1177
QY	1199	CNGKSASGRLARALFPDDPPLDGDADDENLSKGERVRAWIRAPLPACYLERDSWSAYI	1258
Db	1178	CNGKSASGRLARTLRTDDPQLDGDADDENLSKGERIQAWVRSLPACCRERDSWSAYI	1237
QY	1259	FPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLNFIET	1318
Db	1238	FPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLNFIET	1297
QY	1319	AVFLAEMTVKVALGCFGEQAYLRSSWNVDGLLVLISVIDILVSMVSDSGTKILGMLR	1378
Db	1298	AVFLAEMTVKVALGCFGEQAYLRSSWNVDGLLVLISVIDILVSMVSDSGTKILGMLR	1357
QY	1379	VLRLRLTLRPLRVISRAQGLKLVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKGF	1438
Db	1358	VLRLRLTLRPLRVISRAQGLKLVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKGF	1417
QY	1439	FVCGEDTRNITNKSDCAEASRVRWRHKYNFNDNLGQALMSLFVLASKDGVWDIMYDGLDA	1498
Db	1418	FVCGEDTRNITNKSDCAEASRVRWRHKYNFNDNLGQALMSLFVLASKDGVWDIMYDGLDA	1477
QY	1499	VGVDQOPIMNHNPMMLLYFTISFLLIIVAFVFLNMFVGVVVENFHKCRHQHEEARRREK	1558
Db	1478	VGVDQOPIMNHNPMMLLYFTISFLLIIVAFVFLNMFVGVVVENFHKCRHQHEEARRREK	1537
QY	1559	RLRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFIITGVIGLVNVTMA	1611
Db	1538	RLRLEKKRRSKEKQMAEAQCKPYSDYSRFRLLVHHLCTSHYLDLFIITGVIGLVNVTMA	1597
QY	1612	MEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQOLDLAIVLLSIMG	1671
Db	1598	MEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQOLDLAIVLLSIMG	1657
QY	1672	ITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGRALLDTVMQALPQVGNLGLL	1731
Db	1658	ITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGRALLDTVMQALPQVGNLGLL	1717
QY	1732	FMLLFFIFAALGVLEFGDLECDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK	1791
Db	1718	FMLLFFIFAALGVLEFGDLECDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK	1777
QY	1792	DTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVLKHLEESNKEAELEA	1851
Db	1778	DTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVLKHLEESNKEAELEA	1837
QY	1852	ELEEMKTLSPQHPSPGLGSPFLWPVGEGPDPSPKPGALHPAAHARSASHFSLEHPTMQ	1911
Db	1838	ELEEMKTLSPQHPSPGLGSPFLWPVGEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMV	1897
QY	1912	PHPTLP--GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGLGHRGWGLPKAQSGSV	1968
Db	1898	PHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAEKSLGHRGWGLPKAQSGSI	1957
QY	1969	LSVHSQPADTSYILQPKDAPHLLQPHSAPTWCTIPKLPSPGRSPLAQRLRRQAAIRTD	2028
Db	1958	LSVHSQPADTSCILQPKDVHYLLQPHGAPTGAIPKLPSPGRSPLAQRLRRQAAIRTD	2017
QY	2029	SLDVQGLSREDLLAEVSGSPPLARAYSFWGQSTQAQHSRSHSKISKHMTTPPAPCPG	2088
Db	2018	SLDVQGLSREDLLSEVSGSPCLTRSSFWGSSSIQVQQRSGIQSKVSKHRLPAPCPG	2077
QY	2089	PEPNWKGPPETRSSLELDTLSWISGDLPLPPGGQREPPSPRDLKKCYVSEAQSCORRPT	2148
Db	2078	LEPSWAKDPPETRSSLELDTLSWISGDLPLPSSQREHPLFPRDLKKCYSVETQSCRRRPG	2136

Db 61 FFYLSQDSRPRSWCLRTVCNPWFERSVMLVILLNCVTGLMFERPCEDIACDSQRCRILQAF 120

QY 121 DDPIFAFFAVEMVVMVALGIFGKKCYLGD TNRLDFFIVIA GML EYSLDLQNVFSAVR 180

Db 121 DDPIFAFFAVEMVVMVALGIFGKKCYLGD TNRLDFFIVIA GML EYSLDLQNVFSAVR 180

QY 181 TVRVLRLRAINRVPSMRILVTL LLD T L P M L G N V L L C F F V F F I G I V G V Q L W A G L L R N R 240

Db 181 TVRVLRLRAINRVPSMRILVTL LLD T L P M L G N V L L C F F V F F I G I V G V Q L W A G L L R N R 240

QY 241 CFLPENFSLPLSVDLERYYQ TENEDESPFI CSQPRENGMRSCRSVPTLRGDGGGPPCGL 300

Db 241 CFLPENFSLPLSVDLERYYQ TENEDESPFI CSQPRENGMRSCRSVPTLRGE GGGPPCSL 300

QY 301 DYEAYNSSNTCVNWNQY YTNCSAGEHNPFKGA INFDNIGYAWIAIFQVITLEGWVDIM 360

Db 301 DYETYNSSNTCVNWNQY YTNCSAGEHNPFKGA INFDNIGYAWIAIFQVITLEGWVDIM 360

QY 361 YFVMDAHSFYNFIFILLIIVGSPFMINLCLVVIATQFSETKQRESQLMREQVRFLSNA 420

Db 361 YFVMDAHSFYNFIFILLIIVGSPFMINLCLVVIATQFSETKQRESQLMREQVRFLSNA 420

QY 421 STLASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPSS 480

Db 421 STLASFSEPGSCYEELLKYLVIYILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPSS 480

QY 481 SCSRSHRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

Db 481 SCSRSHRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540

QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600

Db 541 TPGGPPRGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600

QY 601 TLKEKALVEAASSGPPTLTSLNIPPGPYSSMHKILLETQSTGACQSSCKISSPCLKADSG 660

Db 601 ILKDKALVEVAPSGPPTLT SFNIPPGPFSSMHKILLETQSTGACHSSCKISSPCLKADSG 660

QY 661 ACGPDCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS - RRQRS LGPD 719

Db 661 ACGPDCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS LGPD 720

QY 720 AEPSSVLAFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISN 779

Db 721 AEPSSVLAFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISN 780

QY 780 IVFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGQGGGLSVLRTFRM 839

Db 781 IVFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVISVWEIVGQGGGLSVLRTFRM 840

QY 840 RVLKLVRLPALQRLVVLMTMDNVATFCMLLMFIFISILGMHLFGCKFASERDGD 899

Db 841 RVLKLVRLPALQRLVVLMTMDNVATFCMLLMFIFISILGMHLFGCKFASERDGD 900

QY 900 LPDRKNFDSLLWAI VTFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNVYVLFNLL 959

Db 901 LPDRKNFDSLLWAI VTFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNVYVLFNLL 960

QY 960 VAILVEGFQAEISKREDASGQLSCIQLPVD SQGDANKSESEPDFFSPLDGDGRKKC 1019

Db 961 VAILVEGFQAE-----GDATKSESEPDFFSPLDGDGRKKR 997

QY 1020 LALVSLGHEPHELKSLPLPLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGA 1079

Db 998 LALVALGEHAELKSLPLPLIHTAATPM SHPKSSSTGVGEALGSGRRRTSSGSAEPGA 1057

QY 1080 A-HEMKSPPSARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1138

Db 1058 AHHEMKCPPSARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1117

QY 1139 SQDEESSEERASPAGSDHRRHGRSLEREAKSSFDPD TLQVPGHLRTASGRGSAEHQD 1198

Db 1118 SQDEESSEEDRASPAGSDHRRHGRSLEREAKSSFDPD TLQVPGHLRTASGRGSAEHQD 1177

QY 1199 CNGKSASGLARALRPDDPPLDGD DADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258

Db 1178 CNGKSASGLARALRTDDPQLDGD DDDNDEGNLSKGERIQAWVRSLPACCRERDSWSAYI 1237

QY 1259 FPQSRFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318

Db 1238 FPQSRFRLLCHRIITHKMFHDVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297

QY 1319 AVFLAEMTVKVVALGWC FGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR 1378

Db 1298 AVFLAEMTVKVVALGWC FGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSGTKILGMLR 1357

QY 1379 VLRLRLRLPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438

Db 1358 VLRLRLRLPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1417

QY 1439 FVCQGEDTRNITNKSDCAEASVRVHRHKYNFDNLGQALMSLFLVASKDGVVDIMYDGLDA 1498

Db 1418 FVCQGEDTRNITNKSDCAEASVRVHRHKYNFDNLGQALMSLFLVASKDGVVDIMYDGLDA 1477

QY 1499 VGVDQOQIMNHPWMLLYFISFLLI VAFVVLNMFVGVVVENFHKCRHQHEEARRREK 1558

Db 1478 VGVDQOQIMNHPWMLLYFISFLLI VAFVVLNMFVGVVVENFHKCRHQHEEARRREK 1537

QY 1559 RLRLLEKKRR-----KAQCKPYSDYSRFRLLVHLC TSHYLDL FIT 1600

Db 1538 RLRLLEKKRRNMLDDVIASGSSASAASEAQCKPYSDYSRFRLLVHLC TSHYLDL FIT 1597

QY 1601 GVIGLNVVTMAMEHYOQPQILDEALKICNYIFTVIVLESVFKLVAFGFRFFQDRWNQL 1660

Db 1598 GVIGLNVVTMAMEHYOQPQILDEALKICNYIFTVIVLESVFKLVAFGFRFFQDRWNQL 1657

QY 1661 DLAI VLLSIMGITLEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGM RALLDVTVMQ 1720

Db 1658 DLAI VLLSIMGITLEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGM RALLDVTVMQ 1717

QY 1721 ALPQVGNLGLLFMLFFIFAALGVELFGDLECDETHPC EGLGRHATFRNFGMAFLTFRV 1780

Db 1718 ALPQVGNLGLLFMLFFIFAALGVELFGDLECDETHPC EGLGRHATFRNFGMAFLTFRV 1777

QY 1781 STGDNWNGIMKDTLRDCDQESTCYNTVTSPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN 1840

Db 1778 STGDNWNGIMKDTLRDCDQESTCYNTVTSPIYFVSFVLTAQFVLVNVVIAVLMKHLEESN 1837

QY 1841 KEAKEEAEELEAELEMKTLSPQHPSPGLSPFLWPVGVEGPDSPDKPGALHPAAHARSA 1900

Db 1838 KEAKEEAEELEAELEMKTLSPQHPSPGLSPFLWPVGVEGYNSTDSPKPGAPHTTAHIGAA 1897

QY 1901 SHFSLEHPTMQPHPTLP---GPDLITVRKSGVSRTHSLPNDSYMCRHSGSTAEGPLGHRG 1957

Db 1898 SGFSLEHPTMVPHPEEVVPLGPDLLITVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHG 1957

QY 1958 WGLPKAQSGSVLSVHSQPADTSLILQPKDAPHL LQPHSAPTWTGTPKLP PPGRSPLAQ 2017

Db 1958 WGLPKAQSGSVLSVHSQPADTSLILQPKDVHYLLQPHGAPTWGAIPKLP PPGRSPLAQ 2017

QY 2018 PLRQQAIRTDSL DVQGLGSRD LLAEVSGSPPLARAYSFWQSQSSTQAQHSRSHSKIS 2077

Db 2018 PLRQQAIRTDSL DVQGLGSRD LLAEVSGSPCLTRSSSFWGSSIQVQORSGIQSKVS 2077

QY 2078 KEMTPPAPCPGPEPNWKGPPETRSSLELDTLSWISGDL LPPGGQEEPPSPRDLKKCYS 2137

Db 2078 KHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDL L-PSSQEEPLFRDLKKCYS 2136

QY 2138 VBAQSCQRRPTSWLDEQRRHSIAVCLDSGSQLHLGTDPSNLGGQPLGPGSRPKKLSP 2197

Db 2137 VETQSCRRRPGFWLDEQRRHSIAVCLDSGSQLCPSPSSLGQPLGGPGSRPKKLSP 2196

QY 2198 PSITIDPPESQGRPTPPSPGICLRRRAPSDSKDPLASGPPD SMAASP KKDVL SGL 2257

Db 2197 PSISIDPPESQGRPPCSPGVCLRRRAPASDSKDP SVSSPILDSTAASP KKTOTLSL SGL 2256

QY	2258	SSDPADLDP	2266	
Db	2257	SSDPTDMDP	2265	
RESULT 12				
AAAY14592				
ID	AAAY14592	standard; protein;	2272	AA.
XX	AAAY14592;			
AC	AAAY14592;			
XX	07-DEC-1999	(first entry)		
DT				
DE	Rat T-type voltage-gated Ca channel alpha-1-G	(rCavT1c).		
XX				
KW	Human; T-type voltage-gated calcium channel;	membrane; pore; ion;		
KW	activation; current; rat; screen; drug;	cardiomyopathy; epilepsy.		
XX				
OS	Rattus sp.			
XX	WO9929847-A1.			
PN	17-JUN-1999.			
XX				
PD	30-OCT-1998;	98WO-US023161.		
XX				
PF	05-DEC-1997;	97US-00985809.		
XX				
PR	(LOYO) UNIV LOYOLA CHICAGO.			
XX	Perez-Reyes E, Cribbs LL;			
PI				
XX	WPI; 1999-394972/33.			
DR	N-PSDB; AAX83487.			
DR				
XX	New T-type voltage-gated calcium channels.			
PT				
XX	Disclosure; Page 85-94; 138pp; English.			
PS				
XX				
CC	This sequence represents a rat T-type voltage-gated calcium (Ca) channel			
CC	alpha-1-G designated rCavT1c. Voltage gated channels are membrane bound			
CC	glycosylated proteins formed of several subunits. The large alpha			
CC	subunits form a pore in the membrane that is selective for a given ionic			
CC	species. Each alpha subunit contains 4 domains (I, II, III and IV) and			
CC	each domain contains 6 putative transmembrane helical segments (S1-S6). T			
CC	-type Ca channels are activated at a lower voltage than L- or N-type			
CC	channels. Characteristics of T-type channels include short current time,			
CC	slow activation kinetics near threshold, fast inactivation kinetics and			
CC	slow tail current. The sequences AAX83481-X83492 represent novel T-type			
CC	voltage-gated Ca channel genes from humans and rats. Each of the novel Ca			
CC	-channels contains a putative IVS4 region comprising the amino acid			
CC	sequence AAY14598. Cells expressing the T-type voltage-gated calcium			
CC	channel proteins can be used to screen for drugs which affect calcium			
CC	channels. Methods are also disclosed for treating a disease or disorder			
CC	associated with a deficiency in a native T-type calcium channel nucleic			
CC	acid, e.g. to treat cardiomyopathy, epilepsy, etc			
XX				
SQ	Sequence 2272 AA;			
Query Match 91.8%; Score 10925; DB 2; Length 2272;				
Best Local Similarity 91.7%; Pred. No. 0;				
Matches 2106; Conservative 33; Mismatches 103; Indels 54; Gaps 6;				
QY	1	MDEEDGAGAEESGQPRSEFRLNDLSGAGRPGSGAEKDPGSADSEAGLPALAPVV	60	
Db	1	MDEEDGAGAEESGQPRSFITLNDLSGAGRQPGSGTEKDPGSADSEAGLPALAPVV	60	
QY	61	FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTILGMFRPCEDIACDSQRCILQAF	120	
Db	61	FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTILGMFRPCEDIACDSQRCILQAF	120	
QY	121	DDFIFAFFAVEMVMVALGIFGKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR	180	

QY 1259 FPPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
Db 1238 FPPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297
QY 1319 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLR 1378
Db 1298 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLR 1357
QY 1379 VLRLRLRTRPLRVISRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGF 1438
Db 1358 VLRLRLRTRPLRVISRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGF 1417
QY 1439 FVCOGEDTRNTKSDCAEASYSRWVRHKYNFDNLGOALMSLFVLASKDGVIMYDGLDA 1498
Db 1418 FVCOGEDTRNTKSDCAEASYSRWVRHKYNFDNLGOALMSLFVLASKDGVIMYDGLDA 1477
QY 1499 VGVDQOPIMNHNPMWMLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRQHQQEEEEARRREEK 1558
Db 1478 VGVDQOPIMNHNPMWMLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRQHQQEEEEARRREEK 1537
QY 1559 RLRRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSH 1593
Db 1538 RLRRLEKKRRSKEKOMADMLDLDVIASSSASAASEAQCKPYSDYSRFRLLVHHLCTSH 1597
QY 1594 YLDFITGVIGLVNVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFF 1653
Db 1598 YLDFITGVIGLVNVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFF 1657
QY 1654 QDRWNQDLAIVLLSIMGITLEIEVNVASLPINPITIRIMRVLRIARVLKLLKMAVGMRA 1713
Db 1658 QDRWNQDLAIVLLSIMGITLEIEVNVLSLPINPTIRIMRVLRIARVLKLLKMAVGMRA 1717
QY 1714 LLDVTMQALPOVGNLGLLPMLLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMA 1773
Db 1718 LLHTVMQALPOVGNLGLLPMLLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMA 1777
QY 1774 FLTFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLM 1833
Db 1778 FLTFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLM 1837
QY 1834 KHEESNKEAKEAELEAELEMLEMTLSPOQHSPLGSPFLWPVGEGDSDSPDKPGALHP 1893
Db 1838 KHEESNKEAKEAELEAELEMLEMTLSPOQHSPLGSPFLWPVGEGVNSTDSPKPGAPHT 1897
QY 1894 AAHARSASHFLEHPTMQPHPTLP--GPDLITVRKSGVSRTHSLPNDSYMCRHGSTAE 1950
Db 1898 TAHIGAASGFSLEHPTWVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAE 1957
QY 1951 GPLGHRGWGLPKAQSGSVLSVHSQPADTSTVILQPKDAPHLLOPHSAPTWGTIPKLPPPG 2010
Db 1958 RSLGHRGWGLPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHCAPTWGAIPKLPPPG 2017
QY 2011 RSPLAQRPLRQAARTDSDLVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQHS 2070
Db 2018 RSPLAQRPLRQAARTDSDLVQGLGSRREDLLSEVSGSPCLTRSSSFWGSSIQVQORS 2077
QY 2071 RSHKISKHMTTPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPLPGGQEEPPSPR 2130
Db 2078 GIQKSVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLPSSQEEPLFPR 2136
QY 2131 DLKKCYSEVAQSCORRPTSWLDEQRHRSIAVSCLDGSGQHLGTDPSNLGGQPLGGPGSR 2190
Db 2137 DLKNCYSVETQSCRRRPGFWLDEQRHRSIAVSCLDGSGQHLGTDPSNLGGQPLGGPGSR 2196
QY 2191 PKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPPKKD 2250
Db 2197 PKKLSPPSISIDPPESQGSRRPPCGVCLRRRAPASDSKDPSPVSSPLDSTAASPPKKD 2256
QY 2251 VLSLSGLSSDPADLDP 2266
Db 2257 TLSLSGLSSDPTDMDP 2272

RESULT 13
AAB66475
ID AAB66475 standard; protein; 2287 AA.
XX AAB66475;
AC AAB66475;
XX 09-APR-2001 (first entry)
DT
XX Rat alpha-IG calcium channel protein.
DE
XX Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
KW hypotensive; cardiant; nootropic; T-type calcium channel subunit;
KW cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
KW epilepsy; alpha-IG calcium channel.
XX
OS Rattus sp.
XX
PN WO200102561-A2.
XX
PD 11-JAN-2001.
XX
PF 04-JUL-2000; 2000WO-CA000794.
XX
PR 02-JUL-1999; 99US-00346794.
XX
PA (NEUR-) NEUROMED TECHNOLOGIES INC.
XX
PI Snutch TP, Baillie DL;
XX
DR WPI; 2001-123111/13.
DR N-PSDB; AAF31677.
XX
PT Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT epilepsy.
XX
PS Disclosure; Page 63-72; 103pp; English.
XX
CC The present sequence is given in a specification providing sequences and
CC partial sequences for three types of mammalian (human and rat) T-type
CC calcium channel subunits. An expression cassette has been generated which
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC subunit operably linked to control sequences to effect its expression.
CC The novel calcium channel nucleic acids and proteins are useful for
CC treating conditions characterised by undesirable levels of T-type calcium
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC hypertension, sleep disorder and epilepsy
XX
SQ Sequence 2287 AA;
Query Match 90.5%; Score 10774; DB 4; Length 2287;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 2075; Conservative 33; Mismatches 105; Indels 36; Gaps 6;
QY 30 GRPGPGSAEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPSWCLRTVCNPFERISML 89
Db 62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVFFYLSQDSRPSWCLRTVCNPFERISML 121
QY 90 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG 149
Db 122 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLG 181
QY 150 DTWNRDLDFFIAGMLESYLDLQNVSFSAVTRVRLPLRAINRVPSMRILVLLDTP 209
Db 182 DTWNRDLDFFIAGMLESYLDLQNVSFSAVTRVRLPLRAINRVPSMRILVLLDTP 241
QY 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPSVDLERYQTENEDESPF 269
Db 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPSVDLERYQTENEDESPF 301
QY 270 ICSQPRENGMRSCRSVPTLRGDGGGPPCGLDYEAYNSSNTTCVNWNYQYTCNSAGEHN 329

Db 302 ICSQPRENGMRSCRSVPTLRGEGGGPPCSDLYETYNSSNTTCVNWNQYNTCSAGEHN 361

Qy 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFYFILLIIVGSFFMINL 389

Db 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIFYFILLIIVGSFFMINL 421

Qy 390 CLVVIATQSETKQRESQOLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 449

Db 422 CLVVIATQSETKQRESQOLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAAR 481

Qy 450 RLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRRLSVHHLVHHHHHHHHYHLGN 509

Db 482 RLAQVSRAGVRVGLLSSPVARSGQEPQPSGSCTRSHRRRLSVHHLVHHHHHHHHYHLGN 541

Qy 510 GTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGAESVHSFYHADCHLEPVRQ 569

Db 542 GTLRVPRASPEIQDRDANGSRRLMLPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRQ 601

Qy 570 APPPRSPSEASGRIVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPY 629

Db 602 APPPRCPSEASGRIVGSGKVYPTVHTSPPPETLKEKALVEVAPSPGPPTLTSLNIPPGPF 661

Qy 630 SSMHKLLETQSTGACOSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSD 689

Db 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 721

Qy 690 SEAVYEFTQDAQHSDLRDPHS-RRQSLGPDABPSSVLAFWRLICDTFRKIVDSKYFGRG 748

Db 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDABPSSVLAFWRLICDTFRKIVDSKYFGRG 781

Qy 749 IMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVVGPFGYIKNPYN 808

Db 782 IMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVVGPFGYIKNPYN 841

Qy 809 IFDGVIVVISWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDNVATF 868

Db 842 IFDGVIVVISWEIVGQGGGLSVLRTFRMLRVLKLVRFLPALQRLVLMKTMNDNVATF 901

Qy 869 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNKV 928

Db 902 CMLMLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTFQILTQEDWNKV 961

Qy 929 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEIEISKREDASGQUSCQLP 988

Db 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEIEISKREDASGQUSCQLP 1003

Qy 989 VDSQGGDANKSESEPDDFFSPSLDGDGRKKCLALVSLGEHPELRKSLPLPLIHTAATPM 1048

Db 1004 -----GDATKSESEPDDFFSPVGDGDKRKLALVALGEHAELRKSLLPLIHTAATPM 1058

Qy 1049 SLPKSTSTGLGEALGPASRRTSSSGSABPGAA-HEMKSPPSARSSPHSPWSAASWTSRR 1107

Db 1059 SHPKSSSTGVGEALGSGSRRTSSSGSABPGAAHEMKPPSARSSPHSPWSAASWTSRR 1118

Qy 1108 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEERASPGSDHHRHGSLERE 1167

Db 1119 SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEERASPGSDHHRHGSLERE 1178

Qy 1168 AKSSFDLPDTLQVPLGHTASGRGSASEHQDCNGKSASGRLARALRPDDPPLDGDADDDE 1227

Db 1179 AKSSFDLPDTLQVPLGHTASGRSSASEHQDCNGKSASGRLARALTURDDPQLDGDNDDE 1238

Qy 1228 GNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRLIITHKMFHDHVLVLIIF 1287

Db 1239 GNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLLCHRLIITHKMFHDHVLVLIIF 1298

Qy 1288 LNCITIAMERPKIDPHSAERIFLTLSNYIIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1347

Db 1299 LNCITIAMERPKIDPHSAERIFLTLSNYIIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1358

Qy 1348 VLDGLLVLSVIDILVMSVSDSGTKILGMLRVLRLLRPLRPLRVISRAQGLKLVVETLMS 1407

Db 1359 VLDGLLVLSVIDILVMSVSDSGTKILGMLRVLRLLRPLRPLRVISRAQGLKLVVETLMS 1418

Qy 1408 SLKPIGNIWVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKY 1467

Db 1419 SLKPIGNIWVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKY 1478

Qy 1468 NFDNLGOALMSLFVLASKDGNVDIMYDGLDVGVDQOPIMNHNPMMLLYFISFLLIVAFF 1527

Db 1479 NFDNLGOALMSLFVLASKDGNVDIMYDGLDVGVDQOPIMNHNPMMLLYFISFLLIVAFF 1538

Qy 1528 VLNMFVGVVVENFHKCRHQHEEAEARRREKRLRRLEKKRR-----KAQCKPYYSYDS 1580

Db 1539 VLNMFVGVVVENFHKCRHQHEEAEARRREKRLRRLEKKRSKEKQMAEAQCKPYYSYDS 1598

Qy 1581 RFRLLVHHLCTSHYLDLFTITGVGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLES 1640

Db 1599 RFRLLVHHLCTSHYLDLFTITGVGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLES 1658

Qy 1641 VFKLVAFGFRFFQDRWNQLDLAIVLLSIMGITLEEIEFVNASLPINPTIIRIMRVLIAR 1700

Db 1659 VFKLVAFAFRFFQDRWNQLDLAIVLLSIMGITLEEIEFVNLSLPINPTIIRIMRVLIAR 1718

Qy 1701 VLKLLKMAVGMRALDVTMQALPOVGNLGLLMLLFFIFAALGVELFGDLECDETHPCEG 1760

Db 1719 VLKLLKMAVGMRALHTVMQALPOVGNLGLLMLLFFIFAALGVELFGDLECDETHPCEG 1778

Qy 1761 LGRHATERNFGMAFLTFRVSTGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTA 1820

Db 1779 LGRHATERNFGMAFLTFRVSTGDNWNGIMKDPSPRDCQESTCYNTVISPIYFVSFVLTA 1838

Qy 1821 QPVLNVVIAVLMKHLEESNKEAKEEAELAELELEMKTLSPQSPHSPGLSGPFLWPGEVP 1880

Db 1839 QPVLNVVIAVLMKHLEESNKEAKEEAELAELELEMKTLSPQSPHSPGLSGPFLWPGEVP 1898

Qy 1881 DSPDSPKPGALHPAAHARSASHFSLEHPTMQPHTELP---GPDLLTVRKSGVSRTHSLP 1937

Db 1899 NSTDSPKPGAPHTTAHICAAAGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLP 1958

Qy 1938 NDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYIQLPKDAPHLLQPHSA 1997

Db 1959 NDSYMCRNSTAESRSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGA 2018

Qy 1998 PTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSDVQGLGSRREDLLAEVSGSPPLARAYS 2057

Db 2019 PTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSDVQGLGSRREDLLSEVSGSPCLTRSSS 2078

Qy 2058 FWGQSSTQAQOHSRSHSKISKHMTPPAPCPGPEPNWKGPPETRSSLELDELTSWISGDL 2117

Db 2079 FWGSSIQVQORSGIOQSVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDELTSWISGDL 2138

Qy 2118 LPPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDP 2177

Db 2139 L-PSSQEEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPHLGTDP 2197

Qy 2178 NLGGQPLGGGSRPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDKDPLASGP 2237

Db 2198 SLGGQPLGGGSRPKKLSPPSISIDPPESQGSRRPPCSPGVCLRRRAPASDKDPSVSSP 2257

Qy 2238 PDSMAASPSPKKDVLSLSGLSSDPADLDP 2266

Db 2258 LDSTAASPSPKKDTLSLSGLSSDPTDMDP 2286

RESULT 14

AAU00474

ID AAU00474 standard; protein; 1207 AA.

XX

AC AAU00474;

XX

DT 18-JUL-2001 (first entry)

XX

DE Human T-type calcium channel CACNA1G protein.

XX

KW Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;

cellular proliferative disorder; colorectal cancer; age related disease; apolipoprotein B; APOB; caudal type homeobox transcription factor 2; CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1; MINT31; G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B; HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2; PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL; patched A; patched B; PTCH; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4; chromosome 17.

XX Homo sapiens.
OS WO200119845-A1.
XX 22-MAR-2001.
XX 14-SEP-2000; 2000WO-US025479.
XX 15-SEP-1999; 99US-00398522.
XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX Issa J;
XX WPI; 2001-244777/25.
XX N-PSDB; AAS01624.

New nucleic acid molecule for use as a marker for screening cancer, comprises the coding region for a T-type calcium channel and regulatory sequences associated with the channel.
XX Claim 9; Fig 3B; 125pp; English.
XX The present sequence representing a novel human T-type calcium channel CACNA1G maps to chromosome 17. The methylation state of specific regions within CpG islands associated with the CACNA1G gene correlate with several cancerous phenotypes involving various tissue and cell types. Since aberrant methylation of normally unmethylated CpG islands is often observed in immortalised and transformed cells, CACNA1G is implicated in cellular proliferative disorders e.g. leukaemia, colorectal, lung, breast and other cancers. The nucleic acid coding for CACNA1G is useful as a marker for screening cancer and age related diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for amplification of a CpG-containing nucleic acid, where the primer hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can be used for detecting aberrant methylation. The CpG island sequences (AAS01677-AAS01692) are selected from genes encoding CACNA1G, apolipoprotein B (APOB), caudal type homeobox transcription factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B; HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-activated receptor 2 (PAR2), paired-like homeodomain transcription factor 2 (PITX2), patched A and B (PTCH; PTCHB) and syndecan 1 and 4 (SDC1; SDC4) or a MINT 31 sequence

Sequence 1207 AA;
Query Match 53.1%; Score 6315.5; DB 4; Length 1207;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1207; Conservative 0; Mismatches 0; Indels 23; Gaps 1;
1 MDEEDGAGAEESGQPRSMRLNDLSGAGRPGGSAEKDPGSADSEAGLPYPALAPVV 60
1 MDEEDGAGAEESGQPRSMRLNDLSGAGRPGGSAEKDPGSADSEAGLPYPALAPVV 60
61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLMGFRPCEDIACDSQRCRILQAF 120
61 FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTLMGFRPCEDIACDSQRCRILQAF 120
121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
181 TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

Db	181	TVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240
Qy	241	CFLPENFSLPLSVDLERYQTENEDESPFICQPRENMRSCRSVPTLRDGGGGPPCGL	300
Db	241	CFLPENFSLPLSVDLERYQTENEDESPFICQPRENMRSCRSVPTLRDGGGGPPCGL	300
Qy	301	DYEAYNSSNTTCVNMNQYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM	360
Db	301	DYEAYNSSNTTCVNMNQYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM	360
Qy	361	YFVMDAHSFYFIYFILLIIVGSFFMINICLVVIATQFSETKQRESQLMREQVRFLSNA	420
Db	361	YFVMDAHSFYFIYFILLIIVGSFFMINICLVVIATQFSETKQRESQLMREQVRFLSNA	420
Qy	421	STLASRSEPGSCYEELLKYLVIILRKAARRLAQVSRAGVRVGLSSPAPLGGQETQSS	480
Db	421	STLASRSEPGSCYEELLKYLVIILRKAARRLAQVSRAGVRVGLSSPAPLGGQETQSS	480
Qy	481	SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQORDANGSRRRLMLPPSTP	540
Db	481	SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQORDANGSRRRLMLPPSTP	540
Qy	541	ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE	600
Db	541	ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE	600
Qy	601	TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLTETQSTGACOSSCKISSPCLKADSG	660
Db	601	TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLTETQSTGACOSSCKISSPCLKADSG	660
Qy	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQSLGPDA	720
Db	661	ACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQSLGPDA	720
Qy	721	EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHEQPELTNALEISNI	780
Db	721	EPSSVLAFWRLICDTFRKIVDSKYFGRGIMIALVNTLSMGIEYHEQPELTNALEISNI	780
Qy	781	VFTSLFALEMLLKLVLVGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR	840
Db	781	VFTSLFALEMLLKLVLVGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR	840
Qy	841	VKLVRFLPALQRLVLMKTMNDNVATFCMLLMFLFIFISILGMHLFGCKFASERDGTIL	900
Db	841	VKLVRFLPALQRLVLMKTMNDNVATFCMLLMFLFIFISILGMHLFGCKFASERDGTIL	900
Qy	901	PDRKNFDSLLWALVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLV	960
Db	901	PDRKNFDSLLWALVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLV	960
Qy	961	AILVEGFAEEISKREDASGQLSCIQLPVDVDSQGGDANKSESEDFPSLDGDRKKCL	1020
Db	961	AILVEGFAEEISKREDASGQLSCIQLPVDVDSQGGDANKSESEDFPSLDGDRKKCL	1020
Qy	1021	ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA	1080
Db	998	ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA	1057
Qy	1081	HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1140
Db	1058	HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQ	1117
Qy	1141	DEESSEERASPAAGSDHRRHRSGLEREAKSSFDLPDTLQVPLHRTASGRGSASEHQDCN	1200
Db	1118	DEESSEERASPAAGSDHRRHRSGLEREAKSSFDLPDTLQVPLHRTASGRGSASEHQDCN	1177
Qy	1201	GKSASGRILARALRPDDPPLDGDADDEGNL	1230
Db	1178	GKSASGRILARALRPDDPPLDGDADDEGNL	1207

ID	AAB66476	standard; protein; 2359 AA.
XX		
AC	AAB66476;	
XX		
DT	09-APR-2001	(first entry)
XX		
DE	Rat alpha-IH calcium channel protein.	
XX		
KW	Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;	
KW	hypotensive; cardiant; nootropic; T-type calcium channel subunit;	
KW	cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;	
KW	epilepsy; alpha-IH calcium channel.	
XX		
OS	Rattus sp.	
XX		
PN	WO200102561-A2.	
XX		
PD	11-JAN-2001.	
XX		
PF	04-JUL-2000; 2000WO-CA000794.	
XX		
PR	02-JUL-1999; 99US-00346794.	
XX		
PA	(NEUR-) NEUROMED TECHNOLOGIES INC.	
XX		
PI	Snutch TP, Baillie DL;	
XX		
DR	WPI; 2001-123111/13.	
DR	N-PSDB; AAF31678.	
XX		
PT	Novel T-type calcium channel alpha-1 subunit gene useful for treating	
PT	cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and	
PT	epilepsy.	
XX		
PS	Disclosure; Page 75-85; 103pp; English.	
XX		
CC	The present sequence is given in a specification providing sequences and	
CC	partial sequences for three types of mammalian (human and rat) T-type	
CC	calcium channel subunits. An expression cassette has been generated which	
CC	comprises a nucleotide sequence encoding a T-type calcium channel alpha_1	
CC	subunit operably linked to control sequences to effect its expression.	
CC	The novel calcium channel nucleic acids and proteins are useful for	
CC	treating conditions characterised by undesirable levels of T-type calcium	
CC	channel activity such as cardiac hypertrophy, cardiac arrhythmia,	
CC	hypertension, sleep disorder and epilepsy	
XX		
SQ	Sequence 2359 AA;	
	Query Match 52.2%; Score 6218; DB 4; Length 2359;	
	Best Local Similarity 56.4%; Pred. No. 0;	
	Matches 1369; Conservative 228; Mismatches 509; Indels 322; Gaps 62;	
QY	2 DEEDGAGAEESGQPRSMRLNDLS-GAGGRP---GPGS---AEKDPGS---AD---SEA 48	
Db	9 DEVRVPLGASPPA-PAAPVRASPAPGAPGREGGSGGVLAPESPTECGADLGADDEE 67	
QY	49 EGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTILGMFRPCEDIA 108	
Db	68 QVPYPALAAATVFCLGQTTRPRSWCLRLVCNPFWEHVSMVLVMLNCVTILGMFRPCEDVE 127	
QY	109 CDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLLDFFIIVAGMLEYS 168	
Db	128 CRSERCSILEAFDDFIFAFFAVEMVVMVALGLFGQKCYLGDTWNRLLDFFIIVAGMMEYS 187	
QY	169 LDIQNVSFSAVRTVRLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIV 228	
Db	188 LDGHKVSLSAIRTVRLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIV 247	
QY	229 GVQLWAGLLRNRCFLPENFSLPLSVD-LERYQOTENEDESPFICSQPRENGMRCRSVPT 287	
Db	248 GVQLWAGLLRNRCFLDSAFVRNNLTFLRPYQTEGEENPFICSSRRDNGMQKCSHIPS 307	
QY	288 ---LRGDGGGGPPCGLDYEAY-----NSSNTTCVNNQYITNCSAGEHNPFKGAINF 337	

Db	308 RREL-----VQCTLGWEAYGQQAEDGGAGRNACINWNQYINVCRSGEFPHNGAINF 361
QY	338 DNIGYAWIAFOVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQ 397
Db	362 DNIGYAWIAFOVITLEGWVDIMYVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQ 421
QY	398 FSETKQRESQLMREQVRFLSNASTIASFSEPGSCYEELLKYLVLKAAARLAQVSRA 457
Db	422 FSETKQRENQLMREQVARYLSNDSTLASFSEPGSCYEELLKYVGHIFRKVRRSLRYAR 481
QY	458 AGVRVGLLSSP-APLGGQETQPSSCSRSRHR-LSVHVLV-HHHHHHHHHYHLNGTTLRA 514
Db	482 WQSRWRKKVDSSTVHGQ--GPGRRPRRAGRRTASVHLVYHHHHHHHHYHFSHGPPR 539
QY	515 PRASPEIQDRDANGSRRLM--LPPPTPALSGAPPGGAESVHSFYHADCHLEPVRCAAPP 572
Db	540 P--SPE---PGAGDNRLVRACAPSPSPGHGPP-DSESVHSIYHADCHVEGQERARV 592
QY	573 PRSPSEASGRTVSGS--KVYPTVHTSPPTETLKEKALVEVAASGPTLTSLNIP---- 625
Db	593 AHSIATAASLKLASGLTMNYPTI---LPSTVNSKG----GTSSRPKGLRGAGAPGA 645
QY	626 -----PGPYSSMHKLLETQSTGACQS-----SKISSPCLKADSGACGPDSCP 670
Db	646 HSPLSLGSPRPYEKIQDVVGEQGLGRASSHLSGLSVPCPLSP--QAGTLTCELKSCP 703
QY	671 ARA-GAGEVELADREMPDSDSEAVYEFTQDAQSDLRDP-----HS--RRQSL 716
Db	704 ASALEDPFEFSGSESDSDAHGYEFTQDVHGDGCDPVOQPHEVGTGPHGSNERRRTP 763
QY	717 GDAEPSSVLAFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHQPEELTNALE 776
Db	764 RKASQPGGIGHLWASFSGKLRRIIVDSKYFNRGIMAAILLVNTLSMGVEYHQPEELTNALE 823
QY	777 ISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIPDGVIVVISWEIVGQCGGLSLV 836
Db	824 ISNIVTSMFALEMLLKLACGPLGYIRNPYNIPFDGIVVVISWEIVGQADGQSV 883
QY	837 RLMRVLKLVRFLPALQRLVILMKTMDNVATFCMLMLFIFISILGMHLFGCKPASE 896
Db	884 RLLRVLKLVRFLPALRRQLVILMRTMDNVATFCMLMLFIFISILGMHLFGCKPS 943
QY	897 -GDTLPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFG 955
Db	944 SGDTVPDRKNFDSLLWAIIVTFQILTQEDWNVLNGMASTSSWAALYFVALMTFG 1003
QY	956 FNLLVAILVEGFQAEIEISKREDASGQLSCIQLPVDSDGDKANKSESEPFSPSLD 1015
Db	1004 FNLLVAILVEGFQAE-----GDATRSDDTDEKTSQLEGD 1040
QY	1016 RKKCL-----ALVSLGEHPELRKSLPPLIHTAATPMSLPKSTSTGLGEALGP 1066
Db	1041 KLRLDRATEMKMYS LAVTPNGHLEGRGSLPPLITHAATPMPTPKS-SPNLDVAHAL 1099
QY	1067 RRTSSSGSAEPGAAHEMKSPPSARSPHSPWASAASWTSRRSSRNSLGRAPSLKR 1126
Db	1100 SRRSSSGSVDPQLG-DQKSLASLRSSPCTPWGPNAGSSRRSSRNSLGRAPSLKR 1158
QY	1127 ERRSLLSGEGESQDEESESSEERAS-----PAGSDHHRGSLEREAKSSFDL-- 1174
Db	1159 ERESLLSGEGKSTDE--AEDSRPSTGTHPGASPGPRATPLRAESLDH--RSTLD 1214
QY	1175 ----PDTLQVPGHLRTASGRGSAHEHQDCNGKSAASGRALARALRPDDPPLDGD 1230
Db	1215 PRPAPPVQV-----HDCNGQMVALPSEFFLRIDSHKEDAAEFDDIED 1258
QY	1231 SKGERVRAWIRARLPACYLERDSWSAYIFPPQSRRLCHRIITHKMFHDHVLVIFL 1290
Db	1259 SCCFRLHKVLEPYAPQWCRSRESWALYLFPPQNRRLRVSCQKVIHAKMFDHVL 1318
QY	1291 ITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVVALGWCFGEQAYLR 1350

Db	1319	ITIALERPDIDPGSTERAPFLSVSNYIFTAIFVVMVMKVVALGLLWGEHAYLOQSSWNVLD	1378
Qy	1351	GLLVLSIVDILVSMVSDSGTKILGMLRLVRLRLTLRPLRVISRAQGLKLVVETLMSLKL	1410
Db	1379	GLLVLSLVDIIVAMASAGGAKILGVLRVVRLLRTLRLPLRVISRAPGLKLVVETLISLR	1438
Qy	1411	PIGNIWVICCAFFIIFGILGVOLFKGKFFVCQGEDTRNITNKSDCAEASYSVRHRYKNFD	1470
Db	1439	PIGNIWVICCAFFIIFGILGVOLFKGKFFYCEGTDTRNITTKAECHAAHYRWRKYNFD	1498
Qy	1471	NLGOALMSLFLVASKDQWVDIMYDGLDAVGVDQQPIMHNHPWMLLYFISFLLIIVAFVLN	1530
Db	1499	NLGOALMSLFLVSSKQGWVNIYDGLDAVGIDQQPVQNHNPWMLLYFISFLLIIVSFFVLN	1558
Qy	1531	MFVGVVVENFHKCRQHQQEAEARRREKRRLRLEKKRKAQCKPYVSDYSRFRLLVHHLC	1590
Db	1559	MFVGVVVENFHKCRQHQQEAEARRREKRRLRLEKKRKAQCKPYVSDYSRFRLLVHHLC	1618
Qy	1591	TSHYLDLFTITGVLNVTMAMEHYQQPQILDEALKICNVIFTVIFVLESVFKLVAFGFR	1650
Db	1619	TSHYLDLFTITGVLNVTMAMEHYQQPQILDEALKICNVIFTVIFVLESVFKLVAFGFR	1678
Qy	1651	RFFQDRWNQLDLAIVLLSIMGITLLEEIVNASLPINPTIIRIMRVLRIARVLKLLKMAVG	1710
Db	1679	RFFQDRWNQLDLAIVLLSIMGITLLEEIVNASLPINPTIIRIMRVLRIARVLKLLKMAVG	1738
Qy	1711	MRALLDTVMQALPOVGNLGLLPMLLFFIFAALGVLELFGDLECDTHPCGELGRHATFRNF	1770
Db	1739	MRALLDTVMQALPOVGNLGLLPMLLFFIFAALGVLELFGDLECDTHPCGELGRHATFRNF	1798
Qy	1771	GMAFLTFRVSTGDNWNGIMKDTLRDC--DQESTCYNTVISPIYFVSFVLTAQFVLVNV	1827
Db	1799	GMAFLTFRVSTGDNWNGIMKDTLRDC--DQESTCYNTVISPIYFVSFVLTAQFVLVNV	1858
Qy	1828	VIAVLMKHLEESNKEAKEEAELEAELEMLEKTLSPQPHSPGLSPFLWPGVEGPDSPDSPK	1887
Db	1859	VVAVLMKHLEESNKEAREDAEMDAEIELEM-----1888	
Qy	1888	PGALHPAAHARSASHFSLEHPTMQPHPT--ELPG-----PDLLTVRKSGVSRTHSLPND	1940
Db	1889	-----AQGSTAQPPPTAQESQGTQDTPNLLVVRKVSVRMLSLPND	1931
Qy	1941	YMCRHGSTAEGPLGHRGWGLP-----KAQSGSVLSVHSQPADTSYILQLPKDAPELLQP	1994
Db	1932	YMFPRVAPAAAPHSH-----PLQEVEMETITGPVTSAHSPPLEPRASFQVPSAA-----	1980
Qy	1995	HSAPTWTGTP--KLPPPG--RSPLAQRPLRRQAARTDSDL--VQGLSREDLLAEVSGP	2048
Db	1981	--SSPARVSDPLCALSPRGTPRSLSLSRILCRQEAHSESLEGVDDVGG--DSIPDYTEP	2037
Qy	2049	SPPLARAYSFWG-----QSSTOQQHRSRSHSKISKHMTPPAPCPGPEPNWKGPP	2098
Db	2038	AENMSTSQASTGAPRSPPCSPRPASVTRKHTFGORCISR--PPT-----LGGD	2085
Qy	2099	ETRSSLLEDTLSWISGDLLP-----PGQEEPP-----SPRDLKKCYSVBAQSC	2143
Db	2086	EAEAADPADEEVSHITSSAHPWPATEPHSPEASPTASPVKGTWGSGRDPRRFCVDAQSF	2145
Qy	2144	QRRPTSWLDEQRRHSIAVSCLDGSGPHLGTDPNSNLGGQPLG-----GPGSRPKKLS	2196
Db	2146	LDKP-GRPDAQRWSSVE--LDNG-ESHLES-----GEVGRASELEPALGSRKKKMS	2194
Qy	2197	PPSITIDPP--ESQGPRTPPSP---GICLRRRAPSSDSK-----DPLASG	2236
Db	2195	PPCISIEPPTKDEGSSRPAAEGGNTTLRRRTPSCEALHRDCPEPTEGPGTGDGPFVAKG	2254
Qy	2237	PPDSMAASPSPKKDVLSLGLSSDPADL	2264
Db	2255	ERWGQA---SCRAEHLTVPNFAFEPLDM	2279

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:41 ; Search time 40.3132 Seconds
(without alignments)
3727.727 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEDGAGAEESGQPRSF.....PKKDVLSLGLSPADLDP 2266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	11862.5	99.7	2273	3	US-09-426-998-5
2	6315.5	53.1	1207	4	US-09-398-522-52
3	6211	52.2	2353	3	US-08-984-709A-50
4	5492.5	46.1	2175	3	US-09-404-650-2
5	5492.5	46.1	2175	4	US-09-935-541-2
6	5484	46.1	2188	3	US-09-404-650-4
7	5484	46.1	2188	4	US-09-935-541-4
8	5366	45.1	1835	3	US-09-404-650-5
9	5366	45.1	1835	4	US-09-935-541-5
10	1750.5	14.7	2343	3	US-09-268-163-4
11	1749	14.7	2337	3	US-08-713-118-2
12	1749	14.7	2337	3	US-09-452-007-2
13	1748.5	14.7	2339	1	US-08-455-543A-47
14	1748.5	14.7	2339	2	US-08-223-305C-47
15	1746.5	14.7	2339	3	US-09-268-163-6
16	1743	14.6	2237	1	US-08-455-543A-48
17	1743	14.6	2237	2	US-08-223-305C-48
18	1741	14.6	2237	3	US-09-268-163-8
19	1722	14.5	2336	3	US-09-268-163-10
20	1632.5	13.7	1873	1	US-08-435-675B-4
21	1622.5	13.6	1873	1	US-08-336-257A-7
22	1619.5	13.6	1984	3	US-08-836-325-10
23	1619.5	13.6	1984	4	US-09-457-571-10
24	1619.5	13.6	1985	4	US-09-495-714C-6
25	1616	13.6	1872	6	5386025-6
26	1615.5	13.6	1989	3	US-08-836-325-12
27	1615.5	13.6	1989	4	US-09-457-571-12

28	1607.5	13.5	2516	3	US-08-374-077C-2	Sequence 2, Appli
29	1607.5	13.5	2516	3	US-08-895-590-2	Sequence 2, Appli
30	1607.5	13.5	2516	4	US-09-539-879A-2	Sequence 2, Appli
31	1601	13.4	1977	4	US-09-495-714C-4	Sequence 4, Appli
32	1601	13.4	2509	2	US-08-149-097D-35	Sequence 35, Appli
33	1587	13.3	2016	4	US-09-514-907A-2	Sequence 2, Appli
34	1587	13.3	2016	4	US-09-896-994-2	Sequence 2, Appli
35	1586	13.3	1969	3	US-08-836-325-16	Sequence 16, Appl
36	1586	13.3	1969	4	US-09-457-571-16	Sequence 16, Appl
37	1586	13.3	2016	3	US-09-634-920-4	Sequence 4, Appli
38	1586	13.3	2016	4	US-09-840-125-4	Sequence 4, Appli
39	1583	13.3	1977	4	US-09-976-594-757	Sequence 757, App
40	1583	13.3	1977	4	US-09-919-039-367	Sequence 367, App
41	1573.5	13.2	1912	4	US-09-495-714C-2	Sequence 2, Appli
42	1569.5	13.2	1968	1	US-08-455-543A-45	Sequence 45, Appl
43	1569.5	13.2	1968	2	US-08-223-305C-45	Sequence 45, Appl
44	1560.5	13.1	2161	1	US-08-455-543A-51	Sequence 51, Appl
45	1560.5	13.1	2161	2	US-08-223-305C-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-426-998-5
; Sequence 5, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 5
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-426-998-5

Query Match	99.7%	Score	11862.5	DB	3	Length	2273
Best Local Similarity	99.4%	Pred. No.	0				
Matches	2260	Conservative	4	Mismatches	2	Indels	7
Gaps	1						
QY	1	MDEEDGAGAEESGQPRSFMRNLDSGAGRPGPGSAEKDPGSADSEAEGLYPALAPVV	60				
Db	1	MDEEDGAGAEESGQPRSFMRNLDSGAGRPGPGSAEKDPGSADSEAEGLYPALAPVV	60				
QY	61	FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTILGMFPCEDIAACDSQRILQAF	120				
Db	61	FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTILGMFPCEDIAACDSQRILQAF	120				
QY	121	DDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAAGMLEYSLDLQNVFSFAVR	180				
Db	121	DDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAAGMLEYSLDLQNVFSFAVR	180				
QY	181	TVRVLRLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240				
Db	181	TVRVLRLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240				
QY	241	CFLPENFSLPSVDLERYYTENEDESPFICSPRENGMRSCRSVPTLRDGGGGPPCGL	300				
Db	241	CFLPENFSLPSVDLERYYTENEDESPFICSPRENGMRSCRSVPTLRDGGGGPPCGL	300				
QY	301	DYEAYNSSNTTCVNNQYTNCSAGEHNPFKAINFDNIGYAWIAIFQVITLEGWVDIM	360				
Db	301	DYEAYNSSNTTCVNNQYTNCSAGEHNPFKAINFDNIGYAWIAIFQVITLEGWVDIM	360				

QY 361 YFVMDAHSFYNFYIFILLIIVGSPFMINCLVVIATOFSETKQRESQLMREQVRFLSNA 420
Db
QY 361 YFVMDAHSFYNFYIFILLIIVGSPFMINCLVVIATOFSETKQRESQLMREQVRFLSNA 420
Db
QY 421 STLASFEPGSCYEELLKYLVLILKAARRLAQVSRAGVRVGLLSSPAPLGSGQETQPS 480
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QY 421 STLASFEPGSCYEELLKYLVLILKAARRLAQVSRAGVRVGLLSSPAPLGSGQETQPS 480
Db
QY 481 SCSRSHRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db
QY 481 SCSRSHRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db
QY 541 ALSGAPPGAESVHSFYHADCHLEPVCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600
Db
QY 541 ALSGAPPGAESVHSFYHADCHLEPVCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600
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QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
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QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
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QY 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSGLPDA 720
Db
QY 661 ACPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSGLPDA 720
Db
QY 721 EPSSVLAFWRLICDTRFKIVDSKYFGRGIMIAILLVNTLSMGIEYHEQPEELTNALEISNI 780
Db
QY 721 EPSSVLAFWRLICDTRFKIVDSKYFGRGIMIAILLVNTLSMGIEYHEQPEELTNALEISNI 780
Db
QY 781 VFTSLFALEMLLKLVLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR 840
Db
QY 781 VFTSLFALEMLLKLVLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMR 840
Db
QY 841 VLKLVRLPALQRLVLMKTMNDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGTIL 900
Db
QY 841 VLKLVRLPALQRLVLMKTMNDNVATFCMLLMLFIFIFSILGMHLFGCKFASERDGTIL 900
Db
QY 901 PDRKNFDSLWAIIVTVFQILTOEDWNKVLNGMASTSSWAALFYFALMTFGNYVLFNLLV 960
Db
QY 901 PDRKNFDSLWAIIVTVFQILTOEDWNKVLNGMASTSSWAALFYFALMTFGNYVLFNLLV 960
Db
QY 961 AILVEGQAEIISKREDASQGLSCIQLPVDPSQGGDANKSESEPDPFSPSLDGDGRKKCL 1020
Db
QY 961 AILVEGQAEIISKREDASQGLSCIQLPVDPSQGGDANKSESEPDPFSPSLDGDGRKKCL 1020
Db
QY 1021 ALVSLGEHPELRKSLIPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
Db
QY 1021 ALVSLGEHPELRKSLIPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
Db
QY 1081 HEMKSPPSARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERSLLSGEQESQ 1140
Db
QY 1081 HEMKSPPSARSPPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERSLLSGEQESQ 1140
Db
QY 1141 DEEESSEERASPAGSDHHRGSLEREAKSSFDLPDTLQVPLHRTASGRGSASEHQDCN 1200
Db
QY 1141 DEEESSEERASPAGSDHHRGSLEREAKSSFDLPDTLQVPLHRTASGRGSASEHQDCN 1200
Db
QY 1201 GKSASGRALARLPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260
Db
QY 1201 GKSASGRALARLPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260
Db
QY 1261 PQSRFLLCHRIITHKMFHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
Db
QY 1261 PQSRFLLCHRIITHKMFHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
Db
QY 1321 FLAEMTVKVALGWCFCGEQAVLRSSWNVDGLVLISVIDILVSMVSDSGTKILGMLRVL 1380
Db
QY 1321 FLAEMTVKVALGWCFCGEQAVLRSSWNVDGLVLISVIDILVSMVSDSGTKILGMLRVL 1380
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QY 1381 RLLRTLRLRVISRAOGLKLVVETLMSSLLKPIGNIWVICCAFFIIFGILGVQLFKGKFFV 1440
Db
QY 1381 RLLRTLRLRVISRAOGLKLVVETLMSSLLKPIGNIWVICCAFFIIFGILGVQLFKGKFFV 1440

QY 1441 CQGEDTRNITNKSDCAEASYSRWVRHKYNFNDLGOALMSLFLVASKDQGWVDIMYDGLDAVG 1500
Db
QY 1441 CQGEDTRNITNKSDCAEASYSRWVRHKYNFNDLGOALMSLFLVASKDQGWVDIMYDGLDAVG 1500
Db
QY 1501 VDQOPIMNHNPMWLLYFISFLLIVAFFVLNMFVGVVVFHFKCRQHQQEERARRREKRL 1560
Db
QY 1501 VDQOPIMNHNPMWLLYFISFLLIVAFFVLNMFVGVVVFHFKCRQHQQEERARRREKRL 1560
Db
QY 1561 RRLEKKR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITVIGLNVVTMAME 1613
Db
QY 1561 RRLEKKR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITVIGLNVVTMAME 1620
Db
QY 1614 HYQOPQILDEALKICNYIFTVIFVLESVFKLVAFGRFFQDRWNQDLAIIVLLSIMGIT 1673
Db
QY 1621 HYQOPQILDEALKICNYIFTVIFVLESVFKLVAFGRFFQDRWNQDLAIIVLLSIMGIT 1680
Db
QY 1674 LEEIEVNASLPINPTIIRIMRVRIARVLKLLKMAVGNRALLDTVMQALPQVGNLGLLFM 1733
Db
QY 1681 LEQIEVNASLPINPTIIRIMRVRIARVLKLLKMAVGNRALLDTVMQALPQVGNLGLLFM 1740
Db
QY 1734 LLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1793
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QY 1741 LLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1800
Db
QY 1794 LRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAELEAEL 1853
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QY 1801 LRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEAKEAELEAEL 1860
Db
QY 1854 ELEMKTLSPOPHSPGLSPFLWPVGEGPDSPPSKPGALHPAAHARSASHFSLEHPTMQPH 1913
Db
QY 1861 ELEMKTLSPOPHSPGLSPFLWPVGEGPDSPPSKPGALHPAAHARSASHFSLEHPTMQPH 1920
Db
QY 1914 PTELPGDLLTVRKSGVSRTHSLPNDNSYMCRHGSTAEGPLHGRGWGLPKAQSGSVLSVHS 1973
Db
QY 1921 PTELPGDLLTVRKSGVSRTHSLPNDNSYMCRHGSTAEGPLHGRGWGLPKAQSGSVLSVHS 1980
Db
QY 1974 QPADTSYILQLPKDAPHLLOPHSAPTWTGTPKLPGRSPPLAQRPLRRQAAIRTDSDLDVQ 2033
Db
QY 1981 QPADTSYILQLPKDAPHLLOPHSAPTWTGTPKLPGRSPPLAQRPLRRQAAIRTDSDLDVQ 2040
Db
QY 2034 GLGSREDLLAEVSGSPPLARAYSFWSGSTQAQHSRSHSKISHKMTPPAPCPGPEPNW 2093
Db
QY 2041 GLGSREDLLAEVSGSPPLARAYSFWSGSTQAQHSRSHSKISHKMTPPAPCPGPEPNW 2100
Db
QY 2094 GKGPPETRSSLELDELTELSSWISGDLPPGQEEPPSPRDLKKCYVSAQSCQRRPTSWLDE 2153
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QY 2101 GKGPPETRSSLELDELTELSSWISGDLPPGQEEPPSPRDLKKCYVSAQSCQRRPTSWLDE 2160
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QY 2154 QRRHSIAVSCLDSSQPHLGTDPNSNLGGQPLGGSRPKKLSPPSITIDPPESQGPRT 2213
Db
QY 2161 QRRHSIAVSCLDSSQPHLGTDPNSNLGGQPLGGSRPKKLSPPSITIDPPESQGPRT 2220
Db
QY 2214 PSPGICLRRRAPSSDSKDPLASGPPDMSMAASPSPKDVLSSLSSDPADLDP 2266
Db
QY 2221 PSPGICLRRRAPSSDSKDPLASGPPDMSMAASPSPKDVLSSLSSDPADLDP 2273

RESULT 2
US-09-398-522-52
; Sequence 52, Application US/09398522
; Patent No. 6783933
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNAIG POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/09/398,522
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1207
; TYPE: PR

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CACNA1G - a gene ecoding a T-type calcium channel
US-09-398-522-52

Query Match 53.1%; Score 6315.5; DB 4; Length 1207;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1207; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

QY 1 MDEEEDGAGAEESGQPRSFMRNLNLSGAGRPGPGSAEKDPSADSEAEGLPYPALAPVV 60
Db 1 MDEEEDGAGAEESGQPRSFMRNLNLSGAGRPGPGSAEKDPSADSEAEGLPYPALAPVV 60

QY 61 FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLGMFRPCEDIAQDSQRCRILQAF 120
Db 61 FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLGMFRPCEDIAQDSQRCRILQAF 120

QY 121 DDFIFAFFAVEMVVMVALGIFGKKCYLGDWTNRDLFFIVIAGMLEYSLDLQNVFSFSAVR 180
Db 121 DDFIFAFFAVEMVVMVALGIFGKKCYLGDWTNRDLFFIVIAGMLEYSLDLQNVFSFSAVR 180

QY 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Db 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240

QY 241 CFLPENFSLPLSVDLERYQTENEDESPFICSPRENGMRSCRSVPTLRGDGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYQTENEDESPFICSPRENGMRSCRSVPTLRGDGGGPPCGL 300

QY 301 DYEAYNSSNTTTCVNNQYVYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360
Db 301 DYEAYNSSNTTTCVNNQYVYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360

QY 361 YFVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQRESQMLREQVRFLSNA 420
Db 361 YFVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQFSETKQRESQMLREQVRFLSNA 420

QY 421 STLASFSEPGSCVEELLKYLVIYILRKAARLAQVRAAGVRVGLLSSPAPLGGQETQPS 480
Db 421 STLASFSEPGSCVEELLKYLVIYILRKAARLAQVRAAGVRVGLLSSPAPLGGQETQPS 480

QY 481 SCSRRHRLSVHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db 481 SCSRRHRLSVHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP 540

QY 541 ALSGAPPGABSVHSFYHADCHLEPVRCAQPPRSPSEASGRVSGKVYPTVHTSPPE 600
Db 541 ALSGAPPGABSVHSFYHADCHLEPVRCAQPPRSPSEASGRVSGKVYPTVHTSPPE 600

QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660

QY 661 ACGPDSCTPCARAGAGEVELADREMPDSDSEAVYEFTQDQHSDLRDPHSRRQRSLGPDA 720
Db 661 ACGPDSCTPCARAGAGEVELADREMPDSDSEAVYEFTQDQHSDLRDPHSRRQRSLGPDA 720

QY 721 EPSSVLAFWRLLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780
Db 721 EPSSVLAFWRLLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780

QY 781 VFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVSVWEIVGQGGGLSVLRTFRLMR 840
Db 781 VFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVSVWEIVGQGGGLSVLRTFRLMR 840

QY 841 VLKLVRLPALQRLVLMKTMNDNVATFCMLLMFIFIFSILGMHLFGCKFASERDGDTL 900
Db 841 VLKLVRLPALQRLVLMKTMNDNVATFCMLLMFIFIFSILGMHLFGCKFASERDGDTL 900

QY 901 PDRKNFDSLLWAIIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNVVLFNLLV 960
Db 901 PDRKNFDSLLWAIIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNVVLFNLLV 960

QY 961 AILVEGFQAEELISKREDASGQLSCIQLPVDVSQGGDANKSESEDPFFSPSLDGDGRKKCL 1020
Db 961 AILVEGFQAE-----GDANKSESEDPFFSPSLDGDGRKKCL 997

QY 1021 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
Db 998 ALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1057

QY 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEQESQ 1140
Db 1058 HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEQESQ 1117

QY 1141 DEESSEERASPGSDHRRHRSGLEREAKSSFEDLPDITLQVPLHRTASGRGSAEHQDCN 1200
Db 1118 DEESSEERASPGSDHRRHRSGLEREAKSSFEDLPDITLQVPLHRTASGRGSAEHQDCN 1177

QY 1201 GKSASGRLARALRPDDPPLDGDADDDEGNL 1230
Db 1178 GKSASGRLARALRPDDPPLDGDADDDEGNL 1207

RESULT 3
US-08-984-709A-50
; Sequence 50, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,709A
; FILING DATE: 02-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 587-5360
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2353 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-984-709A-50

Query Match 52.2%; Score 6211; DB 3; Length 2353;
Best Local Similarity 56.6%; Pred. No. 0;
Matches 1365; Conservative 214; Mismatches 523; Indels 310; Gaps 60;

QY 7 GAGAEESGQP-RSFMRLNLSGAGRPGPGSAEKDPSADSEAEGLPYPALAPVVFFYLS 65

Db 27 GASPSPGAPGREAERGSEL-GVSPSESP-AAERGAELGADEEQRVFPALAAATVFFCLG 84
QY 66 QDSRPRSCLRTVCNPNWFERISMLVILLNCVTILGMPERPCEDIAQDSQRCRIILQAFDDFIF 125
Db 85 QTRRPRSCLRLVCNPNWFEHVSMVLVIMLNCVTILGMPERPCEDVECGSERCNILEAFDAFIF 144
QY 126 AFFAVEMVVMKVALGIFGKKCYLGDWTNRLLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRVL 185
Db 145 AFFAVEMVIMKVALGLFGQKCYLGDWTNRLLDFFIVVAGMWEYSLDGHNVSLSAIRTVRVL 204
QY 186 RPLRAINRVPSMRILVTLTLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNCFLPE 245
Db 205 RPLRAINRVPSMRILVTLTLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNCFLDS 264
QY 246 NFSPLPLSVD-LERYYQTENEDESPFICSQPRENGMRSCRVP---TLRGDGGGGPPCGLD 301
Db 265 AFVRNNLTFLRPYYQTEEGEENPFICSSRRDNGMQKCSHIPGRREL- ----MPCTLG 318
QY 302 YEAYN-----SSNTTCVNWNQYYTNCSEAGHNPFKGAJNFDNIGYAWIAIFQVITLE 354
Db 319 WEAYTQQAEGVGAARNACINWNQYYNVCRSGDSNPHNGAINFDNIGYAWIAIFQVITLE 378
QY 355 GWVDIMYFVMDAHSFYNIYFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQRV 414
Db 379 GWVDIMYFVMDAHSFYNIYFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQRA 438
QY 415 RFLSNASTLASFSEPGSCYEELLKYLVLILKAARRLAQVSRAGVVRVGLLSSPAPLGGQ 474
Db 439 RHLSDNSTLASFSEPGSCYEELLKYVGVHIFRKVKRRSLRLYARWQSRWRKKVDPSPAVQOQ 498
QY 475 ETQPSSSCSRSHRR-LSVHLV-HHHHHHHHHVHLNGTTLRAPRASPEIQDRDANGSRL 532
Db 499 --GPGHRQRRAGRHTASVHHLVYHHHHHHHHYHSHGSPRRPGPEGCAD-----TRLV 551
QY 533 MLPPPSTPALSGAPPGGAESVHSFYHADCHLE--PVRQAPPPRSPSEASGR-TVGSGKV 589
Db 552 RAGAPSPSPGRRGPPDAESVHSIYHADCHIEGQERARVAHAATAAASRLATGLGTM 611
QY 590 -YPTV-----HTSP-----PPETLKEKALVEVAASSGPPTLTSLNIPPGPY 629
Db 612 NYPTILPSGVGSGKGSTSPGPKGWAGPPGT-----GGHGPLSLNS-----PDY 657
QY 630 SSMHKLLETQSTGACQS-----SKSISSPCLKADSGACGPDSCPYCARA-GAGEVELA 681
Db 658 EKIPHVVEHGLGQAPGHLGSLVPCPLPSP--PAGTILTELKSCPYCTRALDPEGELS 715
QY 682 DREMPDSSEAVYEFTQDAQHSDLRDP-----HSSRQORSLGPDAPSSV 725
Db 716 GSESGDSGRGVYEFTQDVRHGDRWDTPRPRATDTPGPGPGSPORRAQQAAPGEPGWM 775
QY 726 LAFWRLICDTPFRKIVDSKYFGRGIMAILVNTLSMGIEYHQPEELTNALEISNIVFTSL 785
Db 776 GRLWVTFSKLRRIIVDSKYFSRGIMAILVNTLSMGVEYHQPEELTNALEISNIVFTSM 835
QY 786 FALEMILLKLVVGPFGYIKNPYNIYFDGVIIVISVWEIVGQCGGLSVLRTFRLMRVLKIV 845
Db 836 FALEMILLKLLACGPLGIYRNPYNIYFDGVIIVISVWEIVGQADGGLSVLRTFRLLRVLKIV 895
QY 846 RFLPALQRLVLMKTMNDNVATFCMLMLFIFIFSILGMHIFGCKFASERD-GDTLPDRK 904
Db 896 RFLPALRRQLVVLVKTMDNVATFCTLLMLFIFIFSILGMHIFGCKFSLKTDGTGTVDRK 955
QY 905 NFDLSLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAILV 964
Db 956 NFDLSLWAIIVTFQILTQEDWNVLYNGMASTSSWAALYFVALMTFGNYVLFNLLVAILV 1015
QY 965 EGFQAEISKREDASGQLSCIQLPVDVDSQGGDANKSESEPDFFSPSLDGD-----GD 1015
Db 1016 EGFQAE-----GDANRSDTDEKTSVHFEEDFHKLRELQTE 1052
QY 1016 RKKCLALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSA 1075

Db 1053 LKMCSLAVTPNGHLEGRGSLSPPLIMCTAATPMPTPKSSPFLDAAPSLPDSRRRGSSSGD 1112
QY 1076 EPGAHEMKSPPSARSSPHSPWSAASSWTSSRSNSLGRAPSLKRRSPSGERRSLLSGE 1135
Db 1113 PP--LGDQKPPASLRSSPCAPWPGSGAWSSRRSSWSLGRAPSLKRRGQCGERESLLSGE 1170
QY 1136 GQESQDEESESSEERASPA--GSDHRHRGSLEREAKSSFDLPDTL-----QVPGLH--- 1184
Db 1171 KGKSTDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPTKCRDRDQGVVALPSDF 1228
QY 1185 --RTASGRGSASEHQDCNGKSASGRLARALRPDDPPLDGDADDEGNLSKGERVAVIRA 1242
Db 1229 FLRIDSHREDAEAELDDSDSDSCCLRLHKVLEPKP-----QWCRS 1268
QY 1243 RLPACYLERDSWYIFPPQSRFRLLCHRIITHKMFHVVVLVIIFLNCITIAMERP KIDP 1302
Db 1269 -----PEAWALYLFSPQNRFRVSCQKVIITHKMFHVVVLVIFLNCVTIALERPDIDP 1320
QY 1303 HSAERIFLTLNYSIYFTAVFLAEMTVKVVALGWCFCGEAYLRSWNVLDGLLVLSVIDIL 1362
Db 1321 GSTERVFLSVSNYIFTAIFVAEMVMKVVALGLLSGEHAYLQSSWNLLDGLLVLSVLDIV 1380
QY 1363 VSMVSDSGTKILGMLRVLRLLRTRLPLRVISRAOGLKLVVETIMSSLKPIGNIVVICAF 1422
Db 1381 VAMASAGGAKILGVLRVLRLLRTRLPLRVISRAPGLKLVVETLSSLRPIGNIVLICAF 1440
QY 1423 FIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYSRWRHXYKYNFDNLGQALMSLFLV 1482
Db 1441 FIIFGILGVQLFKGKFFYCEGPDTRNISTKAQCRAAHYRWRKYNFDNLGQALMSLFLV 1500
QY 1483 ASKDGWVDIMYDGLDAVGVDQOPIMNHNPMMLLYFISFLLVIAFFVLNMFVGVVVENFHK 1542
Db 1501 SSKDGWVNIYDGLDAVGVDQOPVQNHNPWMLLYFISFLLVISFFVLNMFVGVVVENFHK 1560
QY 1543 CRHQEEEEARRREEKRLRLEKKR-----KAQCKPYSDYSRERLLVHHLCTSHYLD 1596
Db 1561 CRHQEAEEARRREEKRLRLERRRSTFPSPQAQRPPYADYSPTRRSIHSLCTSHYLD 1620
QY 1597 LFTGVIGLVNVTMAMEHYQQPQILDEALKICNVITVIFVLESVFKLVAFGRFRFFQDR 1656
Db 1621 LFTFIICNVITMSMEHYNQPKSLDEALKYCNVYFTIVFVFEAALKLVAFGRFRFFKDR 1680
QY 1657 WNQDLAIVLLSIMGITLEIEVNASLPPINPTIIRIMRVLRIARVLKLLKMAVGMRALLD 1716
Db 1681 WNQDLAIVLLSLMGITLEIEIEMSAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLD 1740
QY 1717 TVMQALPQVGNLGLLFFLFFIPAALGVLEFGDLECDETHPCCEGLGRHATERNFGMAFLT 1776
Db 1741 TVVQALPQVGNLGLLFFLFFIYAALGVLEFGRLCEDSNPCEGLSRHATFSNFGMAFLT 1800
QY 1777 LFRVSTGDNWNGIMKDTLRDC--DQESTCYNTVTSPIYFVSFVLTAQFVLNVVIAVLM 1833
Db 1801 LFRVSTGDNWNGIMKDTLRCSREDKHLCLSYLPALSPYFVTVFVLVAQFVLNVVVAVLM 1860
QY 1834 KHLEESNKEAKEAEAELEAELEBMKTLSPQPHSPLGSPFLWPGVEGPDSP---DSPKPGA 1890
Db 1861 KHLEESNKEAREDAELDAEIELEM-----AQGPSARRVDADRP-- 1899
QY 1891 LHPAAHARSASHFSLEHPTMQPHPTLP-----PDLLTVRKSGVSRTHSLPNDSYMCRHG 1946
Db 1900 -----PLPQESPGARDAPNLV-ARKVSVSRMLSLPNDSYMFRPV 1937
QY 1947 STAEGP-----LGHRGWGLPKAOSGVSLSVHSQPADTSYILQLPKDAPHLLQPHSA 1997
Db 1938 VPASAPHPRPLQEVEMETYGAGTP---LGSVASVHSPPAESCASLQIP-----LAVSSPA 1989
QY 1998 PTWGTIPKLPPPG--RSPLAQRPRLRQAAIRTDSDLVQGLSGREDLL--AEVSGPSP--P 2051
Db 1990 RSGEPLHALSPRGTAARSPSLRLLCRQEAHVHTDSLEKG-IDSPRDTLDPAPGKTPVRP 2048
QY 2052 LARAYSFWG--QSTQAAQHRSRSHSKISHMTTPAP-CPGPEPNWGKPPETRSSLELDT 2108
Db 2049 VTQGSLSQSPPRSPPASVRTRKHT-FGQHCVSRRPAAFGGE-----EAEASDPADE 2099

Qy	2109	ELSWISGDLLP-----PGQEEPP---SPRDLKKCYSEVAQSCQRRPTSWLDEQRHSI	2159
Db	2100	EVSHITSSACPWQTAAPHGPEASPVAGGERDLRLLYSDVAQGFLDKP-GRADQWRPSA	2158
Qy	2160	AVSCLDSGSQPHLGTDPNSNLGGQPLGGPGRPKKLSPSITIDPP-ESQGPRTPPSP--	2216
Db	2159	ELSGEPGEAKAWGE-----AEP--ALGARRKKNSPPCISVEPPAEDEGSARPSAAEG	2211
Qy	2217	-GICLRRRAPSSDSK-----DPLASGPPDSMAASPSPKDVLSLSLGLSS	2259
Db	2212	GSTTLRRRTPSCEATPHRESLEPTEGSGAGGDPAAKGERWGQA---SCRAEHLTVPSFAF	2268
Qy	2260	DPADL-----DP	2266
Db	2269	EPLDLGVPSGDP	2280

```

RESULT 4
US-09-404-650-2
; Sequence 2, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-650-2

```

Query Match	46.1%	Score 5492.5	DB 3	Length 2175
Best Local Similarity	51.3%	Pred. No. 0		
Matches 1233	Conservative 214	Mismatches 508	Indels 447	Gaps 55
QY	31	RPGPSAEKDPGSADSEAG----	LPYPALAPVVFYLSQDSRPSRWCLRTVCNPFERI	86
Db	25	QGPGRSPSPSGLEELPDGADPHVHPDLAPIAFFCLRQTTSRNCWKIMVCNPFECV	84	
QY	87	SMLVILLNCVTILGMRPCEDIAQDSQRCRILQAFDDIFAFFAVEMVVKMVALGIFGKKC	146	
Db	85	SMLVILLNCVTILGMYQPCDDMDCLSDRCKILQVEDDFIFIFFAMEMVLKMAVGIFGKKC	144	
QY	147	YLGDTWNRLLDFFIVIAQMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLD	206	
Db	145	YLGDTWNRLLDFFIVMAGMVEYSLDLQINILSAIRTVRVLRPLKAINRVPSMRILVNLLLD	204	
QY	207	TPLMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSLPLSVDLERYYQTENEDE	266	
Db	205	TPLMLGNVLLLCFFVFFIFGIIIGVQLWAGLLNRNRCFLEENFTIQGDVALPPYQPEEDE	264	
QY	267	SPFICSQPRENGMRSCRSVPTRLRGDGGGPPCGL-----DYEAYNSSNTT--CVNWNQ	318	
Db	265	MPFICSLSGDNGIMGCHEIPLKEQ---GRECCLSKDDVDFGAGRQDLNASGLCVNWNR	321	
QY	319	YYTNCSGAHEHNPFGAINFEDNIGYAWIAIFQVITLEGWDIMYFVMDAHSFYNFIFYILL	378	
Db	322	YYNVCRTGSANPHKGAINFDNIGYAWIVFQVITLEGWVEIMYVMDAHSFYNFIFYILL	381	
QY	379	IIVGSFFMINLCLVVIATQFSETKQRESQLMRQORVRFLSNASTLASFSEPGSCYEELLK	438	
Db	382	IIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLS--SSTVASYAEPGDCYBEIFQ	440	
QY	439	YLVYLIRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRHRRLSVHHLVHHH	498	
Db	441	YVCHILRKAKR-----RALGLYQALQSRRAQALG-----	468	

QY 1521 LLIVAFVLMFVGVVVENFHKCRQHQQEAEARRREKRLRRLEKKRRKAQCKPYYSDYS 1580
Db 1380 LLIVSFFVLMFVGVVVENFHKCRQHQQEAEARRREKRLRRLEKKRRKAQRLPYATYC 1439
QY 1581 RFRLLVHLCTSHYLDLFTIGVIGLVNVTWAMEHYQQQILDEALKICNYIFTVIFVLES 1640
Db 1440 HTRLLIHSCTSHYLDIFITFIICLVNVTMSLEHYNQPTSLETALKYCNMFTTVPVLEA 1499
QY 1641 VFKLVAFGRRFQDRWNQDLDAIVLLSIMGITLEEIEVNASLIPNPTIIRIMRVLIAR 1700
Db 1500 VLKLVAFGLRRFFKDRWNQDLDAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLIAR 1559
QY 1701 VLKLLKMAVGMRALLDTVMQALPOVGNLGLLFWLLFFIFAALGVLEFGDLECDETHPCBG 1760
Db 1560 VLKLLKMATGMRALLDTVVQALPOVGNLGLLFWLLFFIYAALGVLEFGKLVNDENPCBG 1619
QY 1761 LGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV 1817
Db 1620 MSRHATFENFGMAFLTFRVSTGDNWNGIMKDTLRDCTHDSRCLSLQFVSPLYFVSFV 1679
QY 1818 LTAQFVLNVVIAVLMKHLEESNKEAEAELEAELEEM-KTLLSPQHSPLGSPFLWPG 1876
Db 1680 LTAQFVLINVVAVLMKHLDDSNKEAQEDAEMDAELEMAHGLGPGRLPTGSPGA-PG 1738
QY 1877 VEGPDSPD-----SPKPGAL-----HPAAHA----- 1897
Db 1739 -RGPAGAGGGDTGGLCRRCYSPAQDSLEGELTIIDNLSGSIFFHYSSPAGCKKCHDK 1797
QY 1898 -----RSAS-----HFSLEHPTMQP-----HPTELPGPDLTLVRKSG-- 1929
Db 1798 QEVQAEAFSLNSDRSSILLGDDLSLEDTACPPCRKDSKGELDPPEPMRVGDLGEC 1857
QY 1930 ---VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLP 1985
Db 1858 FFPLSTAVSPDPENFLCEMEEIPFPNV--RSW--LKHDSSQAPSPSPDASSPLPMP 1913
QY 1986 KDAPH-----LLQPHSAPTWTGTPKLP--RSLAQRPLRROAAIRTDSDVQG 2034
Db 1914 AEFFHPAVSASQKPEKGTGTGLPKIALQGSWASLRSRPNCTLLRQATGSDTSLD--- 1970
QY 2035 LGSREDLLAEVSGSPPLARAYSFWGQSSTQAQHSRSHSKISKHMTPPAPCPGEPNMG 2094
Db 1971 -----ASPSSAGSLQTTLEDSLTSDSPRRA-----LGPPAPAPGPRAGLS 2012
QY 2095 KGPETRSLELDTLSWISGDLPLPGGQEBPPSPRDLKKCVSVEAQSCQRRPTSWLDEQ 2154
Db 2013 ---PAARRLSL-----RGRGLFSLRLRA-----HQ 2036
QY 2155 RHHSIAVSCLDGSGQPHLGTDPN---LGQPLGGPGSRPKKLSPPSIT---IDPPESQ 2208
Db 2037 RSHSSGGS-TSPGCTHDSMDPSDEEGRGAGGGAGSEHSETLSLSLTSLFCPPP--- 2092
QY 2209 GPRTPPSPGICLRRAPSSDS-----KDPLASGPPDSMAASPSPKDVLSLSGLSSDPADL 2264
Db 2093 ---PPPAPGLTPARKFSSSTSLAAGRPHAAALAHGLARSPSWAAD-----RSKDPFGR 2143
QY 2265 DP 2266
Db 2144 AP 2145

RESULT 5
US-09-935-541-2
; Sequence 2, Application US/099335541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175.
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-541-2

Query Match 46.1%; Score 5492.5; DB 4; Length 2175;
Best Local Similarity 51.3%; Pred. No. 0;
Matches 1233; Conservative 214; Mismatches 508; Indels 447; Gaps 55;

QY 31 RPPGSAEKDPGSADSEAEAG---LPPALAPVVFFYLSQDSRPSWCLRTVCNPFERI 86
Db 25 QPGRSPSPSPGLEEPLDGADPHVPHDLAPIAFFCLRTSPRNWCIKMWCNPFECV 84
QY 87 SMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVMVALGIFGK 146
Db 85 SMLVILLNCVTLGMVQPCDDMDCLSDRCKILQVDFDFIFIFFAEMVLMVALGIFGK 144
QY 147 YLGDWTNRLDFFIVTAGMLEYSLDLQNVFSAVRTVRVLRPLRAINRVPSMRILV 206
Db 145 YLGDWTNRLDFFIVMAGWVEYSLDLQINLSAIRTVRVLRPLKAINRVPSMRILV 204
QY 207 TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCFLPENSLPLSVDLERYYTENE 266
Db 205 TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCFLPENFTIQGDVALPPYQPEED 264
QY 267 SPFICSPQPRENGMRSCRSVPTLRGDGGGPPCG---DYEAYNSSNTT--CVNWNQ 318
Db 265 MPFICSLSGDNGIMGCHEIPLKEQ---GRECCSKDDVDYDFGAGRQDLNASGLCV 321
QY 319 YNTNCSAGEHNPFGAINFDNIGYAWIAIQVITLEGWVDIMYFVMDAHSFNFYIFILL 378
Db 322 YNVNCTGSANPHKGAINFNDNIGYAWIVIFQVITLEGWVEIMYVMDAHSFNFYIFILL 381
QY 379 IIVGSFFMNLCLVVIATQFSETKQRESQLMREQRVFLSNASTLASFSEPGCYEELLK 438
Db 382 IIVGSFFMNLCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYEEIFQ 440
QY 439 YLVYILRKAARLQAQVSRAAGVRVGLLSPPAPLGGQETQPSSSCSRSHRRLSVH 498
Db 441 YVCHILRKAKR-----RALGLYQALQSRQALG----- 468
QY 499 HHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPSPALSGAPPGAESVHSFYH 558
Db 469 -----PEAPA--PAKEGP-----H 480
QY 559 ADCHLEPVRCQAPPPRSPSEASGRVTGSGKVYPTVHTSPPPETLKEKALVEVAASGPPT 618
Db 481 AK--EPRHYQLCPQHSPLDATPHTL-----VQPIPAIL----- 511
QY 619 LTSLNIPPGPYSSMHKLLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR----- 672
Db 512 -----ASDPASCPCCQHEDGRRP 529
QY 673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDDLDPHSRRQRSLGPDAPSSVL----- 726
Db 530 SGLGSTD-SGQEGSGSGSSAGGE--DEADCGDARSSSEDGASSELGKEEEEEQADGAVWL 586
QY 727 --AFWRLLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFTS 784
Db 587 CGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNALEICNVVFTS 646
QY 785 LFALEMLLLKLLVYGPFGYIKPNYINFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKL 844
Db 647 MFALEMILKLAAGLFDYLRPNYINFDISIIVISIWEIVGQADGGLSVLRTFRLLRVLKL 706
QY 845 VRFLPALQRLVLMKTMNDVATFCMLLLMFLFIFISILGMHLFGCKFASERD-GDTLPDR 903
Db 707 VRFMPALRRQLVLMKTMNDVATFCMLLLMFLFIFISILGMHIFGCKFSLRTDGTVPDR 766

QY	904	KNFDSLLWAI	VTFQIL	TQEDWNKVL	YNMGASTSSWAALFYIALMTFGNYVLFNLLVAIL	963
Db						
Db	767	KNFDSLLWAI	VTFQIL	TQEDWNVVL	YNMGASTSPWASLYFVALMTFGNYVLFNLLVAIL	826
QY	964	VEGFOAEEI	SKREDASQL	SCIQLPVD	SQGKDANKSESEPDPFPSPS-----LDGD	1013
Db	827	VEGFOAE	-----	-----	-----GDANRSYDEDOSSSIEEFDKLQEGLDSS	863
QY	1014	GDRKKCLAL	VSUGEHP	ELRKSLLPPLI	IHTAATPMSLPKSTSTGLGEALGPASRRT----	1069
Db	864	GDPKLCPI	PMTPNH-	-----LDP	-----SLPLGGHLGPAGAAGPAPRLSLQPDP	906
QY	1070	-----	SSSGSAEPGA	AHEMKSPPSARSSPHSPWSAASSWT	SRSSRNLSLRAPSCLK	1120
Db	907	PMLVALGRK	SSVMSLGRMSYDQR	SSLSSRSSYYGPGWGRAAWASRRSWN-----	SLK	960
QY	1121	RRSPSGERR	SLLSGE-QGESQDBESSEE--ERASPAGSDH-----	RHRG	1162	
Db	961	HKPPSAEHES	LlsaERGgGARvCEVAADegPPRAAPLHtPhAHIIHHGPHLAHRHRHRR	1020		
QY	1163	SLREAKSSF	DLPTLTQVPGLHRTASGR--GSASEHQDCNGKSASGRLARALRPDDPPLD	1220		
Db	1021	TLSDLNRDS	VSDLAELVPAVGHPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMGRGDR	1080		
QY	1221	GDADDEGNL	SKGERVRAMTRARLPACYLERSWSAVIFPPQSRFRLLCHRIITHKMFHDH	1280		
Db	1081	GED-EEEIDY	TLCFVRVKMIDVYPDWCEVEDWSVLFSPENRFRVLCOTIAHKLFDY	1139		
QY	1281	VVLVIIFLNC	ITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFFEQA	1340		
Db	1140	VVLAFIFLNC	ITALERPQIEAGSTERIFLTVSNIYFTAIFVGEMTKVVSGLYFFGEQA	1199		
QY	1341	YLRSSWNVL	DGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLRTLRLPLRVISRAOGLKL	1400		
Db	1200	YLRSSWNVL	DGFLVFYSIIDIVWSLASAGGAKILGVRLVRLRLRTLRLPLRVISRAPGLKL	1259		
QY	1401	VVETLMSSL	KPIGNIVVICCAFFIIFGILGVQLFKGKFVCQGEDTRNITNKSDCAEASY	1460		
Db	1260	VVETLISSL	KPIGNIVLICCAFFIIFGILGVQLFKGFHYHCLGVDTNRNITNRSDCMAANY	1319		
QY	1461	RWRHKYNFN	DNLGOALMSFLVASKDGWDIMYDGLDAVGVDQQPINHNPNWMLLYFISF	1520		
Db	1320	RWHHKYNFN	DNLGOALMSFLVASKDGWVNIMYNGLDAVADQQPVTHNPWMLLYFISF	1379		
QY	1521	LLIVAFFVL	NMFVGVVVNFHCKROHQEEEEARRREEKRRLRLEKKRRKAQCKPYYSDES	1580		
Db	1380	LLIVSFFVL	NMFVGVVVNFHCKROHQEAEEARRREEKRRLRLEKKRRKAQRLPYAYATYC	1439		
QY	1581	RFRLLVHHL	CTSHYLDLFI	TGVIGLVNVVTNAMEHYQQPILDEALKICNYIFTVIVFVLES	1640	
Db	1440	HTRLIIHSM	CTSHYLDIFITFIICLVNVVTMSLEHYNQPTSLETALKYCNMYFTTVFVLEA	1499		
QY	1641	VFKLVAFGR	FRRFFQDRWNQLDLAI	VLLSIMGITLEEIEVNASLIPINPTTIIRIMRVLRIAR	1700	
Db	1500	VKLVAFLGR	FRFFKDRWNQLDLAI	VLLSVMGITLEEIEINAALPINPTTIIRIMRVLRIAR	1559	
QY	1701	VLKLLKMAV	GMRALDITVMOALPOVGNLGLLFM	LLFFIFAALGVLEFGDLECDETHPCEG	1760	
Db	1560	VLKULKMAT	GMRALDITVVQALPOVGNLGLLFM	LLFFIYAALGVLEFGKLCVNDENPCEG	1619	
QY	1761	LGRHATERFN	FGMAFLTILFRVSTGDNWNGIMKOTLRDC-DQESTCYNTV--ISPIYFVSFV	1817		
Db	1620	MSRHATERFN	FGMAFLTILFQVSTGDNWNGIMKOTLRDCTHDERSCLSLQFVSPLYFVSFV	1679		
QY	1818	LTAQFVLNV	VVIAVLMKHLEESNKEAKEBAELEAELELEM-KTLSQPSPHSPGPFWPWG	1876		
Db	1680	LTAQFVLINV	VVAVLMKHLDDSNEKAQEDAEMDAELELEMAHGLGPGPRLFTGSPGA-PG	1738		
QY	1877	VEGPDSPD	-----	--SPKPGAL-----HFAAHA-----	1897	
Db	1739	-RGPGAGGG	GTTEGGLCRRCYSPAQDSLEGELTIIDNLGSIHFHYSSPAGCKKCHDK	1797		

QY	1988	-----RSAS-----HFSLEHPTMQP-----HPTELPGPDLITVRKSG--	1929
Db	1798	QEVQLAETEAFSLNSDRSSILLGDDLSLEDPTACPGRKDSKGELDPPEPMRVGDLGEC	1857
QY	1930	---VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLP	1985
Db	1858	FFPLSSTAVSPDPENFLCEMEEIPFNPV--RSW--LKHDSSQAPPSPSFDDASSPLLPMP	1913
QY	1986	KDAPH-----LLQPHSAPTWTGIPKLPPLPG-----RSPLAQRPLRQAAIRTDSDLVQG	2034
Db	1914	ABFFHPAVSASQKGEKGTGTLPKIALQGSWASLRSRPNCTLLRQATGSDTSLD---	1970
QY	2035	LGSREDLLAEVSGPSPPLARAYSFWQSSITQAQHSRSHSKI SKHMTTPAPCPGPEPNWG	2094
Db	1971	-----ASPSAGSLQTTLEDSTLSDSPRRA-----LGPPAPAPGPRAGLS	2012
QY	2095	KGPPETRSSLLELDTLSWISGDLPLPGGQHEPPSPRDLKKCYSEVAQSCQRRPTSWLDEQ	2154
Db	2013	---PAARRRLSL-----RGRGLFSLRGLRA-----HQ	2036
QY	2155	RRHSIAVSLDGSQPHLGTDPN---LGGQPLGGPGSRPKKLSPPSIT---IDPPESQ	2208
Db	2037	RSHSSGGS-TSPGCTHDSMDPSDEEGRGAGGGAGSEHSETLSLSLTSLFCPPP---	2092
QY	2209	GPRTPPSPGICLRRRAPSSDS---KDPLASGPPDMSMAASPSKKDVLSSLGLSSDPADL	2264
Db	2093	---PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD-----RSKDPPGR	2143
QY	2265	DP	2266
Db	2144	AP	2145

RESULT 6

US-09-404-650-4

; Sequence 4. Application IIS/09404650

; Patent No. 6309858

GENERAL INFORMATION:

APPLICANT: Dietrich. paul s.

APPLICANT: McGovern. Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL. VARIANTS. COMPOSITIONS. METHODS

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/404.650

; CURRENT FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Pat

; SEQ ID NO 4

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; LENGTH: 2
; TYPE: FREE

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; TYPE: PRT
; OPERATOR: TYPE

```

; ORGANISM: H
IIS-09-404-CEC 4

Query Match 46.1%; Score 5484; DB 3; Length 2188;
Best Local Similarity 51.4%

31 PRCPCGCEYVDPCCACDCEPC

87 31 RFGGSAENDFGSAUSEAEG-----LPYPALAPVFFYLSQDSRPSRWCLRTVCNPWFERI

QY
87 SMLVIIJNCVTI.GMERPCEDTACDSORCETI.CAERDCEPACBCTE

67 S...E...L...A...C...V...I...E...M...F...R...E...C...D...I...A...C...S...Q...R...C...R...I...L...Q...A...F...D...D...F...I...F...A...F...F...A...V...E...M...V...K...W...A...L...G...I...F...G...K...K...C...140

QY 147 YLGDTWNRLLDFFI VIAGMLEYSLDLONVSFSAVRTVPVI.PPI PAINRYDQMBTTTTTTTTT

[illegible]

QY 207 TPLMGNVLLCFFVFFIFGI VGVOLWAGLLRNRCFT.PENESL.PI.SYDI.FP.VVYOTNEDE 200

[illegible]

QY 267 SPFICSPRENGMRSCRSVPTLRDGGGGPPCGL-----DYEAYNSSNTT--CVNWNQ 318
Db 265 MPFICSLSGDNGIMGCHEIPLKEQ---GRECCLSKDDVDFGAGRQDLNASGLCVNWR 321
QY 319 YYTNCSSAGEHNPFGAINFDNIGYAWIAFQVITLEGWVDIMYFVMDAHSFYNFYFILL 378
Db 322 YYNVCRGTSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYVMDAHSFYNFYFILL 381
QY 379 IIVGSFFMINCLVVIATQFSETKQRESQIMREQVRFLSNASTLASFSEPGSCYEELLK 438
Db 382 IIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQYLS-SSTVASYAEPGDCYEETIQ 440
QY 439 YLVYILRKAARLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHH 498
Db 441 YVCHILRKAKR-----RALGLYQALQSRQALG----- 468
QY 499 HHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSAGAPPGAESVHSFYH 558
Db 469 -----PEAPA--PAKPGP-----H 480
QY 559 ADCHLEPVRCQAPPPRSPSEASGRTVGSKVYPTVHTSPPPETLKEKALVEVAASSGPPT 618
Db 481 AK--EPRHYQLCPQHSPLDATPHTL-----VQIPATL----- 511
QY 619 LTSLNIPPGPYSSMHKLTQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR----- 672
Db 512 -----ASDPASCPCCQHEGDRRP 529
QY 673 AGAGEVELADREMFDSDSEAVYEFQTQDAQHSDLRDPHSRRQRSLGPDAPSSVL----- 726
Db 530 SGLGSTD-SQEGSGSGSSAGGE--DEADGDGARSSEDDGASSELGKEEEEBEQADGAVWL 586
QY 727 --AFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALIEISNIVFTS 784
Db 587 CGDVWRETRAKLRGIVDSKYFNEGIMMAILNVTSMGIEHHEQPEELTNILEICNVVFTS 646
QY 785 LFAEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRIMRVLKL 844
Db 647 MFAEMILKLAAGLFDYLRNPYNIFDSIIIVIISIWEIVGQADGGLSVLRTFRLLRVLKL 706
QY 845 VRFLPALQQLVVLMTMDNVATFCMLLMFIFIFISILGMHLFGCKFASERD-GDTLPDR 903
Db 707 VRFPALRQLVVLMTMDNVATFCMLLMFIFIFISILGMHLFGCKFSRLRTDGTIVPDR 766
QY 904 KNFDSLLWALVTVFQILTQEDWNKVLYNGMASTSSWAALPIALMTFGNVVLENLVAIL 963
Db 767 KNFDSLLWALVTVFQILTQEDWNVLYNGMASTSPWASLVFVALMTFGNVVLENLVAIL 826
QY 964 VEGFOAEIISKREDASQLSCIQLPVDSQGDANKSESEPPDFSPS-----LDGD 1013
Db 827 VEGFOAE-----GDANRSYSDQSSNIEEFKLOEGLDSS 863
QY 1014 GDRKKCLALVSLGHEPBLRKSLLPPLIHTAATPMSLPKSTSTGELGALGPASRRT---- 1069
Db 864 GPKLCPIMPTPNGH-----LDP-----SLPLGGHLGPAGAGPAPRLSLQPD 906
QY 1070 -----SSSGSAEPGAAHEMKSPPSARSSPHSPWSAASSWTSSRRSSRNSLGRAPSLK 1120
Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSRSSSYGPGWGRSAAMASRRSSWN-----SLK 960
QY 1121 RRSPPSGERRSLLSGE-QOESQDEEBESSEE--ERASPAAGSDH-----RHRG 1162
Db 961 HKPPSAEHESLLSAERGGGARVCEVADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHR 1020
QY 1163 SLIERAKSSFDLPTDTLQVPLGHRHTASGR--GSASEHQDCNGKSASGRALARALRPPDPLD 1220
Db 1021 TLSLNRDSDVDAELVPAVGAPRAAWRAAGAPAPGHEDCNGRMPSIAKDVFTKMGDRGDR 1080
QY 1221 GDDADDEGNLSKGERVRAWIRARLPACYLERDSWAIYIPPPQSRFRLLCHRIITHKMFEDH 1280
Db 1081 GED-EEIDYTLCFVRVKMIDVYKPDWCVEVDWSVYLFSPENRFRVLQCTIIAHKLFDY 1139
QY 1281 VLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQA 1340

Db 1140 VVLAIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGMTLKVVSGLGFEGEQA 1199
QY 1341 YLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMRLVRLRLTLRPLRVISRAOGLKL 1400
Db 1200 YLRSSWNVLDGFLVFVSIIDIVVSLASAGAKILGVLRLRLTLRPLRVISRAPGLKL 1259
QY 1401 VVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEAS 1460
Db 1260 VVETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTNRNITNRSDCMA 1319
QY 1461 RWVRHKYNFDNLGQALMSLFLVASKDGVVDIMYDGLDAVGVDQOQIMNHNPMWMLLYFIS 1520
Db 1320 RWVHHKYNFONLQALMSLFLVASKDGVNIMYNGLDAAVADQOQVTNHNPMWMLLYFIS 1379
QY 1521 LLIVAFFVLNMFVGVVVENFHKRQHQBEEEEARRRREKRLRLEKKRKAQCKPYYSYS 1580
Db 1380 LLIVSFFVLNMFVGVVVENFHKRQHQBEEEEARRRREKRLRLEKKRKAQRLPYATYC 1439
QY 1581 RFRLLVHHLCTSHYLDLFIITGVIGLVNVTNAMEHYQOQIILDEALKICNYIFTVIFVLES 1640
Db 1440 HTRLLIHSMTCTSHYLDIFITFIICLVNVTMSLEHYNQPTSLTALKYCNMYFTTVFVLEA 1499
QY 1641 VPKLVAFGRFRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIAR 1700
Db 1500 VLKLVAFGLRRFFKDRWNQDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIAR 1559
QY 1701 VLKLLKMAVGMRALDITVMQALPOVGNLGLLPMLLFFIFAALGVLEFGLECDETHPCBG 1760
Db 1560 VLKLLKMATGMRALDITVVQALPOVGNLGLLPMLLFFIYAALGVLEFGKLVNCDENPCBG 1619
QY 1761 LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DOESTCYNTV--ISPIYFVSFV 1817
Db 1620 MSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCLSLQFVSPLYFVSFV 1679
QY 1818 LTAQFVLNVVIAVLMKHLBESNKEAKEEAELEAELELEM-KTILSPQHPHSLGSPFLWPG 1876
Db 1680 LTAQFVLNVVAVLMKHLDDSNKEAQEDAEMDAELEMAHGLGPGPRLPTGSPGA-PG 1738
QY 1877 VEGPD-----SP-----HARSAS-----HFSLEHPTMQP-----HPTLP 1918
Db 1739 -RGPAGAGGGDTEGGLCRRCYSPAENLWLDVSLIKDSLEGELTIIDNLSSIFHHY 1797
QY 1893 --PAA-----HARSAS-----HFSLEHPTMQP-----HPTLP 1918
Db 1798 SSPAGCKKCHDKQEVQLAETAEPALNSDRSSILLGDDLSEDDTACPPGRKDSKGELD 1857
QY 1919 GPDLLITVVKSG-----VSRTHSLFN-DSYMCRHGSTAEGPLHGRGWGLPKAQSGSVLSVH 1972
Db 1858 PPEPMRVGLGECFFPLSSTAVSPDENFLCEMEEIPEPNV--RSW--LKHDSSQAPPS 1913
QY 1973 SQPADTSYILQLPKDAPH-----LLQPHSAPTWTGTIPKLPPPG-----RSPLAQRPLR 2021
Db 1914 FSPDASSPDLPEPAEFFHPAVSASOKGPEKGTGTGLPKIALQGSWASLRSPRVNCTLLR 1973
QY 2022 QAAIRTDSDVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQQHSHRSKISHMT 2081
Db 1974 QATGSDTSLD-----ASPSAGSLQTTLEDLSLSDSPRA-----LG 2012
QY 2082 PPAPCPGPEPNWGKPPETRSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSVEAQ 2141
Db 2013 PPAPAPGPAGLS--PAARRRLSL-----RGRGLFSLRGLRA- 2047
QY 2142 SCQRRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDPN---LGGQPLGGGSRPKKLSP 2198
Db 2048 -----HQRSHSSGGS-TSPGCTHDSMDPSDEGRGGAGGAGSEHSETLSSL 2095
QY 2199 SIT---IDPPESQGRTPPSPGICLRRRAPSSDS---KOPLAGPPDSMAASPSPKDV 2251
Db 2096 SLTSLFCPPP-----PPAPGLTPARKFSSTSSLAAPGRPHAAALAHCLARSPSWAAD- 2148
QY 2252 LSLSGLSSDPADLDP 2266

Db 2149 -----RSKDPGGRAP 2158

RESULT 7
US-09-935-541-4
; Sequence 4, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-4

Query Match 46.1%; Score 5484; DB 4; Length 2188;
Best Local Similarity 51.1%; Pred. No. 0;
Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;

QY 31 RPPGSAEKDPGSADSEAE-----LPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERI 86
Db 25 QPGPRSPSPSPGLEPLDGDADPHVPHDLPAPIAFFCLRQTTSRPNWCIKMCNPNWFEV 84

QY 87 SMLVILLNCVTLGMFRPCEDIAQSRQRILOAFDDFIAPFAFVAVMVVVMVALGIFGKKC 146
Db 85 SMLVILLNCVTLGMYPQCDMDCLSDRCKILOQVDFDIFIFFAMEMVLKMAVGIFGKKC 144

QY 147 YLGDWNRLLDFFIVAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLED 206
Db 145 YLGDWNRLLDFFIVMAGMVEYSLDLQNLNSAIRTVRVRPLKAINRVPSMRILVTLLED 204

QY 207 TPLMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFILPENFSLPSLDLERYQTENEDE 266
Db 205 TPLMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLEENFTIQGDVALPPYQPEEDE 264

QY 267 SPFICSQPRENGMRSCRSVPTLRGDDGGGPPCGL-----DYEAYNSSNTT--CVNNWQ 318
Db 265 MPFICSLSGDNGIMGCHIEPPLKEQ--GRECCLSKDDVDYDFAGRQDLNASGLCVNWR 321

QY 319 YTNCSAGEHNPFPKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILL 378
Db 322 YNVNCRGTSANPHKGAINFNDNIGYAWIVIFQVITLEGWVEIMYVMDAHSFYNFYIFILL 381

QY 379 IIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRLSNASTLASFSEPGSCYEELK 438
Db 382 IIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQYLS-SSTVASYAEPGDCYEEIFQ 440

QY 439 YLVYILRKAARLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHH 498
Db 441 YVCHILRKAKR-----RALGLYQALQSRQALG----- 468

QY 499 HHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPSPSTPALSAPPGAESVHSFYH 558
Db 469 -----PEAPA--PAKPGP-----H 480

QY 559 ADCHLEPVRQAPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEAASSGPPT 618
Db 481 AK--EPRHYQLCPQHSPLDTPHL-----VQIPATL----- 511

QY 619 LTSLNIPPGPYSSMHKLLLETSQSTGACQSSCKISSPCLKADSGACGPDSCPYPAR----- 672
Db 512 -----ASDPASCPCQCHDGRRP 529

QY 673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLSGPDAPSSVL----- 726
Db 530 SGLGSTD-SGQEGSGSGSAGGE--DEADGDGARSSEDGASSELGKEEEEEQADGAVWL 586

QY 727 --AFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFTS 784
Db 587 CGDVWRETRAKLRGIVDSKYFNRRGIMAILVNTVSMGIEHHEQPEELTNALEICNVVFTS 646

QY 785 LFALEMLLKLVYGPFGYIKPNYNIFDGVIVVISVWEIVGQQGGSLSVLRTFRLMRVLKL 844
Db 647 MFALEMILKLAAPGLFDYLRPNYNIFDSIIVISIWEIVGQADGSLSVLRTFRLLRVLKL 706

QY 845 VRFLPALQRLVVLMTMDNVATFCMLLMFIFIFISILGMLHFGCKPFASERD-GDTLPDR 903
Db 707 VRFPALRRQLVVLMTMDNVATFCMLLMFIFIFISILGMLHFGCKFSLRDTGTDPDR 766

QY 904 KNFDSLLWAIWTVFQILTQEDWNVLYNGMASTSSWAALYFTALMTFGNYVLNLLVAIL 963
Db 767 KNFDSLLWAIWTVFQILTQEDWNVLYNGMASTSPWASLYFVALMTFGNYVLNLLVAIL 826

QY 964 VEGFOAEELSKREDASGQLSCIQLPVDSSQGDANKSESEDPFFSPS-----LDGD 1013
Db 827 VEGFOAE-----GDANRSYDEQSSSNIIEFCLKQEGLDSS 863

QY 1014 GDRKKCLALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRT----- 1069
Db 864 GPKLCPIMPMPNGH-----LDP-----SLPLGHLGPAGAAGPAPLSLQPD 906

QY 1070 -----SSGSAEPGAHAHEMKSPPSARSPPHSPWSAASSWTSRRSSRNSLGRAPSLK 1120
Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSYYGWRSAAWASRRSSWN-----SLK 960

QY 1121 RRSPPGERRSLSGE-GQESQDEEESSEE--ERASPDGSDH-----RHRG 1162
Db 961 HKPPSAEHESLLSAERGCGGARVCEVADEGPPRAAPLHTPHAHHIHHGPHLAHRHRHRR 1020

QY 1163 SLERAKSSFDLPDTLQVPLHRTASGR--GSASEHQDCNGKSASGRALARALRPDDPPLD 1220
Db 1021 TSLDNRDSVDLAEVPAVGAHPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMGDRGR 1080

QY 1221 GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFH 1280
Db 1081 GED-EEEDYTLCFRVRKMDVYKPDWCCEVEDWSVYLFSPENRFRVLCQTLIAHKLFDY 1139

QY 1281 VVLVIFLNCITIAMERPDKIDPHSAERIFLTLNSYIFTAVELAEMTVKVVALGWCFCGEQA 1340
Db 1140 VVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSGLYFGEQA 1199

QY 1341 YLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLRLRPLRPLRVISRAQGLKL 1400
Db 1200 YLRSSWNVDGLVLFVSIIDIVVSLASAGAKILGVLRLRLRPLRPLRVISRAQGLKL 1259

QY 1401 VVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCOGEDTRNITNKSDCAEASY 1460
Db 1260 VVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCOGEDTRNITNRSDCMAANY 1319

QY 1461 RWVRHKYNFNLGQALMSLFLVASKDGWVDIMYDGLDVGVDQOPIMHNPNWMLLYFISF 1520
Db 1320 RWVHKYNFNLGQALMSLFLVASKDGWVIMYNGLDVAVDQOQPVNHNPNWMLLYFISF 1379

QY 1521 LLIVAFFVLNMFVGVVVENFHKROHQBEEEAARRRREKRLRLEKKRKAQCKPYSDYS 1580
Db 1380 LLIVSFFVLNMFVGVVVENFHKRQHQEAEEARRRREKRLRLEKKRKAQRLPYATYC 1439

QY 1581 RFRLLVHLCCTSHYLDLFIITVIGLNVVVTMAMEHYQQOQILDEALKICNYIFTVIFVLES 1640
Db 1440 HTRLLIHSMTCTSHYLDIFITFIICLNVVVTMSLEHYNQPTSETALKYCNMFTTVPVLEA 1499

QY 1641 VFKLVAFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRMRVLRIAR 1700
Db 1500 VLKLVAFGLRRFFKDRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRMRVLRIAR 1559

QY 1701 VLKLLKMAVGMRALLDVTVMQALPOVGNLGLLFLMLFFIFAALGVLFGLDECEDETHPCEG 1760

Db	1560	VLKLLKMATGRALDDTVVQALPQVGNLGLLFFIYAALGVLFGLVCNDENPC	1619	Db	19	GITEQGPSPSPSPGLEEPLEGTPDVPHPDLAPVAFFCLRQTTSPRNCIKMVCNFW	78
QY	1761	LGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV	1817	QY	83	FERISMLVILLNCVTLMFRPCEDIACDSQRCRILQAFDFFIFAFFAVEMVVMVALGIF	142
Db	1620	MSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERSCSLSLQFVSPLYFVSFV	1679	Db	79	FECVSMVLVILLNCVTLMQYPCDDMECLSDRCKILQVDFDFFIFFAMEMVLKMWALGIF	138
QY	1818	LTAQFVLNVVAVLMMKHLSESNKEABEALEALEM-KTILSPQPHSPGLSPFLWPG	1876	QY	143	GKKCYLGDITWNRDLFFIVIAGMLEYSILDQNVSFSAVRTVRVLRPLRAINRVPSMRILVT	202
Db	1680	LTAQFVLINVVAVLMMKHLDDSNKEAQEDAEADAELEMAHGLGPGPRLPTGSPGA-PG	1738	Db	139	GKKCYLGDITWNRDLFFIVMAGMVEYSILDQNLNLSAIRTVRLRPLKAINRVPSMRILVN	198
QY	1877	VEGPD-----SP-----DSPKPGALH--	1892	QY	203	LLDITLPMNLGNVLLLCFFVFFIFIGVGVQVWAGLLRNRCFLPENFSLPLSVDLERYOTE	262
Db	1739	RGPGGAGGGDTGGLCRRCYSPAQENLWLDVSLLIHKDSLEGELTIIDNLSGSIFHHY	1797	Db	199	LLDITLPMNLGNVLLLCFFVFFIFIGIIGVQVWAGLLRNRCFLEENFTIQGDVALPPYQOE	258
QY	1893	--PAA-----HARSAS-----HFSLEHPTMQP-----HPTLTP	1918	QY	263	NEDESPFICSPQPRENGMRSCRSVPTLRGDGGGGPPCGL-----DYEAYNSSNTT--CV	314
Db	1798	SSPAGCKKCHDKQEVQLAETAFAFSLNSDRSSILLGDDLSLEDPACPPGRKDKSGELD	1857	Db	259	EDDEMPFICSLTGDNGIMGCHEIPPLKEQ---GRECCLSKDDVYDFGAGRQDLNASGLCV	315
QY	1919	GPDLITVRKSG-----VSRTHSLPN-DSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVH	1972	QY	315	NWNQYNTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDMYFVMDAHSFYNFYI	374
Db	1858	PPEPMRVGDLGECFFPLSSTAVSPDPENFLCEMEEIPFPV--RSW--LKHDSSQAPPSP	1913	Db	316	NWNRYNVNCRGTGNANPHKGAINFDNIGYAGIVIFQVITLEGWVEIMYVMDAHSFYNFYI	375
QY	1973	SQPADTSYILQPKDAPH-----LLQPHSAPTWTIPKLP--RSPLAQRPLRR	2021	QY	375	FILLIIVGSFFMINCLVVIATQFSETKQRESQMLREQVRFLSNASTLASFEPGSCYE	434
Db	1914	FSPDASSPLLPMPAEFFHFAVSASQKGPKEGTGTGTLFKIALQGSWASLRSRPNVCTLLR	1973	Db	376	FILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYE	434
QY	2022	QAARTDSDVQGLSGREDLLAEVSGSPPLARAYFWGQSSTQAQQHSHRSKISKHMT	2081	QY	435	ELLKYLVIILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQFSSSCSRSHRRLSVHHL	494
Db	1974	QATGSDTSLD-----ASPSAGSLQTTLEDSTLSDSPRA-----LG	2012	Db	435	EIPQYVCHILRKAARRALGLYQALQNR-----	461
QY	2082	PPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPPGQEEPPSPRDLKKCYVSAEQ	2141	QY	495	VHHHHHHHHYHLNGNGLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGAESVH	554
Db	2013	PPAPAGPGRAGLS---PAARRRLSL-----RGRGLFSLRGLRA-2047	2047	Db	462	-----RQAMG-----PGTPA--PAKPGP-----	477
QY	2142	SCQRRPTSWLDEQRHRSIAVSCLDSDSGSQPHLGTDPN---LGGQPLGGPGSRPKKLSP	2198	QY	555	SFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKVYPTVHTSPPTLKEKALVEVAASS	614
Db	2048	-----HQRSHSSGGS-TSPGCTHDSMDPSDEGRGAGGAGGAGSEHSETLSSL	2095	Db	478	--HAK--EPSHCKLCPRHSPLD-----PTPHLLVQ-----	504
QY	2199	SIT---IDPPESQGPRTPPSGICLRRRAPSSDS---KDPLASGPPDSMAASPSPKKDV	2251	QY	615	GPPTLSLNIPIPGPYSSMHKLLETQSTGACQSSCKTSSPCLKADSGACGPDSCPYCAR--	672
Db	2096	SLTSLFCPPP-----PPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD-	2148	Db	505	-----ISAILASD-----PSSCFHCQHEA	523
QY	2252	LSLSGLSDPADLDP 2266		QY	673	-----AGAGEVELADREMPDSDSAVVEFTQDAQHSDLRDPHSRRQRSLGPDAPSSVLA-	727
Db	2149	-----RSKDPGGRAP 2158		Db	524	GRRPSGLSTD-SQEGSGSGSAAEAEANGDG---LQSESDGVSSDLGKEEEOEDGAAR	578
RESULT 8				QY	728	-----FWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHQPEELTNALEISNIVFT	783
US-09-404-650-5				Db	579	LCGDVWRETRKKLRGIVDSKYFNRGIMMAILVNTVSMGIEHQPEELTNALEICNVVFT	638
; Sequence 5, Application US/09404650				QY	784	SLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLK	843
; Patent No. 6309858				Db	639	SMFALEMILKLAAGLFDYLRNPYNIFDSIIIVISWEIVGQADGGLSVLRTFRLRVLK	698
; GENERAL INFORMATION:				QY	844	LVRFLPALQRLVLMKTMNDNVATFCMLMLFIFIFISILGMHLFGCKFASERD-GDTLPD	902
; APPLICANT: Dietrich, Paul S.				Db	699	LVRFPALRRQLVLMKTMNDNVATFCMLMLFIFIFISILGMHLFGCKFSLRTDGTDPD	758
; APPLICANT: McGivern, Joseph G.				QY	903	RKNFDSLLWAIWTFQILTQEDWNKVLNGMASTSSWAAALYFIALMTFGNVLFNLVVAI	962
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;				Db	759	RKNFDSLLWAIWTFQILTQEDWNVVLNGMASTTPWASLYFVALMTFGNVLFNLVVAI	818
; TITLE OF INVENTION: AND USES				QY	963	LVEGFQAEIISKREDASQGLSCIQLPVDSDQGDANKSESEPDFFSPS-----LDG	1012
; FILE REFERENCE: R0043B-RFG sequence listing				Db	819	LVEGFQAE-----GDANRSCDEQSSNLEEFDKLPEGLDN	855
; CURRENT APPLICATION NUMBER: US/09/404,650				QY	1013	DGDRKKCLALVSLGEHPELRKSLPLPLIHTAATPMSLPKSTGTGLGEALGPA-SRRTSS	1071
; CURRENT FILING DATE: 1999-09-23				Db	856	SRDLKLCPIPMTPNGH-----LDP-----SLP-----LGAHLGPAGTMGTAP	892
; NUMBER OF SEQ ID NOS: 12				QY	1072	SCSAEPG-----AAHEMKSPPSARSSPHSPWASASSWTSRRSRNSL	1113
; SOFTWARE: PatentIn ver. 2.0						::: : : :	
; SEQ ID NO 5						: : :	
; LENGTH: 1835						: : :	
; TYPE: PRT						: : :	
; ORGANISM: Rattus sp.						: : :	
US-09-404-650-5						: : :	
Query Match						45.1%; Score 5366; DB 3; Length 1835;	
Best Local Similarity						56.8%; Pred. No. 0;	
Matches 1138; Conservative 183; Mismatches 346; Indels 336; Gaps 38;							
QY	27	GAGGRPGPSAEKDPGSADSAEG-----LPYPALAPVFFYLSQDSRRPRSWCLRTVCNFW	82				

Db 893 RLSLQDPVLVALDSRKSSVMSLGRMSYDQRLSSSRSSYYGPWGRSGTWASRRSSWN-- 950

QY 1114 GRAPSLKRRSPSGERRSLLSGEQESQDEE-ESSEEE---RASPAGSDH----- 1158

Db 951 ----SLXHKPPSAEHESLLSGEGGSCVRACEGAREEAPRTAPLHAPHAHAHGHPLA 1006

QY 1159 -----RHGSLEREAKSFDLPDTLQVPLHRTAS--GRGSASEHQDCNGKSASGLRAL 1212

Db 1007 HRRHRRRTLSLDRSDVDLGELVPVVGAHSRAAWRGAGQAPGHEDCNGRMPNIAKDVFT 1066

QY 1213 RPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRI 1272

Db 1067 KMDDRRDRGED-EEEDYTLCFRVRKMDIVYKPDWCEVREDWSVLFSPENKFRILCQTI 1125

QY 1273 ITHKMFHVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVAL 1332

Db 1126 IAHKLFYVVLAFILNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVS 1185

QY 1333 GWCFFEQAAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTRPLRVI 1392

Db 1186 GLYFGEQAAYLRSSWNVDGLFVFSIIDIVSVASAGGAKILGLVLRVLRLLRTRPLRVI 1245

QY 1393 SRAQGLKVVFETLMSLKPIGNIVIVCCAFFIIFGILGVLFKGFVFCQGEDTRNITNK 1452

Db 1246 SRAPGLKVVFETLMSLKPIGNIVILICAFFIIFGILGVLFKGFYHCLGVDTRNITNR 1305

QY 1453 SDCAEASVVRHKYNFNDNLQALMSLFLVASKDGVIMYDGLDVGVDQQPIMNHNPW 1512

Db 1306 SDCVAANYRWHHKYNFNDNLQALMSLFLVASKDGVIMYDGLDVGVDQQPIMNHNPW 1365

QY 1513 MLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEAEARRREEKRLRLEKRRKAQC 1572

Db 1366 MLLYFISFLLIIVFFVLNMFVGVVVENFHKCRHQHEEAEARRREEKRLRLEKRRKAQR 1425

QY 1573 KPYYSYSRFRLLVHLCTSHYLDLFTGVIGLVNVTMAHEHYQQOILDEALKICNYIF 1632

Db 1426 LPYATYCPTRLIHSMTCTSHYLDIFITFIICLVNVTMSLEHYNQPTSLETALKYCNMF 1485

QY 1633 TVIFLESVFKLVAFGFRFFQDRWNQDLAIIVLLSIMGITLEEIEVNASLPINPTIIRI 1692

Db 1486 TVFVLEAVLKLVAFLRRFKDRWNQDLAIIVLLSVMGITLEEIEINAALPINPTIIRI 1545

QY 1693 MRVLRARVLKLLKMAVGMRALDVTVMQALPQVGNLGLLFFIFAALGVLELFGDLEC 1752

Db 1546 MRVLRARVLKLLKMATGMRALDVTVMQALPQVGNLGLLFFIFAALGVLELFGKLV 1605

QY 1753 DETHPCEGLRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDC-DQESTCYNVT--IS 1809

Db 1606 NDENPCEGMSRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDCDTHBERTCLSSLOFVS 1665

QY 1810 PIYFVSFVLTAQFVLVNVVIAVLMKHEESNKEAEAELEAELEEM-KTLSPQPHSPL 1868

Db 1666 PIYFVSFVLTAQFVLVNVVIAVLMKHLDDSNKEAQEDAEMDAEIELEMAHGLGPCP 1721

QY 1869 GSPFLWPVGEGDSDSPKPGALHPAAHARSASHPSLEHPTMQPHTELPGPDLLTV--- 1925

Db 1722 -----GPCPG-----PCPCPCPCPCAGRLPTSSPG 1747

QY 1926 ---RKSGVSRTHSLPNDSYMCRH 1945

Db 1748 APGRSGGAGAGG-DTESHLCHR 1769

RESULT 9

US-09-935-541-5

; Sequence 5, Application US/09935541

; Patent No. 6589787

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/09/935,541

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 1835

; TYPE: PRT

; ORGANISM: Rattus sp.

US-09-935-541-5

Query Match 45.1%; Score 5366; DB 4; Length 1835;

Best Local Similarity 56.8%; Pred. No. 0;

Matches 1138; Conservative 183; Mismatches 346; Indels 336; Gaps 38;

QY 27 GAGRPGPGSAEKDPGSADSEAE-----LPYPALAPVVFVYLSQDSRPRSWCLRTVCNPW 82

Db 19 GITEQPGPRSPPPSPGLEEPLGPNPDVPHPDLPAPVAFCLRTTSPRNWCIKMWVCNPW 78

QY 83 FERISMLVILLNCVTLMGFRPCEDTACDSQRCRILQAFDDFFIAFFAVEMVVMKVALGTF 142

Db 79 FECVSMVLVILLNCVTLMGYQPCDDMECLSDRCKILQVDDDFIFIFFAMEMVLKMAVGIF 138

QY 143 GKCYLGTWNRLDFFIVIAAGMLEYSLDLQNVSFSAVRTVRLRPLRAINRVPSMILVT 202

Db 139 GKCYLGTWNRLDFFIVMAGMVEYSLDLQNLNLSAIRTVRVLRPLKAINRVPSMILVN 198

QY 203 LLDDTLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFPLPENFSLPLSVDLERYQTE 262

Db 199 LLDDTLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLEENFTIOGDVALPPYYQPE 258

QY 263 NEDESPFICSQPRENGMRSRCSVPTLRDGGGGGPPCGL-----DYEAYNSSNTT--CV 314

Db 259 EDDMPFICSLTGDNGIMGCHIEIPPLKEQ---GRECLSKDDVDYDFGAGRQDLNASGLCV 315

QY 315 NWNQYVTCNSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYI 374

Db 316 NWNRYNVVTCRTGNANPHKGAINFNIGYAGIVIFQVITLEGWVEIMYVMDAHSFYNFYI 375

QY 375 FILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTILASFEPGSCYE 434

Db 376 FILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRYLS--SSTVASYAEPGDCYE 434

QY 435 ELLKYLVIYILRKAARLAQVSRAGVRVGLSSPAPLGGQETQPSSSCSRSRHRRLSVHHL 494

Db 435 EIFQYVCHILRKAKRALGLYQALQNR-----

QY 495 VHHHHHHHHYHLGNGTILRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGAESVH 554

Db 462 -----RQANG-----PGTFA--PAKPGP----- 477

QY 555 SFYHADCHLEPVQCAPPSPSPSEASGRVSGKVYPTVHTSPPETLKEKALVEVAASS 614

Db 478 ---HAK---EPHCKLCPRHSPLD-----PTPHTLVQP----- 504

QY 615 GPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR-- 672

Db 505 -----ISAILASD-----PSSCPHCQHEA 523

QY 673 ----AGAGEVELADREMPDSDSEAVYFTQDAQHSLDRPHSRQRSLGPDPAEPSSVLA- 727

Db 524 GRRPSGLGSTD-SQEGSGSGSAAEANGDG---LQSSDGVSSDLGKEEQEDGAAR 578

QY 728 ----FWRLICDTRFKIVDSKYFGRGIMIAILLVNTLSMGIEYHEQPEELTNALEISNVFT 783

Db 579 LCGDVWRTRTKLRGIVDSKYFNRGIMMMAILVNTVSMGIEHHEQPEELTNALEISNVFT 638

QY 784 SLFALEMLLKLIVGPFYIKNPYNIFDGVIVVSVWEIVGQGGGLSVLRTFRLMRVLK 843

Db 639 SMFALEMILKLAAGLFDYLRNPYNIFDSIIIVISWEIVGADGGLSVLRTFRLMRVLK 698

QY 844 LVRFLPALQRLVLMKTMNVATFCMLLMFLIFIPFILGMHLFGCKFASERD-GDTLPD 902

Db 1722 -----GPCPG-----PCPCPCPCPCAGRLPTSSPG 1747
 QY 1926 ---RKSGVSRTHSLNDSYMCRRH 1945
 Db 1748 APGRSGGAGAGG-DTESHLCRH 1769
 RESULT 10
 US-09-268-163-4
 ; Sequence 4, Application US/09268163B
 ; Patent No. 6353091
 ; GENERAL INFORMATION:
 ; APPLICANT: Lipscombe, Diane
 ; APPLICANT: Schorge, Stephanie
 ; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
 ; FILE REFERENCE: B1055/7000
 ; CURRENT APPLICATION NUMBER: US/09/268,163B
 ; CURRENT FILING DATE: 1999-03-12
 ; EARLIER APPLICATION NUMBER: US 60/077,901
 ; EARLIER FILING DATE: 1998-03-13
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 2343
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-268-163-4
 Query Match 14.7%; Score 1750.5; DB 3; Length 2343;
 Best Local Similarity 24.2%; Pred. No. 2.4e-133;
 Matches 639; Conservative 363; Mismatches 827; Indels 815; Gaps 84;
 QY 27 GAGGRPGPGSAEKDPGSADSEAEGLFPALAPVVF-----FYLSDSRP 70
 Db 25 GAGGAGGPGGGLQPGQRLVYKQSIQARTMALYNPIPVKQNCFTVNRSLFVSEDNV 84
 QY 71 RSWCLRTVCNPFBEISMLVILLNCVTGLMFRPCEDIACDSQRCRILQAFDD---FIFAF 127
 Db 85 RYAKRITTEWPPFEYMLATIIANCIVLAL---EQHLPDGDKTFMSERLDDTEPYFIGI 140
 QY 128 FAVEMVVKMVALG-IFGKKCYLGDWNRLDFFIIVAGMLEYS---LDLQNVSFSAVRTVR 183
 Db 141 PCFEAGIKIIALGFVFKGSLRNGWNVMDFVVVLTGILATAGTDFDLR-----TLRAVR 195
 QY 184 VLRLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFL 243
 Db 196 VLRLKLVSGIPSLQVVLKSIKAMVPLQLGILLFFAILMFAIIGLEFFYMGKFKACF- 254
 QY 244 PENFSLPLSVDLERYQYQTENEDESPFICSPQRENGMRSCRSVPTRLGDDGGGPPCGLDYE 303
 Db 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273
 QY 304 AYNSSNTTCVNNQYNTNCSAGEHNPFKAINFDNIGYAWIAIFQVITLEGWVDIMYFV 363
 Db 274 ARLCGDETC--REYWP-----GPNFGITNFDNILFAILTVOFCITMEGTDLILYNT 323
 QY 364 MD-AHSFYNFIYFILLIIVGSFFMINCLVVIATQFSETKQRES-----QLMRQVRVF 416
 Db 324 NDAAGTNWNLWFYFIPLIIGSFMLNLVLGVLSEFAKERERVENRRRAFLKLRQQQIE- 382
 QY 417 LSNASTLASFSEPGSCYEELKYLVIILRKAARRLAQVSRAGVRVGLLSSAPLGGQET 476
 Db 383 -----RELNGYLEWIFKAEVMLAEEDNA-----EER 410
 QY 477 QPSSSCSRSHRRLSVHHLVHHHHHHHHLNGTLRAPRASPEIQDRDANGSRRLMLPP 536
 Db 411 SPLDVLKRAATFKSRNDLIH-----AEEGEDRFAD----- 440
 QY 537 PSTPALSGAPPGAESVHSFYHADCHLEPVRCAOPPPRSPSEASGRTVSGKVYPTVHTS 596
 Db 441 ----- 440
 QY 597 PPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLETTQSTGACQSSCKISSPCLK 656

APPLICANT: Sun Chen, Ai Ru
 APPLICANT: Suey, David J.
 TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
 TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173-4799
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/713,118
 FILING DATE: 16-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mata, Elizabeth W.
 REGISTRATION NUMBER: 38,236
 REFERENCE/DOCKET NUMBER: ACC96-01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2337 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-713-118-2

Query Match	14.7%;	Score 1749;	DB 3;	Length 2337;
Best Local Similarity	24.3%;	Pred. No. 3.1e-133;		
Matches 645:	Conservative 359;	Mismatches 832;	Indels 820;	Gaps 86;

QY	14	QQPRSFMRNLDSL	GAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVF	-----	61			
					:			
Db	13	GGPGSGERARG	-GGAGGAGGPGGLQPGQRLVKYQSIQAQRARTMALYNPIPVKQNCFTV	71				
					:			
QY	62	----FYL	SQDSRPRSWCLRTVCNPWFERISMLVILLNCVTGLMFRPCEDIA	CDSQRCIL	117			
					:			
Db	72	NRSLFV	SESDNVVRKYAKRITETWPPFXYMILATIIANCIVLAL	-----EQHLPDGD	KTPMS	127		
					:			
QY	118	QAFDD---	FIFAFFAVEMVKMVALG-IFGKCYLGDTWNRLDFFIV	IAGMLEYS	---LD	170		
					:			
Db	128	ERLDDTEPY	FIFGFCFEAGIKIIALGFVFKGSYLRGNWNVDFVVVL	TGILATAGTDFD	187			
					:			
QY	171	LQNVFS	AVRTVRVLRLPRAINRVPSMRILVTLLD	TPLMGNVLLCFFVFF	IFGIVGV	230		
					:			
Db	188	LR-----	TLRAVRVLRLKLVSGIPSLQVVLKSI	MKAMVPLLQIGLLFFAILMFAI	IIGL	242		
					:			
QY	231	QLWAGLL	NRCLPENFSLPSVDLERYYQ	TENEDES	PFICSQPRENGMR	SCRSVPTLRG	290	
Db	243	EFYMGK	FKHKACF-----PNSTDAE	-----PV	---	263		
QY	291	DGGGPP	CGLDYEAYNSSNTTCVNWNQYYTNC	SAGEHNPFK	GAINEDNIGYAWIA	IFQV	350	
Db	264	--GD	PPCGKEAPARLCEGDTEC---REYWP	-----GPNFGIT	NFDNILF	AILTVFQC	310	
QY	351	ITLEGV	VDIMYFVMD-AHSFYNF	IYFTILLIIVGSFF	MINCLVVIATQ	PSETKQRES	---406	
Db	311	ITMEG	TDILYNTNDAAGNTWNWLYFI	PLIIIGSFF	MLNLVLGVL	SGEFAKER	VENRR	370
QY	407	---Q	LMREQRVRFLSNASTLASFSEPG	SCYEBELLKYL	VYILRKAAR	LQAQVSR	AAGVRVG	463
Db	371	AF	LKLRQQQIE-----RELNGYLEW	IFKAEV	VMLAE	DRNA-----	407	
QY	464	LLSS	PAPLGQETQPS	SSCSRHRRLSVHHLVHHHHHHHHH	YHLGNGT	LFRAS	PEIQD	523

Db 1264 RLPKLVKAVFDCVNSLKNVLNIIIVYMLFMFIEAVIAQLFKGKFFCYCTDESKELERDCR 1323

QY 1448 N--ITNKSDCAEASR-WVRHKYNFDNLGOALMSLFVLASKDGVIMYDGLDAVGVDQ 1504

Db 1324 GQVLDYEKEEVEAQPROWKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEEQG 1383

QY 1505 PIMNHNPMWLLLYFISLIIIVAFFVLNMFVGVVVFNFHKKRQHQQEERARRREKRLRLE 1564

Db 1384 PSPGYRMELSIYVYVVFVFFFFVNFVFIITF-----QEQGDKVMSE-----CSLE 1433

QY 1565 KKRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTIGVIGLNVVTMAMEHY 1615

Db 1434 KNERACIDFAISAKPLTRYMPQNRSQFYKTFVVSPPFEYFIMAMIALNTVVLMMKFY 1493

QY 1616 QQPQILDEALKICNYIFTVIFVLESVEKLVAFGRFFQDRWNQDLAIVLLSIMGITLE 1675

Db 1494 DAPYEYELMKCLNIVFTSMFMECVLKIAGVNLNYFRDANVDFVTVLGSITDILVT 1553

QY 1676 EIEVNASLPINPTIIRIMRVLRIARVLKLLKQAVGMRRALLDTVMQALPOVGNLGLLEMLL 1735

Db 1554 EIANNF--IN--LSFLRLFRAARLIKLLRQGYTIRILLWTFVQSFKALPYVCLLIAML 1607

QY 1736 FFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLR 1795

Db 1608 FFIYAIIGMQVFNIALDDD--TSINRHNFRFTLQALMLLFRSATGEAWHEIMLSCLS 1664

QY 1796 D--CDQE--STCYNTVISPIYFVSFVLTAQFVLNVVIAVLM-----KHL 1836

Db 1665 NQACDEQANATECGDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHL 1724

QY 1837 EE-----1838

Db 1725 DEFIRVWAEDPAACGRISYNDMFEMLKHMSPPGLGKKPCPARVAYKRLVRMNMPISNED 1784

QY 1839 -----SNKEAKEEAELEAELEMKTLSPQPHSLGSPFLW 1874

Db 1785 MTVHFTSLMALIRTALEIKLAPAGTKHQCDALKEISVWVANL-PQKTLDLLVP--- 1840

QY 1875 PGVEGDPSPSPKPGALHPA-----AHARSASHFLEHPTM--- 1910

Db 1841 -----PHKPDENTVGKVAALMIFDFYKQNTTRDQMOQAPGGLSQMGVPSLFHPLKATL 1895

QY 1911 -QPHPTLPGPDLITVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVL 1969

Db 1896 EQTPAVLRGARVFLRQKSSTLSN-----GGAIQNESGIKE 1933

QY 1970 SVHSQPADTSYIQLPKDAPHLLQP-----HSAPTWTGPTIKLPPGSRPLAQRLRQAA 2024

Db 1934 SV-----SWGTRTQDAPHEARPPLEGRHSTEI-----PVGRSALAVDVQMOSI 1978

QY 2025 IR-----TDSLVOQLGSRREDLLAEVSGP---SPPLARAYSFVGQSTQAOQHSRSHS 2074

Db 1979 TRRGPDGEPQPGLESQGRAASMPRLAAETQPTVDASPMKRSI-----STLAQRPRGTHL 2032

QY 2075 KISKHMTTPAPCPG-----PEPNWKGPPETRSLSLELDTLSWISGDL 2117

Db 2033 CST---TPDRPPPSQASSHHHHRRCHRRRRDRKQRSLEKGP---SLSADMDGAPSSAVPG 2086

QY 2118 LPPGGQEEPPSPRLDKKCYSVAEQAQCORR-PTSWLDEQRRHSIAVSCLDG----- 2167

Db 2087 LPPG--EGPTGCRERRRQERSRQERRQSSSSSEKQRF---YSCDRFGGREPPKPKP 2141

QY 2168 -----SQPHLGTDP-----SNLGGQL-----GGPGSRPKKLSP-PSITI 2202

Db 2142 SLSSHPTSPTAGQEPGPHPGQSGSVNGSPLLSTGASTPGRGRRQLPQTPLTPRPSITY 2201

QY 2203 -----DPPESSQGPRT--PP-SPG-----ICLRRRAPSSDSKDPPLASGPPDSMAASP 2245

Db 2202 KTANSSPIHFAGACTSLPAFSPGRLSRGLSEHNALLQRPDLS---QPLAPG----- 2249

QY 2246 SPKQDVLSLSGLSSDP 2261

Db 2250 -----SRIGSDP 2256

RESULT 12

US-09-452-007-2

; Sequence 2, Application US/09452007

; Patent No. 6140485

; GENERAL INFORMATION:

; APPLICANT: Franco, Rodrigo

; APPLICANT: Sun Chen, Ai Ru

; APPLICANT: Suey, David J.

; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL

; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: USA

; ZIP: 02173-4799

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/452,007

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/713,118

; FILING DATE: 16-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Mata, Elizabeth W.

; REGISTRATION NUMBER: 38,236

; REFERENCE/DOCKET NUMBER: ACC96-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2337 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-452-007-2

Query Match 14.7%; Score 1749; DB 3; Length 2337;

Best Local Similarity 24.3%; Pred. No. 3.1e-133;

Matches 645; Conservative 359; Mismatches 832; Indels 820; Gaps 86;

QY 14 GQPRSMRLNLSGAGRPGPSAEKDPGSADSEAEGLPYPALAPVVF----- 61

Db 13 GPGGGERARG-GGAGGAGGPGGLQPGQVLYKQSIQARRTMALYNPIPVKQNCFTV 71

QY 62 ----FYLQDSRPRSWCLRTVCNWPFERISMLVILLNCVTLGMFPCEDIACDSQRCRIL 117

Db 72 NRSLFVSEDNVVRKYAKRITWPPFEYMLATIIANCIVLAL-----EQHLPDGDKTPMS 127

QY 118 QAFDD---FIFAFFAVEMVVKMVALG-IFGKKCYLGDVTNRLDFFIVIAMLEYS---LD 170

Db 128 ERLDDTEPYFIFGCFEAGIKIIALGFVFKGSLYLRNGWNVDMFVVVLTGILATAGTDFD 187

QY 171 LQNVFSAVRTRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGV 230

Db 188 LR-----TURAVRVLRLKLVSGIPSLQVWLKSIKAMVPLLIQIGLLFFAILMFAIGL 242

QY 231 QLWAGLLNRRCFLPENFSLPLSLDLERYYYQTENEDESPTICSPRENGMRSRCSVPTLRG 290

Db 243 ERYMGKFKHAKCF-----PNSTDAE-----PV--- 263

QY 291 DGGGPPCGLDYEAYNSSSTNTTCVNMWQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQV 350

Db	264	---	GDFFCGKEAPARLCEGDTEC	---	REYWP	-----	GNFGITNFDNILFAILTVFQC	310
QY	351	ITLEGWVDIMYFVMD	-	AHSFYNFIVFILLIIVGSFFMINCLVVIATQFSETKORES	---		406	
Db	311	ITMEGWTDILYNTDAAGNTWNLWFIPLIIIGSFFMLNLVLGVLGSEFAKERERVENRR	370					
QY	407	---	QLMREQRVRFELSNASTLASFSEPGSCYEELLYLVILRKAARRLAQVSRAAGVRVG	463				
Db	371	AFELKRRQQOIE	-----	RELNGYLEWIFXAEVWMLAEEDRNA	-----		407	
QY	464	LLSSPAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLNGTTLRAPRASPEIQD	523					
Db	408	-----	EKSPLDVLKRAATKKSRLDIH	-----	AEEGED	436		
QY	524	RDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRT	583					
Db	437	READ	-----				440	
QY	584	VSGKVYPTVHTSPPPETLKEKALVEVAASSGPTLTSLNIPPGPYSSMHKLLTQSTGA	643					
Db	441	-----		-----			440	
QY	644	COSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHS	703					
Db	441	---	LCAVGSPFARASLKGKTESSESYFRR	-----	KEKMFRR	-----	473	
QY	704	DLRDPHSRRQRSGLPDAPESPVLAFWRLLCDTFRKIVDSKYFGRGIMIALIIVNTLSMGIE	763					
Db	474	-----	FIRRMVKAQSFYVWVLCVVALNTLCVAMV	502				
QY	764	YHEQPEELTNALEISNIVFTSLFALEMLLKLVLVYGPFGYIKNPYNIFDGVIVVISVWEIV	823					
Db	503	HYNQPRRLTTLYFAEFVFLGLFLTEMSLKMVGLGPRSYFRSSFCDFGVIVGSVFEVV	562					
QY	824	GQ	-----	QGGGLSVLRTFRLMRVLKLVFLPALQRLVVLMTMDNVATFCMLLMFLIFI	878			
Db	563	WAAIKPGSSFGISVLRALRLRLRFKVTKYWSSLRNLVSLNSMKSIISLLFLFLFIW	622					
QY	879	FSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTVFQILTQEDWNKVLNGM	933					
Db	623	FALLGMQLFGGQFNQDETPT	---	TNFDTFPAAILTVFQILTGEDWNAMVYHGIESQGG	678			
QY	934	ASTSSWAALYFIALMTFGNYVLFNLVAILVEGF	-	QAEIEISK	-----	REDASGQ	981	
Db	679	VSKGMFSSFYFIVTLFGNYTLLNVLFLAIVDNLANAQELTKDEEMEEAANQKLALQKA	738					
QY	982	-----	LSCIQLPVDSQGDANKSESEPDDFFSPSLDGDGRKKCLALVS	-----			1024	
Db	739	KEVAEVPMSAANISIAARQNSAKARSVWEQASQLRLQNLRASCEALYSEMDPEERLR	798					
QY	1025	---	LGEHPELRKSLPLLIHTAATPMSLP	-----	KSTSTGLGEALGPASR	-----	1067	
Db	799	FATRRHRRPDMKTHLDRPLVLVELGRDGARGVGGKARPEAAEAEPGVDPRRHRRDKD	858					
QY	1068	RTSSSG	-----	SAEPGA	-----	AHEMKSPPSARS	1094	
Db	859	KTPAAGDQDRAEAPKAESGEPGAREERPRPHRSHSKEAAGPPEARSRERGRGPGEGGRRH	918					
QY	1095	---	SPWSAASSWTSR	-	RSSRNSLGRAPSLKRSPSGERRSLLSGEGQESQDEEESSEE	-	1148	
Db	919	HRRGSPEAAERPRRRAHRH	---	QDPSKECAGAKGERARRHRRGGPRAGPREAESGEEP	975			
QY	1149	-----	ERASP	-----	AGSDHRRHSGSLEREAKSSFDLPDIL	1178		
Db	976	ARRHRAHKAQPAHEAVEKETTEKEATEKEAEIVADKEKELRNHQPREPHCDLETSGTV	1035					
QY	1179	QVPGHLRTASGRGSASEHQDCNGKSKASGRLARALRPDDP	---	PLDGDADD	1226			
Db	1036	TVGPMHTLPSTCLQKVEEQPEDADNQNRVTRMGSPDPDNTIVHIPVMLTGPLGEATVVP	1095					
QY	1227	EGNL	-----	SKGER	-----	VRAWIRARLPACYLERDSWSAYIFPPQSRFRLCHRIIT	1274	
Db	1096	SGNVLDLESQAEKGKVEEADDVMRSGPRPIVPYS	-----	SMFCLSPNTLLRRFCHYIVT	1148			

QY 597 PPBETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLX 656
Db 441 -----LCAVGSFAR 450
QY 657 ADGACGPDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRQSL 716
Db 451 ASLKSGETESSYFRR-----KEKWERF----- 473
QY 717 GPDAEPSSVLAFWRLLCOTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEBLTNALE 776
Db 474 -----FIRMVKAQSFYVVLVCVVALNTLVCVAMVHYNQPRRLTTLY 515
QY 777 ISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQ-----QGGLS 831
Db 516 FAEFVFLGLFITEMSLKMYGLGPRSYFRSSFCDFGVIVGSVFEVWAAIKPGSSFGIS 575
QY 832 VLRTFRLMRVLKLVRFLPALORQLVLMKTMNDNVATFCMLLMFLFIFISILGMHLFGCKF 891
Db 576 VLRALRLRLRIFKVTKYWSSLRNLVSSLNSMKSIIISLLFLFLFVVFALLGMQLFGGQF 635
QY 892 ASERDGDTLDPDRKNFDSLLWAIIVTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFTA 946
Db 636 NFQDETPT---TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGVSKGMFSSFFIV 691
QY 947 LMTFGNYVLNLLVAILVEGF-QAEEISK---REDASGQ-----LSCIQ 986
Db 692 LTLFGNYTLNVLVFLAIVDNLANAQELTKDEEMEEAANKLALQAKAEVAEVSMSAAN 751
QY 987 LPVDSQGDANKSESEPFFSPSLDGDGRKKCLALVSLGE-----HPELRK 1033
Db 752 ISIAARQONSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTRHLRPMKT 811
QY 1034 SLLPPLIHTAATPMSLP-----KSTSTGLGEALGPASR-----RTSSG----- 1073
Db 812 HLDRLVLVELGRDGARGPVGKGARPEAAEAPEGVDPPRHRHRDKDTPAAGQDRAEA 871
QY 1074 ----SABPGA-----AHMKSPPSARS-----SPH-----SPWSAASSW 1103
Db 872 PKAESGEPGAREERPRPHRSHSKEAAGPPEARSERGRGPGPEGGRHRHRRGSFEEAERE 931
QY 1104 TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSE-----ERASP- 1153
Db 932 PRRHRAHRH---QDPSKECAGAKERRARRHGGPRAGPRAEAGEEPPARHRHARHKAQPA 988
QY 1154 -----AGSDHHRGSLEREAKSSFDLPDTLQVPLHRTASGRG 1191
Db 989 HEAVEKETTEKEATEKEAEIVEADKEKELRNHQPREPHCDLETSGTVTVGPMHTLPSTCL 1048
QY 1192 SASEHQDCNGKSASGLRALARPDDP-----PLDGDADDENL-----SKGE 1234
Db 1049 QKVEEQPEDADNQNRVTRMGSOQPPDNTIVHPVMTGLPGEATVVPVSGNVLDLESQAEK 1108
QY 1235 R-----VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLVIIIF 1287
Db 1109 KEVEADDVMRSGPRPIVPS-----SMFCLSPTNLLRRFCHYIVTMRYFEVVILVIA 1161
QY 1288 LNCITIAMERPKIDHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1347
Db 1162 LSSIALAAEDP-VRTDSPRNNAALKYLDYIFTGVFTFEMVIKIDGLLLHGPAYFRDLWN 1220
QY 1348 VLDGLLVLSVIDILVSMV-SDSGTKILGMLRVLRLLRTLRLPRVISRAOGLKLVVETLM 1406
Db 1221 ILD-----FIVVSGALVAFAFSGSKGKDINTIKSLRVLRLPLKTIKRLPKLKAVFDCVV 1276
QY 1407 SSLKPIGNIVVICCAFFIIFGILGVQLFKGFFVCQGE-----DTRN--ITNKSDCAEA 1458
Db 1277 NSLKNVLNIIIVMLFMFIFAVIAVQLFKGFFYCTDESELEDRGQYLDYEKEEVEA 1336
QY 1459 SYR-WVRHKYNFDNLGOALMSLFLASKDGWVDIMYDGLDAVGVDQQPIMNHNPMWLLIYF 1517
Db 1337 QPROWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATVEEQGPSGYRMELSIFY 1396

QY 1518 ISPELLIVAFFVLNMFVGVVVENPHKCRHQHEEBEARRREKRLRLEKRRKA-----QC 1572
Db 1397 VYVVFVFPFFVFNIFVALIITF-----QEQDKMSE-----CSLEKNERACIDFAISA 1446
QY 1573 KPY--YSDYSR--FRLLVHHLCTSHYLDLFTIGVIGLNVVTMAMEHYQOQILDEALKIC 1628
Db 1447 KPLTRYMPQNRQSFOYKWTWTFVVSPPFEYFIMAMIALNTVLMKMFYDAPYELMLKCL 1506
QY 1629 NYIFTVIFVLESVKLVAFGFRFFQDRWNOLDLAIVLLSIMGITLEHI-EVNASLPINP 1687
Db 1507 NIVFTSMFSMECVLKIIAFGVNLNYFRDAMNVDFVTVLGSIITDILVTEIAETN-----NF 1561
QY 1688 TIIRIMRVLRIARVLKLLKMAVGMRALLDVTMQALPOVGNLGLLFLMLFFIFAALGVLEF 1747
Db 1562 INLSFLRLFRAARLIKLRQGYTIRILLMTFVQSFKALPYVVCLLIAMLFFIYIIGMQVF 1621
QY 1748 GDLCEDETHPCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMKDTLRD--CDQE--STC 1803
Db 1622 GNIALDDD---TSINRHNFRFTFLOALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE 1678
QY 1804 YNTVISPIYFVSFVLTAQFVLNVVIAVLM-----KHLEE----- 1838
Db 1679 CGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDEFIRVWAEYDP 1738
QY 1839 ----- 1838
Db 1739 AACGRISYNDMFEMLKHMSPPLGLGKKCPARVAYKRLVRMNPISNEDMTVHTSTMAL 1798
QY 1839 -----SNKEAKEEALEAELEEMKTLSPQHSPGLSPFLWPVGVEGPDSPDSP 1886
Db 1799 IRTALEIKLAPAGTKQHQCDAELRKEISVVWANL-PQKTLDLLVP-----PHKPDEM 1849
QY 1887 KPGALHPA-----AHARSASHFSLEHPTM---QPHPTELPGPD 1921
Db 1850 TVGKVYAALMIFDFYKQNKTTTDDQMQQAPGGLSQMGVSLFHLPLKATLEQTQPAVLRGAR 1909
QY 1922 LLTVRKSGVSRTHSLPNDSYNCRHGSTAEGPLGHRGWCLPKAQSGSVLSVHSPADTSYI 1981
Db 1910 VFELQKSSSTLSN-----GGAIQNESGIKESV-----SWG 1940
QY 1982 LQLPKDAPHLLQP-----HSAPTWTGTIPKLPPEGSRPLAQRLRRQAIR-----TDS 2029
Db 1941 TQRTQDAPHEARPLERGHSTEI-----PVGRSGALAVDVQMOSITRRGPDGEPQG 1992
QY 2030 LDVQGLGSREDLLAEVSGP---SPPLARAYSFWGQSSTQAOQHSRSHSKISHMTTPAPC 2086
Db 1993 LESQGRAASMPRLAAETQPVTDASPMKRSI-----STLAQRPRTGTHLCST---TPDRPP 2043
QY 2087 PG-----PEPNWGKGPPEPTSSLELDTLSWISGDLPLPPGGQEEPPSP 2129
Db 2044 PSQASSHHHHRRRRDRKQRSLEKGP---SLSADMKGAPSSAVGPGLPDG--EGPTGC 2098
QY 2130 RDLKKCYSVEAQSCQRR-PTSWLDEQRRHSIAVSCLDG-----SQPHLG 2173
Db 2099 RRERERRQERGRSQERRQPSSSSEKQRF---YSCDRFGGREPKPKPSLSHPTSPTAG 2155
QY 2174 TDP-----SNLGGQPL-----GGPGSRPKKLSP-PSITI-----DPPESEQ 2209
Db 2156 QEPGPHPGQSGSVNGSPLLSTSGASTPGRGRRQLPQTPLTPRPSITYKTANSSPIHFAG 2215
QY 2210 PRT--PP-SPG-----ICLRRRAPSSDSKDPLASGPPDSMAASPCKDVLSSL 2257
Db 2216 AQTSLPAFSPGRLSRGLSEHNALLQDPLS---QPLAPG-----SRI 2254
QY 2258 SSDP 2261
Db 2255 GSDP 2258

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:32:41 ; Search time 178.672 Seconds
(without alignments)
4491.206 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEDGAGAEESGQPRSFM.....PKKDVLSLSGLSDPADLDP 2266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	11815.5	99.3	2377	17	US-10-757-262-16	Sequence 16, Appl
2	11758.5	98.8	2243	16	US-10-408-765A-625	Sequence 625, App
3	11111	93.3	2374	10	US-09-383-894-2	Sequence 2, Appli
4	11111	93.3	2425	10	US-09-383-894-4	Sequence 4, Appli
5	6212	52.2	2353	16	US-10-408-765A-1128	Sequence 1128, Ap
6	5492.5	46.1	2175	9	US-09-935-541-2	Sequence 2, Appli
7	5492.5	46.1	2175	14	US-10-425-800-2	Sequence 2, Appli
8	5484	46.1	2188	9	US-09-935-541-4	Sequence 4, Appli
9	5484	46.1	2188	14	US-10-425-800-4	Sequence 4, Appli
10	5366	45.1	1835	9	US-09-935-541-5	Sequence 5, Appli
11	5366	45.1	1835	14	US-10-425-800-5	Sequence 5, Appli
12	3959.5	33.3	1853	9	US-09-030-482B-19	Sequence 19, Appl
13	3564.5	29.9	1657	14	US-10-369-493-6836	Sequence 6836, Ap

14	1753	14.7	2264	15	US-10-627-370-2	Sequence 2, Appli
15	1750.5	14.7	2343	13	US-10-033-026-4	Sequence 4, Appli
16	1748.5	14.7	2339	15	US-10-375-253-12	Sequence 12, Appl
17	1746.5	14.7	2339	13	US-10-033-026-6	Sequence 6, Appli
18	1746.5	14.7	2339	17	US-10-736-883-32	Sequence 32, Appl
19	1743	14.6	2237	15	US-10-375-253-14	Sequence 14, Appl
20	1741	14.6	2237	13	US-10-033-026-8	Sequence 8, Appli
21	1741	14.6	2237	17	US-10-736-883-34	Sequence 34, Appl
22	1740.5	14.6	2333	17	US-10-736-883-28	Sequence 28, Appl
23	1732.5	14.6	2327	17	US-10-736-883-38	Sequence 38, Appl
24	1729.5	14.5	2331	17	US-10-736-883-44	Sequence 44, Appl
25	1722	14.5	2336	13	US-10-033-026-10	Sequence 10, Appl
26	1722	14.5	2336	17	US-10-736-883-30	Sequence 30, Appl
27	1714	14.4	2288	17	US-10-736-883-40	Sequence 40, Appl
28	1710	14.4	2339	17	US-10-736-883-42	Sequence 42, Appl
29	1673.5	14.1	1745	15	US-10-627-370-4	Sequence 4, Appli
30	1667	14.0	2313	16	US-10-322-696-178	Sequence 178, App
31	1665	14.0	2270	15	US-10-375-253-40	Sequence 40, Appl
32	1663.5	14.0	2251	15	US-10-375-253-38	Sequence 38, Appl
33	1659	13.9	2270	16	US-10-322-696-176	Sequence 176, App
34	1657.5	13.9	2251	16	US-10-322-696-84	Sequence 84, Appl
35	1632	13.7	1873	13	US-10-029-413A-22	Sequence 22, Appl
36	1625.5	13.7	1748	16	US-10-408-765A-1968	Sequence 1968, Ap
37	1619.5	13.6	1984	10	US-09-457-571-10	Sequence 10, Appl
38	1615.5	13.6	1989	10	US-09-457-571-12	Sequence 12, Appl
39	1602	13.5	2016	16	US-10-632-342-2	Sequence 2, Appli
40	1602	13.5	2510	15	US-10-375-253-34	Sequence 34, Appl
41	1598.5	13.4	2015	16	US-10-632-342-6	Sequence 6, Appli
42	1597.5	13.4	2157	16	US-10-467-491-2	Sequence 2, Appli
43	1596.5	13.4	2151	16	US-10-467-491-4	Sequence 4, Appli
44	1594	13.4	2016	16	US-10-632-342-4	Sequence 4, Appli
45	1591	13.4	1854	13	US-10-029-413A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-757-262-16
; Sequence 16, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156

; PRIOR FILING DATE: 2003-07-30									
; PRIOR APPLICATION NUMBER: US 60/499,594									
; PRIOR FILING DATE: 2003-09-02									
; PRIOR APPLICATION NUMBER: US 60/506,332									
; PRIOR FILING DATE: 2003-09-26									
; NUMBER OF SEQ ID NOS: 136									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 16									
; LENGTH: 2377									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-757-262-16									
Query Match 99.3%; Score 11815.5; DB 17; Length 2377;									
Best Local Similarity 95.2%; Pred. No. 0;									
Matches 2264; Conservative 1; Mismatches 1; Indels 111; Gaps 2;									
QY	1	MDEEDGAGAEESGQPRSFMRNLNDSGAGRPGPSAEKDPGSADSEAEGLYPALAPVV	60						
Db	1	MDEEDGAGAEESGQPRSFMRNLNDSGAGRPGPSAEKDPGSADSEAEGLYPALAPVV	60						
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Db	61	FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTILGMFRPCEDIAQDSQRCRILQAF	120						
QY	121	DDFIFAFPAVEMVVKMVALGIFGKKCYLGDWTNRLLDFFIVIAGMLEYSLDLQNVFSFAVR	180						
Db	121	DDFIFAFPAVEMVVKMVALGIFGKKCYLGDWTNRLLDFFIVIAGMLEYSLDLQNVFSFAVR	180						
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Db	181	TVRVLRPLRAINRVPSMRILVTLDDTLPMGLNVLLLCFFVFFIFGIVGVQLWAGLLRNR	240						
QY	241	CFLPENFSLPLSDVLERYQYQ TENEDESPFI CSQPRENGMRSCRSVPTLRGDGGGPPCGL	300						
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QY	901	PDRKNFDSLLWAIWTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLENLV	960						
Db	901	PDRKNFDSLLWAIWTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLENLV	960						
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QY	1381	RLRLTLRLRVLRSRAOGLKLVETILMSSLKPIGNIVVICCAFFIIIFGILGVQLFKGKFFV	1440						
Db	1381	RLRLTLRLRVLRSRAOGLKLVETILMSSLKPIGNIVVICCAFFIIIFGILGVQLFKGKFFV	1440						
QY	1441	CQGEDTRNITNKSDCAEAS YRWRHKNYFNFDNLGQALMSLFVLASKDGVVDIMYDGLDVG	1500						
Db	1441	CQGEDTRNITNKSDCAEAS YRWRHKNYFNFDNLGQALMSLFVLASKDGVVDIMYDGLDVG	1500						
QY	1501	VDQQPMHNHPWMLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQHEEEARREEKRL	1560						
Db	1501	VDQQPMHNHPWMLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQHEEEARREEKRL	1560						
QY	1561	RRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGV	1602						
Db	1561	RRLEKKRRMLDDVIA SGSSASAASEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGV	1620						
QY	1603	IGLNVVTMAMEHYQOQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDL	1662						
Db	1621	IGLNVVTMAMEHYQOQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDL	1680						
QY	1663	AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLDVTMQAL	1722						
Db	1681	AIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLDVTMQAL	1740						
QY	1723	PQVGNLGLLFFLFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVST	1782						
Db	1741	PQVGNLGLLFFLFAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRVST	1800						
QY	1783	GDVWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVVIAMVLMKHLEESNKE	1842						
Db	1801	GDVWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVVIAMVLMKHLEESNKE	1860						
QY	1843	AKBAAEAELEAELEMTLSPQPHSPGLSPFLWPVGEGPDSPPSPKPGALHPAAHARSASH	1902						
Db	1861	AKBAAEAELEAELEMTLSPQPHSPGLSPFLWPVGEGPDSPPSPKPGALHPAAHARSASH	1920						
QY	1903	FSLEHPT-----	1909						

Db 1921 FSLEHPTDRQLFDTISLLIQSLEWELKLMDELAGPGQPSAFPSAPSLGSDPQIPLAE 1980
QY 1910 -----MQPHTELPDGLLTVRKSG 1929
Db 1981 MEALSLTSEIVSEPPSCSLALTDDSLPDDMHTLLLSALESNMQPHTELPDGLLTVRKSG 2040
QY 1930 VSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAP 1989
Db 2041 VSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAP 2100
QY 1990 HLLQPHSAPTWTIPKLPDPGRSPLAQRPLRRQAAIRTDSDVQGLGSREDLLAEVSGPS 2049
Db 2101 HLLQPHSAPTWTIPKLPDPGRSPLAQRPLRRQAAIRTDSDVQGLGSREDLLAEVSGPS 2160
QY 2050 PPLARAYFWGQSSTQAAQHRSRSHKISKHMTPPAPCPGPEPNWGKPPETRSSLELDT 2109
Db 2161 PPLARAYFWGQSSTQAAQHRSRSHKISKHMTPPAPCPGPEPNWGKPPETRSSLELDT 2220
QY 2110 LSWISGDLPPGGQEEPPSPRDLKKCYSVQAEQSCQRRPTSWLDEQRRHSIAVSCLDGSGQ 2169
Db 2221 LSWISGDLPPGGQEEPPSPRDLKKCYSVQAEQSCQRRPTSWLDEQRRHSIAVSCLDGSGQ 2280
QY 2170 PHLGTDPSNLGGQPLGGPSRPPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDS 2229
Db 2281 PHLGTDPSNLGGQPLGGPSRPPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDS 2340
QY 2230 KDPLASGPPDSMAASPSPKKDVLSGLSSDPADLDP 2266
Db 2341 KDPLASGPPDSMAASPSPKKDVLSGLSSDPADLDP 2377

RESULT 2

US-10-408-765A-625
; Sequence 625, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 625
; LENGTH: 2243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-625

Query Match 98.8%; Score 11758.5; DB 16; Length 2243;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2242; Conservative 0; Mismatches 1; Indels 23; Gaps 1;

QY 1 MDEEEDGAGAEESGQPRSFMRNLNLSGAGGPPGSAEKDPGSADSEAEGLPYPALAPVV 60
Db 1 MDEEEDGAGAEESGQPRSFMRNLNLSGAGGPPGSAEKDPGSADSEAEGLPYPALAPVV 60
QY 61 FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLMFRPCEDIACDQSQRILQAF 120
Db 61 FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLMFRPCEDIACDQSQRILQAF 120
QY 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180
Db 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR 180

QY 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVEFFIFGIVGVQLWAGLLNR 240
Db 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVEFFIFGIVGVQLWAGLLNR 240
QY 241 CFLPENFSLPLSVDLERYQYOTENEDESPFICSQPRENGMRSCRSVPTLRDGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYQYOTENEDESPFICSQPRENGMRSCRSVPTLRDGGGPPCGL 300
QY 301 DYEAYNSSNTTCVWNQYNTCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360
Db 301 DYEAYNSSNTTCVWNQYNTCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM 360
QY 361 YFVMDAHSFYNIYFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
Db 361 YFVMDAHSFYNIYFILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
QY 421 STLASFSEPGSCYEELLKYLVIILKAAARLAAQVSRAGVRVGLSSPAPLGQETQPSS 480
Db 421 STLASFSEPGSCYEELLKYLVIILKAAARLAAQVSRAGVRVGLSSPAPLGQETQPSS 480
QY 481 SCSRSRRLSVHLLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPPSTP 540
Db 481 SCSRSRRLSVHLLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPPSTP 540
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600
Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600
QY 601 TLKEKALVEVAASSGPPTILSLNIPPGYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
Db 601 TLKEKALVEVAASSGPPTILSLNIPPGYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
QY 661 ACGPDCPCYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHRRORS LGPDA 720
Db 661 ACGPDCPCYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHRRORS LGPDA 720
QY 721 EPSSVLAFWRLICDTERKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780
Db 721 EPSSVLAFWRLICDTERKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNI 780
QY 781 VFTSLFALEMLLKLVLVYGPFGYIKPNYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMR 840
Db 781 VFTSLFALEMLLKLVLVYGPFGYIKPNYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMR 840
QY 841 VLKLVRLPALQRLVVLKMTMDNVATFCMLLMFIFIFSILGMHLFGCKFASERDGDTL 900
Db 841 VLKLVRLPALQRLVVLKMTMDNVATFCMLLMFIFIFSILGMHLFGCKFASERDGDTL 900
QY 901 PDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALTMTFGNYVLFNLLV 960
Db 901 PDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALTMTFGNYVLFNLLV 960
QY 961 AILVEGFQAEIISKREDASQOLSCIQLPVDSQGGDANKSESEPDFFPSLDGDGDRKKCL 1020
Db 961 AILVEGFQAEIISKREDASQOLSCIQLPVDSQGGDANKSESEPDFFPSLDGDGDRKKCL 997
QY 1021 ALVSLGEHPLEKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1080
Db 998 ALVSLGEHPLEKSLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA 1057
QY 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLSGEGQESQ 1140
Db 1058 HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLSGEGQESQ 1117
QY 1141 DEEESSEERASPAGSDHRRHRSLEFEAKSSFDLPDTLQVPLHRTASGRGSASEHODCN 1200
Db 1118 DEEESSEERASPAGSDHRRHRSLEFEAKSSFDLPDTLQVPLHRTASGRGSASEHODCN 1177
QY 1201 GKSASGRLARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERSWSAYIFP 1260
Db 1178 GKSASGRLARALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERSWSAYIFP 1237
QY 1261 PQSRFRLLCHRIITHKMFHDHVVLVILFNLNCITIAMERFKIDPHSAERIFLTLSNYIFTAV 1320

Db 1238 PQSRFLLCHRIITHKMFHDVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLNYYIFTAV 1297
QY 1321 FLAEMTVKVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVSMVSDSGTKILGMLRVL 1380
Db 1298 FLAEMTVKVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVSMVSDSGTKILGMLRVL 1357
QY 1381 RLRLTLRPLRVISRAQGLKLVWETLMSLLKPIGNIVVICAFFIIFGILGVQLFKGKFFV 1440
Db 1358 RLRLTLRPLRVISRAQGLKLVWETLMSLLKPIGNIVVICAFFIIFGILGVQLFKGKFFV 1417
QY 1441 CQGEDTRNITNKSDCAEASRYRVRHKYNFEDNLQALMSLFVLASKDGVVDIMYDGLDAVG 1500
Db 1418 CQGEDTRNITNKSDCAEASRYRVRHKYNFEDNLQALMSLFVLASKDGVVDIMYDGLDAVG 1477
QY 1501 VDQQPIMNHNPMMLLYFISFLLIIVAFVLMNFVGVVVVENFHKCRQHQBEEHARRREKRL 1560
Db 1478 VDQQPIMNHNPMMLLYFISFLLIIVAFVLMNFVGVVVVENFHKCRQHQBEEHARRREKRL 1537
QY 1561 RRLEKKRRKAQCKPYYSYSRFRLLVHHLCTSHYLDLFIITVIGLNVVVTNAMEHYQQOI 1620
Db 1538 RRLEKKRRKAQCKPYYSYSRFRLLVHHLCTSHYLDLFIITVIGLNVVVTNAMEHYQQOI 1597
QY 1621 LDEALKICNYIFTVIFVLESVEFKLVAFGRFFQDRWNQLDLAIVLLSIMGITLEEIEVN 1680
Db 1598 LDEALKICNYIFTVIFVLESVEFKLVAFGRFFQDRWNQLDLAIVLLSIMGITLEEIEVN 1657
QY 1681 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTMQALPQVGNLGLLPMLLFFIFA 1740
Db 1658 ASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTMQALPQVGNLGLLPMLLFFIFA 1717
QY 1741 ALGVELFGDLECDETHPCBGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDCDQE 1800
Db 1718 ALGVELFGDLECDETHPCBGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDCDQE 1777
QY 1801 STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAEEAELEEMKTL 1860
Db 1778 STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAEEAELEEMKTL 1837
QY 1861 SPQHSPLGSPFLWPVGVEGPDSPDKPGALHPAAHARSASHFSLEHPTMQPHTELPGP 1920
Db 1838 SPQHSPLGSPFLWPVGVEGPDSPDKPGALHPAAHARSASHFSLEHPTMQPHTELPGP 1897
QY 1921 DLLTWRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWLGPKAQSGSVLSVHSPADTSY 1980
Db 1898 DLLTWRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWLGPKAQSGSVLSVHSPADTSY 1957
QY 1981 ILQLPKDAPHLLQPHSAPTWTGTIPKLPPPGRSPLAQRPLRQAAIRTDSDLVQGLGSRED 2040
Db 1958 ILQLPKDAPHLLQPHSAPTWTGTIPKLPPPGRSPLAQRPLRQAAIRTDSDLVQGLGSRED 2017
QY 2041 LLAEVSGPSPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPET 2100
Db 2018 LLAEVSGPSPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPET 2077
QY 2101 RSSLELDTLSWISGDLPLPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRHSTA 2160
Db 2078 RSSLELDTLSWISGDLPLPGGQEEPPSPRDLKKCYSVEAQSCQRRPTSWLDEQRHSTA 2137
QY 2161 VSCLDGSGQPHLGTDPNLGGQPLGGPSRPKKLSPPSITIDPPESQGPRTPPSPGICL 2220
Db 2138 VSCLDGSGQPHLGTDPNLGGQPLGGPSRPKKLSPPSITIDPPESQGPRTPPSPGICL 2197
QY 2221 RRRAPSSDSKOPLASGPPDMSMAASPSPKDVLSLGSLSSDPADLDP 2266
Db 2198 RRRAPSSDSKOPLASGPPDMSMAASPSPKDVLSLGSLSSDPADLDP 2243

RESULT 3
US-09-383-894-2
; Sequence 2, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:

; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2374
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-09-383-894-2

Query Match 93.3%; Score 11111; DB 10; Length 2374;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;

QY 1 MDEEDGAGAEESGQPRSFMRNLDSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
Db 1 MDEEDGAGAEESGQPRSFMRNLDSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVV 60
QY 61 FFVLSQDSRPRSCLRTVCNPFWERISMLVILNCVTLGMFRPCEDIACDSQRCRILQAF 120
Db 61 FFVLSQDSRPRSCLRTVCNPFWERISMLVILNCVTLGMFRPCEDIACDSQRCRILQAF 120
QY 121 DDFIFAFFAVEMVVMKVALGIFGKKCYLGDWTNRDLDFIIVAGMLEYSLDLQNVFSFAVR 180
Db 121 DDFIFAFFAVEMVVMKVALGIFGKKCYLGDWTNRDLDFIIVAGMLEYSLDLQNVFSFAVR 180
QY 181 TVRVLRLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Db 181 TVRVLRLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
QY 241 CFLPENFSLPLSVDLERYQOTENEDESPFICSPRENMRSCRSVPTLRGDDGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYQOTENEDESPFICSPRENMRSCRSVPTLRGDDGGGPPCGL 300
QY 301 DYEAYNSSNTTCVWNQYVYTNCSAGEHNPFGKAINFEDNIGYAWIAIFQVITLEGWVDIM 360
Db 301 DYEAYNSSNTTCVWNQYVYTNCSAGEHNPFGKAINFEDNIGYAWIAIFQVITLEGWVDIM 360
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
Db 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
QY 421 STLASFSEPGSCYEELLKYLVIILKAAARLAQVSRAGVRVGLLSSPAPLGGQETQPS 480
Db 421 STLASFSEPGSCYEELLKYLVIILKAAARLAQVSRAGVRVGLLSSPAPLGGQETQPS 480
QY 481 SCSRRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db 481 SCSRRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600
Db 541 TPSSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE 600
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTQACQSSCKISSPCLKADSG 660
Db 601 ILKDKALVEVAPSPGPTLTLSFNIPPGPYSSMHKLLTQSTQACQSSCKISSPCLKADSG 660
QY 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRS LGPD 719
Db 661 ACPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRS LGPD 720
QY 720 AEPSSVLAFWRLLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHQPELTNALEISN 779
Db 721 AEPSSVLAFWRLLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHQPELTNALEISN 780

QY 780 IVFTSLFALEMLLKLIVYGPFGYIKNPYNIPDGVIVVISVWEIVGQGGGLSVLRTFRM 839
Db 781 IVFTSLFALEMLLKLIVYGPFGYIKNPYNIPDGVIVVISVWEIVGQGGGLSVLRTFRM 840
QY 840 RVLKLVRFPLALQRLVVLMTKMDNVATFCMLLMLFIFIFISILGMHLFGCKFASERDGT 899
Db 841 RVLKLVRFPLALQRLVVLMTKMDNVATFCMLLMLFIFIFISILGMHLFGCKFASERDGT 900
QY 900 LPDRKNFDSLWALVTVFQILTQEDWNKVLNGMASTSSWAALFYIALMTFGNYVLFNLL 959
Db 901 LPDRKNFDSLWALVTVFQILTQEDWNKVLNGMASTSSWAALFYIALMTFGNYVLFNLL 960
QY 960 VAILVEGFAEIEISKREDASGLSCIQLPVD SQGDANKSESPDPFFPSLDGDRKKC 1019
Db 961 VAILVEGFAEIEISKREDASGLSCIQLPVSQGGDATKSESPDPFFPSVVDGDRKKR 1020
QY 1020 LALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGA 1079
Db 1021 LALVALGEHAELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSGRRRTSSGSAEPGA 1080
QY 1080 A-HEMKSPPSARSSPHSPWSAASWTSSRRSSRNLSGRAPSLKRRSPSGERRSLLSGEGQE 1138
Db 1081 AHHEMKSPPSARSSPHSPWSAASWTSSRRSSRNLSGRAPSLKRRSPSGERRSLLSGEGQE 1140
QY 1139 SQDEEESSEERASAPAGSDHRRHRSLEAKSSFDPDLTQVPLHRTASGRGSASEHQD 1198
Db 1141 SQDEEESSEEDRASAPAGSDHRRHRSLEAKSSFDPDLTQVPLHRTASGRGSASEHQD 1200
QY 1199 CNGKSASGLARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWAI 1258
Db 1201 CNGKSASGLARTLRTDDPQLDGDDEGNLSKGERIQAWRSRLPACCRERDSWAI 1260
QY 1259 FPPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318
Db 1261 FPPQSRFRLLCHRIITHKMFHDVVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1320
QY 1319 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVISVIDILVSMVSDSGTKILGMLR 1378
Db 1321 AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVISVIDILVSMVSDSGTKILGMLR 1380
QY 1379 VLRLRLTLRPLRVISRAQGLKLVTETLMSLKPIGNIIVVICCAFFIIFGILGVQLFKGF 1438
Db 1381 VLRLRLTLRPLRVISRAQGLKLVTETLMSLKPIGNIIVVICCAFFIIFGILGVQLFKGF 1440
QY 1439 FVCGEDTRNITNKSDCAEASRVRWRHKYNFNDLQALMSLVFLASKDQWVDIMYDGLDA 1498
Db 1441 FVCGEDTRNITNKSDCAEASRVRWRHKYNFNDLQALMSLVFLASKDQWVDIMYDGLDA 1500
QY 1499 VGVDQOPIMNHNPMMLLYFISFLLI VAFVFLNMFVGVVVENFHKCRHQHEEARRREEK 1558
Db 1501 VGVDQOPIMNHNPMMLLYFISFLLI VAFVFLNMFVGVVVENFHKCRHQHEEARRREEK 1560
QY 1559 RLRLLEKKRR-----KAQCKPYSDYSRFRLLVHLLCTSHYLDLFI 1600
Db 1561 RLRLLEKKRRNMLDDVIAAGSSASAASEAQCKPYSDYSRFRLLVHLLCTSHYLDLFI 1620
QY 1601 GVIGLNVVTMAMEHYQOPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQL 1660
Db 1621 GVIGLNVVTMAMEHYQOPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQL 1680
QY 1661 DLAI VLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMALLDVTMQ 1720
Db 1681 DLAI VLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMALLDVTMQ 1740
QY 1721 ALPQVGNLGLLFMLLFFIFAALGVLFGLDCEDETHPCEGLGRHATERFNGMAFLTFRV 1780
Db 1741 ALPQVGNLGLLFMLLFFIFAALGVLFGLDCEDETHPCEGLGRHATERFNGMAFLTFRV 1800
QY 1781 STGDNWNGIMKDTLRDCDQESTCYNTVISPIVFSVFLTAQFVLNVVIAVLMKHLEESN 1840
Db 1801 STGDNWNGIMKDTLRDCDQESTCYNTVISPIVFSVFLTAQFVLNVVIAVLMKHLEESN 1860
QY 1841 KEAKEAELEAELEEMKTLSPQSPHSPGLSPFLWPGVEGPDSPDSPKPGALHPAAHARSA 1900

Db 1861 KEAKEAELEAELEEMKTLSPQSPHSPGLSPFLWPGVEGVNSPSPKPGAPHTTAHIGAA 1920
QY 1901 SHFSLEHPTMQPHTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957
Db 1921 SGFSLEHPTMVPHPEEVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHG 1980
QY 1958 WGLPKAQSGSVLSVHSQPADTSYIQLPKDAPHLLOPHSAPTWGTIPKLP PPGRSPLAQ 2017
Db 1981 WGLPKAQSGSVLSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLP PPGRSPLAQ 2040
QY 2018 PLRRQAAIRTDSDVQGLSGREDLLAEVSGSPPLARAYSWFQSSSTQAQQHSRSHKIS 2077
Db 2041 PLRRQAAIRTDSDVQGLSGREDLLSEVSGPCLTRSSSPFWGGSSIQQQRSIGIQKVS 2100
QY 2078 KHMTTPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPPGGQEEPPSPRDLKKYS 2137
Db 2101 KHIRLPAPCPGLEPSWAKOPPETRSSLELDTLSWISGDL--PSSQEEPLSPRDLKKYS 2159
QY 2138 VEAQSCQRRTSWLDEQRRHSIAVSCDSGSQLHGTDPNLGGQPLGGGSRPKKLSP 2197
Db 2160 VETQSCRRRPGSWLDEQRRHSIAVSCDSGSQLPCLPSSSLGGQPLGGGSRPKKLSP 2219
QY 2198 PSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKDVLISLGL 2257
Db 2220 PSISIDPPESQGSRRPPCSPGVCLRRRAPASDSKDPVSVPDLSTAASPSPKDVLISLGL 2279
QY 2258 SSDPADLDP 2266
Db 2280 SSDPTDMDP 2288

RESULT 4

US-09-383-894-4
; Sequence 4, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2425
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-383-894-4

Query Match 93.3%; Score 11111; DB 10; Length 2425;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;

QY 1 MDEEEDGAGAEESGQPRSMRLNDLSGAGRPGPSAEKOPGSADSEAGLPYPALAPVV 60
Db 52 MDEEEDGAGAEESGQPRSMRLNDLSGAGRPGPSAEKOPGSADSEAGLPYPALAPVV 111
QY 61 FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 120
Db 112 FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF 171
QY 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDWTNRLDFFI VIAGMLEYSLDLQNVSFSAVR 180
Db 172 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDWTNRLDFFI VIAGMLEYSLDLQNVSFSAVR 231
QY 181 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Db 232 TVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 291

QY 241 CFLPENFSLPLSDLEYYQTENEDESPFICSPRENGMRSCRSVPTLRGDGGGPPCGL 300
Db 292 CFLPENFSLPLSDLEPPYYQTENEDESPFICSPRENGMRSCRSVPTLRGEGGGPPCSL 351
QY 301 DYEAYNSSNTTCVNNQYTYNCISAGEHNPFKGINFDNIGYAWIAIFQVITLEGWVDIM 360
Db 352 DYETYNSSNTTCVNNQYTYNCISAGEHNPFKGINFDNIGYAWIAIFQVITLEGWVDIM 411
QY 361 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKORESOLMREQVRFLSNA 420
Db 412 YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKORESOLMREQVRFLSNA 471
QY 421 STLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAGVRVGLLSSPAPLGGQETQPS 480
Db 472 STLASFSEPGSCYEELLKYLVIILRKAARRLAQVSRAGVRVGLLSSPVARSGQEPQPSG 531
QY 481 SCRSRHRRLSVHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTP 540
Db 532 SCTRSRHRRLSVHHLVHHHHHHHHYHLNGTTLRVPRASPEIQDRDANGSRRLMLPPPSTP 591
QY 541 ALSGAPPGAESVHSFYHADCHLEPVRCAOPPRSPSEASGRTVSGKVYPTVHTSPPE 600
Db 592 TPGGPPRGAESVHSFYHADCHLEPVRCAOPPRSPSEASGRTVSGKVYPTVHTSPPE 651
QY 601 TLKEKALVEVAASSGPPTILTSINIPPGPYSSMHKLLTQSTGACQSSCKISSPCLKADSG 660
Db 652 ILKDKALVEVAPSPGPTILTSFNIPPGPFSSMHKLLTQSTGACHSSCKISSPCKADSG 711
QY 661 ACPDPCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRSGLPD 719
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QY 720 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNLSMGIEYHEQPEELTNALEISN 779
Db 772 AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNLSMGIEYHEQPEELTNALEISN 831
QY 780 IVFTSLFALEMLLKLLVYGPGYIKNPYNIFDGVIVVSVWEIVGQGGGLSVLRTFRIM 839
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QY 840 RVLKLVRFPLPALQRLVLMKTMNDNVATFCMLLMLFIFISILGMHLFGCKFASERDGD 899
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QY 900 LPDRKNFDSLWAIIVTVFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 959
Db 952 LPDRKNFDSLWAIIVTVFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 1011
QY 960 VAILVEGFAEEISKREDASGQLSICQLPVD SQGDANKSESEPDFFSPSLDGDGDRKCC 1019
Db 1012 VAILVEGFAEEISKREDASGQLSICQLPVNSQGGDATKSESEPDFFSPSVDGDGDRKKR 1071
QY 1020 LALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA 1079
Db 1072 LALVALGEHAELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSGRRTSSSGSAEPGA 1131
QY 1080 A-HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLSGEQE 1138
Db 1132 AHHEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLSGEQE 1191
QY 1139 SQDEEESSEEFERASPAGSDHRRHRSLEFEAKSSFDP LPTTLQVPLHRTASGRGSASEHQD 1198
Db 1192 SQDEEESSEEDRASPDAGSDHRRHRSLEFEAKSSFDP LPTTLQVPLHRTASGRSSASEHQD 1251
QY 1199 CNGKSASGRALARALRPDDPPLDGDADDENLSKGERVRAWTRARLPACYLERDSWSAYI 1258
Db 1252 CNGKSASGRILARTLRDDPQLDGDNDNENLSKGERIQAWVRSLPACCRERDSWSAYI 1311
QY 1259 FPPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPSAERIFLTLSNYITFT 1318
Db 1312 FPPQSRFRLLCHRIITHKMFHDHVLVIIIFLNCITIAMERPKIDPSAERIFLTLSNYITFT 1371

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QY 1379 VLRLRLTLRPLRVISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438
Db 1432 VLRLRLTLRPLRVISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1491
QY 1439 FVCQGEDTRNITNKSDCAEASRYRWRHKYNFNDLQALMSLFLVASKDGVVDIMYDGLDA 1498
Db 1492 FVCQGEDTRNITNKSDCAEASRYRWRHKYNFNDLQALMSLFLVASKDGVVDIMYDGLDA 1551
QY 1499 VGVDQQPIMNHNPMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHEEEARRREK 1558
Db 1552 VGVDQQPIMNHNPMMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHEEEARRREK 1611
QY 1559 RLRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFT 1600
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QY 1601 GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVFVLESVFKLVAFGFRFFQDRWNQL 1660
Db 1672 GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVFVESVFKLVAFGFRFFQDRWNQL 1731
QY 1661 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRAALLDTVMQ 1720
Db 1732 DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRAALLDTVMQ 1791
QY 1721 ALPOVGNLGLLFLMLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFCMAPLTLFRV 1780
Db 1792 ALPOVGNLGLLFLMLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFCMAPLTLFRV 1851
QY 1781 STGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMMKHLEESN 1840
Db 1852 STGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMMKHLEESN 1911
QY 1841 KEAKEEAELEAELELEMKLTLSPQSPHSPGLSPFPLWPGVEGPDSPDSPKPGALHPAAHARSA 1900
Db 1912 KEAKEEAELEAELELEMKLTLSPQSPHSPGLSPFPLWPGVEGNSPDSPKPGAPHTAHIGAA 1971
QY 1901 SHFSLEHPTMQPHPTPLP-----GPDLLTVRKSGVSRTHSLPNDSYMCRHSGSTAFGLGHRG 1957
Db 1972 SGFSLEHPTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAESLGHG 2031
QY 1958 WGLPKAQSGSVLSVHSQPADTYSIQLPKDAPHLLOPHSAPTWTGIPKLPPEGRSPLAQ 2017
Db 2032 WGLPKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHCAPTWGAIPKLPPEGRSPLAQ 2091
QY 2018 PLRRQAAIRTDSLDVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQOHSRSHSKIS 2077
Db 2092 PLRRQAAIRTDSLDVQGLGSRREDLLSEVSGSPCLTRSSSFWGGSSIQVQQRSGIQSKVS 2151
QY 2078 KHMTTPAPCPGPEPNWKGPPETRSLSLELDTLSWISGDLPLPGGQEEPPSPRDLKCCYS 2137
Db 2152 KHIRLPAPCPGLEPSWAKDPPETRSLSLELDTLSWISGDLPL-PSSQEEPLSPRDLKCCYS 2210
QY 2138 VEAQSCQRRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDPNLSGQPLGGGSRPKKILSP 2197
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QY 2258 SSDPADLDP 2266
Db 2331 SSDPTDMDP 2339


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; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1128
; LENGTH: 2353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1128

Query Match      52.2%; Score 6212; DB 16; Length 2353;
Best Local Similarity 56.7%; Pred. No. 0;
Matches 1366; Conservative 214; Mismatches 525; Indels 304; Gaps 61;

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Db 27 GASPEPGAPGREAEERGSEL-GVSPSESP-AAERGAELGADEEQRPYPALAAATVFFCLG 84

QY 66 QDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLMFRPCEDIACDSQRCRILQAFFDFIF 125
Db 85 QTRPRSWCLRLVCNPNWFEHVSMVLVIMLNCVTLMFRPCEDVECGSERCNILEAFDAFIF 144

QY 126 AFFAVEMVVKMVALGIFGKCYLGDTWNRLDFFIVAGLMLEYSLDLQNVSPSAVRTVRVL 185
Db 145 AFFAVEMVVKMVALGIFGKCYLGDTWNRLDFFIVAGMMEYSLDGHNVSLSAIRTVRVL 204

QY 186 RPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPE 245
Db 205 RPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLDS 264

QY 246 NFSPLPLSVD-LERYVQTENEDESPFICSPRENQMRSCRSVP---TLRGDGGGPPPCGLD 301
Db 265 AFVRNNNLTLRPPYQTEEGEENPFICSSRRDNGMQKSHIPGRREL-----MPCTLG 318

QY 302 YEAYN-----SSNNTCVNWNQYNTNCSAGHNPPFKGAINFDNIGYAWIAIFQVITLE 354
Db 319 WEAYTQPAEYGVAARNACINWNQYNNVCRSGDSNPHNGAINFDNIGYAWIAIFQVITLE 378

QY 355 GWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQRV 414
Db 379 GWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREORA 438

QY 415 RFLSNASTLASFSEPGSCYEELLYLVYLKKAARLAQVSRAGVRVGLLSSPAPLGQ 474
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QY 475 ETQPSSSCSRSHRR-LSVHHLV-HHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRL 532
Db 499 --GPGHRQRRAGRHTASVHLLVYHHHHHHHHHHYHSHGSRPRRPGPEPGACD-----TRLV 551

QY 533 MLPPPSTPALSGAPPGAESVHSFYHADCHLE--PVRCAQPPPPSPSEASGR-TVSGKV 589
Db 552 RAGAPSPSPGRGPDPAESVHSIYHADCHIEGPQERARVAHAATAAASLRATGLGTM 611

QY 590 -YPTV-----HTSP-----PPELKEKALVEVAASSGPPTLTSLNIPPGPY 629
Db 612 NYPTILPSGVSGSGKSTSPGKKGWAGGPPT-----GGHGPLSLNS-----PDY 657

QY 630 SSMHKLLETQSTGACQS-----SCKISSPCLKADSGACGPDSCPYCARA-GAGEVELA 681
Db 658 EKIPHVVGHEGLQAPGHLGSLSVPCPLSP--PAGTLTCELKSCPYCTRALEDPEGELS 715
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QY 726 LAFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFTSL 785
Db 776 GRLWVTFSGKLRRIVDSKYFSGIMMAILVNTLSMGVEYHEQPEELTNALEISNIVFTSM 835

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Db 836 FALEMLLKLILACGPLGIYRNPYNIFDGIIVVISWEIVQADGGLSVLRTFRLMRVLKIV 895

QY 846 RFLPALQRLVLMKTMNVATFCMLLMLFIFIFISILGMHLFGCKFASERD-GDTLPDRK 904
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QY 905 NFDSLLWAIIVTFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILV 964
Db 956 NFDSLLWAIIVTFQILTQEDWNVVLYNGMASTSSWAALYFVALMTFGNYVLFNLLVAILV 1015

QY 965 EGFOAEISKREDASGQLSCIQLPVDSQGGDANKSESEDPFFSPSLDGD-----GD 1015
Db 1016 EGFOAE-----GDANRSDTDEKTSVHFEEDFKLRELQTTTE 1052

QY 1016 RKKCLALVSLGEHPELRSLLPLIHTAATMSLPKSTSTGLGEALGPASRRTSSSGSA 1075
Db 1053 LKMCSLAVTPNGHLEGRGSLSPPLIMCTAATPMTPKSSPFLDAAAPSLDSRRGSSSGD 1112

QY 1076 EPGAHAHEMKSPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGE 1135
Db 1113 PP--LGDQKPPASLRSSPCAPWPGSPGAWSSRRSSWSLGRAPSLKRRGQCGERESLLSGE 1170

QY 1136 GQESQDEEESSEERASPA--GSDHRRHGRSLEERAKSSFDPDLDTL-----QVPGLH--- 1184
Db 1171 KGSTDDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPPTKCRDRDQGVVALPSDF 1228

QY 1185 --RTASGRGSASEHQDCNGKKSASGRALARALRPDDPPLDGDADDEGNLSKGERVRAWIRA 1242
Db 1229 FLRIDSHREDAAELDDSDSDSCCLRLHKVLEPYKP-----QWCRS 1268

QY 1243 RLPACYLERDSWAYIFPPQSRFLLCRLIITHKMFHDVVLVIIFLNCITIAMERPKIDP 1302
Db 1269 -----REAWALYLFSPQNRFRVSCQKVIHKMFHDVVLVIFILNCVTIALERPDI 1320

QY 1303 HSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLGDLVLISVIDIL 1362
Db 1321 GSTERVFLSVSNYIFTAIFVAEMVKVVALGLLSGEHAYLQSSWNLLDGLLVLSLVDIV 1380

QY 1363 VSMVSDSGTKILGLMLRLRLRLRLRPLRPLRVISRAQGLKLVETLMSLKPIGNIVVICAF 1422
Db 1381 VAMASAGGAKILGVLRVLRLLRPLRPLRPLRVISRAPGLKLVETLISLRPIGNIVLICAF 1440

QY 1423 FIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVL 1482
Db 1441 FIIFGILGVQLFKGKFFYCEGPDTRNISTKAQCRAAHYRWVRKYNFDNLGQALMSLFVL 1500

QY 1483 ASKDGWVDIMYDGLDVGVDQOPIMNHNPMMLLYFISFLIVAFVFLNMFVGVVVENFHK 1542
Db 1501 SSKDGNVIMYDGLDVGVDQOPVQNHNPWMLLYFISFLIVSFFVFLNMFVGVVVENFHK 1560

QY 1543 CRHQHEEEAARRREKRLRRLEKKRR-----KAQCKPYVSDYSRFRLLVHHLCTSHYLD 1596
Db 1561 CRHQHEAEEARRREKRLRRLERRRRSTFPSPAQRPPYADYSPTRRSIHSLCTSHYLD 1620

QY 1597 LFITGVIGLVNVTMAMEHYQQPQIILDEALKICNYIFTVIFVLESVFKLVAFGFRFRFFQDR 1656
Db 1621 LFITFIIICVNVITMSMEHYNQPKSLDEALKYCNYVFTIVFVEAALKLVAFGFRFRFFQDR 1680

QY 1657 WNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMRAALLD 1716
Db 1681 WNQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMATGMRAALLD 1740

QY 1717 TVMQALPQVGNLGLLFLMLFFIFAALGVLEFGDLECDETHPCGELGRHATFRNFGMAFLT 1776
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Db 1741 TVVQALPQVGNLGLLMLFFIYAALGVLELFGRLCESDNPCEGLSRHATFSNFGMAFLT 1800
QY 1777 LFRVSTGDNWNGIMKDLTRDC--DQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVL 1833
Db 1801 LFRVSTGDNWNGIMKDLTRCSREDKHCLSYLPALSPVYFVTFVLVAQFVLNVVVAVLM 1860
QY 1834 KHLEESNKEAELEAELEAELEMTLSPOHSPGLSGPFLWPGVEGPDSP---DSPKPGA 1890
Db 1861 KHLEESNKEAREDAELDAEIELEM-----AQGPSARRVDADRP-- 1899
QY 1891 LHPAAHARSASHFSLHPTMQPHTELPG---PDLLTVRKSGVSRTHSLPNDSYMCRHG 1946
Db 1900 -----PLQESPGLDAPNLV-ARKVSVSRMLSLPNDSYMFRPV 1937
QY 1947 STAEGP-----LHHRGWGLPKAQSGSVLSVHSPADTSYILQLPKDAPHLLOPHSA 1997
Db 1938 VPASAPHRPLQEVEMETYGAGTP--LGSVASVHSPPAESCASLQIP-----LAVSSPA 1989
QY 1998 PTWGVTIPKLPPPG--RSPLAQRLRRQAAIRTDLSLDVQGLSREDLL--AEVSGPSP--P 2051
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QY 2052 LARAYFWG--QSSTQAQOHSRSHSKISKHMTTPAP-CPGPEPNWKGPPETRSSLELDT 2108
Db 2049 VTQGSLSQSPRSPRPASVTRKHT-FGQHCVSSRPAAPGGE-----EAEASDPAD 2099
QY 2109 ELSWISGDLPL-----PGQEEPP---SPRDLKKCYSEVAQSCQRRPTSWLDEQRRHSI 2159
Db 2100 EVSHITSSACPWQPTAEPHGPEASPVAGGERDLRLRLYSVDAQGFLDKP-GRADEQWRPSA 2158
QY 2160 AVSCLDSGQPHLGTDPNSLGGQPLGGGSRPKKLSPPSITIDPP-ESQGPRTPPSP-- 2216
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QY 2217 -GICURRRAPS-----SDSKDPL-----ASGPPDSMA---ASPSPKKDVLSLSGLSSDPA 2262
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QY 2263 DL-----DP 2266
Db 2272 DLGVPSGDP 2280

RESULT 6
US-09-935-541-2
; Sequence 2, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-2
Query Match 46.1%; Score 5492.5; DB 9; Length 2175;
Best Local Similarity 51.3%; Pred. No. 0;
Matches 1233; Conservative 214; Mismatches 508; Indels 447; Gaps 55;
QY 31 RPPGSAEKDPGSDAEAG-----LPYPALAPVVFYLSQDSRPSRWCLRTVCNPFERI 86
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Db 145 YLGDWTNRLLDFFIVMAGMVEYSLDLQNLNSAIRTVRVLRPLRRAINRVPSMRILVNLLD 204
QY 207 TLPMLGNVLLCCFFVFFIFGIVGVQLWAGLLNRNRCFLPENFSPLPSVDLERYQOTENEDE 266
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QY 267 SPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL-----DYEAYNSSNTT--CVNWNQ 318
Db 265 MPFICSLSGDNGIMGCHEIPPLKEQ--GRECCLSKDDVYDFGAGRQDLNASGLCVNWR 321
QY 319 YITNCSAGEHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILL 378
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QY 379 IIVGSFFMINCLVVIATQFSETKQRESQLMREQRVRFSLNASTLASFSFSGSCYEELK 438
Db 382 IIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASAEPGDCYEEIFQ 440
QY 439 YLVYILRKAARLAQVSRRAAGVRVGLLSSPAPLGGQETQPSSSCSRHRRLSVHHLVHH 498
Db 441 YVCHILRKAKR-----RALGLYQALQSRROALG----- 468
QY 499 HHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGAESVHSFYH 558
Db 469 -----PEAPA--PAKPGP-----H 480
QY 559 ADCHLEPVRCQAPPPRSPSEASGRTVGSKVYFVHTSPPTLKEKALVEVAASSGPPT 618
Db 481 AK--EPRHYQLCPQHSPLDATPHTL-----VQIPATL----- 511
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Db 512 -----ASDPASCPCCQHEHGRRP 529
QY 673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRPHSRQRSLGPDAPSSVL----- 726
Db 530 SGLGSTD-SQEGSGSGSSAGGE--DEADGDGARSSEDDGASSELGKEEEEQADGAVWL 586
QY 727 --AFWRLICDTFRKIVDSKYFGRGIMIAILLVNTLSMGIEYHEQPEELTNALISNIVFTS 784
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QY 785 LFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRMLRVLKL 844
Db 647 MFALEMLLKLAAFGFLDYLRNPYNIFDSIIIVISWEIVGQADGGLSVLRTFRLLRVLKL 706
QY 845 VRFLPALQRLVVLMTMDNVATFCMLLMLEFIFISILGMHLFGCKFASERD-GDTLPDR 903
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QY 904 KNFDSLILWAIWTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLLVAIL 963
Db 767 KNFDSLILWAIWTVFQILTQEDWNKVLYNGMASTSPWASLYFVALMTFGNYVLFNLLVAIL 826
QY 964 VEGFQAEIISKREDASGQLSCIQLPVDSQGGDANKSESEPDFFSPS-----LDGD 1013
Db 827 VEGFQAE-----GDANRSYDEDDQSSSNIIEFDKLEGLDSS 863
QY 1014 GDRKKCLALVSLGEHPELRKSLPLPLIHTAATPMSLPKSTSTGLGEALGPASRT----- 1069
Db 864 GDPKLCPIPMTPNGH-----LDP-----SLPLGGLHGPAGAAGPAPRLSLQPD 906
QY 1070 -----SSSGSAEPGAHEMKSPSARSSPHSPWSAASSWTSSRSRNSLGRAPSLK 1120
Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSSYGYPWGRSAAWASRRSSWN-----SLK 960

QY 499 HHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGAESVHSFYH 558
Db 469 -----PEAPA--PAKPGP-----H 480
QY 559 ADCHLEPVRCOAPPPRSPSEASGRTVGSGKVYPTVHTSPPTLKEKALVEVAASSGPPT 618
Db 481 AK---EPRHYQLCPQHSPLDATPHTL-----VQIPATL-----511
QY 619 LTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR-----672
Db 512 -----ASDPASCPCQCHEDGRRP 529
QY 673 AGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRRQRSLGPDAPSSVL-----726
Db 530 SGLGSTD-SQEGSGSGSSAGGE--DEADGDGARSSEDGASSELGKEEEEEEQADGAVWL 586
QY 727 --AFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIYHEQPEELTNALNISNIVETS 784
Db 587 CGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNILEICNVVETS 646
QY 785 LFALEMLLKLIVYGPFGYIKNPYNIFDGIIVVISVWEIVGQGGGLSVLRTFRLMRVLKL 844
Db 647 MFALEMILKLAAGFLDYLRPNYNIFDSIIIVISIWEIVGQADGGLSVLRTFRLLRVLKL 706
QY 845 VRFLPALQRLVLMKTMNDNVATFCMLLMLFIFISILGMHLFGCKFASERD-GDTLPDR 903
Db 707 VREMPALRRQLVLMKTMNDNVATFCMLLMLFIFISILGMHIFGCKFSLRTDGTDTVPDR 766
QY 904 KNFDSLLWAIIVTFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGVYVLFNLLVAIL 963
Db 767 KNFDSLLWAIIVTFQILTQEDWNVLYNGMASTSPWASLYFVALMTFGVYVLFNLLVAIL 826
QY 964 VEGFOAEELSKREDASQGLSCIQLPVDSQGGDANKSESEPDFFS-----LDGD 1013
Db 827 VEGFOAE-----GDANRSYSDQSSNIEEFDKLQEGLDSS 863
QY 1014 GDRKKCLALVSLGEHPELRKSLPLIHTAATPMSLPKSTSTGLGEALGPASRRF-----1069
Db 864 GDXKLCPIPMTPNGH-----LDP-----SLPLGGHLGPAGAAGPAPRLSLQPD 906
QY 1070 -----SSSGSAEPGAHEMKSPSARSSPHSPWSAASSWTSSRRNSLGRAPSLK 1120
Db 907 PMLVALGSRKSSVMSLGRMSYDQRSLSRSSSYGPGWGRSAWASRRSSWN-----SLK 960
QY 1121 RRSPPGERRSLSGE-GQESQDEEESSEE--ERASPAQSDH-----RHRG 1162
Db 961 HKPPSAEHESLSAERGGAARVCEVADEGPPRAAPLHTPHAHIIHGHPLAHRHRHRR 1020
QY 1163 SLERAKSSFDLPDLTQVPLHRTASGR--GSASEHQDCNGKSASGRALARALRPDDPPLD 1220
Db 1021 TSLDNRDSVDLAELVPAVGAHPRAANRAAGPAPGHEDCNGRMPSIAKDVFTKMGDRGR 1080
QY 1221 GDDADDEGNLSKGERVRAWIRARLPACVLERDSWSAYIFPPQSRFRLLCHRIITHKMPDH 1280
Db 1081 GED-EEEDYTLCPFRVKMIDVYKPDWCVEVDWSVYLFSPENRFRVLCQTIIAHKLFDY 1139
QY 1281 VVLVIIIFLNCITITAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQA 1340
Db 1140 VVLAIFLNCITITALERPOIEAGSTERIFLTVSNYIFTAIFVGMETLKVVSLGLYFGEQA 1199
QY 1341 YLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLRLRTPRLRVISRAQGLKL 1400
Db 1200 YLRSSWNVLDGFLVFSIIDIVVSLASAGAKILGVLRLRLRLRTPRLRVISRAPGLKL 1259
QY 1401 VVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITKSDCAEASY 1460
Db 1260 VVETLISLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTNRNITNRSDCMAANY 1319
QY 1461 RWVRHKYNFDNLGQALMSLFLVASKDGVNDIMYDGLDVGVDQDQOPIMNHNPMWMLLYFISF 1520
Db 1320 RWVHKYNFDNLGQALMSLFLVASKDGVNIMVNGLDVAVVDQDQVTVNHNPMWMLLYFISF 1379

QY 1521 LLIVAFFVLNMFVGVVNFHFKCRHQHEEERREKRLRLEKKRRKAQCKPYYSYS 1580
Db 1380 LLIVSFFVLNMFVGVVNFHFKCRHQHEEERREKRLRLEKKRRKAQRLPYATYC 1439
QY 1581 RFRLLVHHLCTSHYLDLFTIGVIGLVNVTVMAMEHYQOQILDEALKICNYIFTVIFVLES 1640
Db 1440 HTRLLIHSMTCTSHYLDLFTIFIIICLVNVTMSLEHYNQPTSLETALKYCNMYFTTTFVLEA 1499
QY 1641 VFKLVAFGFRFFQDRWNQDLALIVLLSIMGITLEEIEVNASLPINPFIIRIMRVLRIAR 1700
Db 1500 VLKLVAFGLRRFFKDRWNQDLALIVLLSVMGITLEEIEINAALPINPFIIRIMRVLRIAR 1559
QY 1701 VLKLLKMAVGMRALLDTVMQALPOVGNLGLLMLFFIFAALGVELFGLECDETHPCGE 1760
Db 1560 VLKLLKMATMRALLDTVVQALPOVGNLGLLMLFFIYAALGVELFGKLVNDENPCGE 1619
QY 1761 LGRHATERNFGMAFLTFRVSTGDNWNGIMKDTLRDC-DQESTCYNTV--ISPIYFVSFV 1817
Db 1620 MSRHATFENFGMAFLTFRVSTGDNWNGIMKDTLRDCTHDERSCSLSLQFVSPLYFVSFV 1679
QY 1818 LTAQFVLNVVIAVLMKHLSEENKEAEAELEAELEEM-KTLPSPQHSPLGSPFLWPG 1876
Db 1680 LTAQFVLNVVIAVLMKHLSDSNKEAQEDAEMDAELEMAHGLGPGRLPTGSPGA-PG 1738
QY 1877 VEGDSDPD-----SPKPGAL-----HPAAHA-----1897
Db 1739 -RPGGAGGGDTEGLCRRCYSPAQDSLEGEITIDNLSGSIFHHYSSPAGCKKCHDK 1797
QY 1898 -----RSAS-----HFSLEHPTMQP-----HPTELPGPDLITVRKSG--1929
Db 1798 QEVQLAETEAFLNSDRSSILLGDDLSLEDPTACPGRKDSKGELDPPEPMRVGDLGEC 1857
QY 1930 --VSRTHSLPN-DSYMCRHGSAEGLGHRGWGLPKAQSGSVLSVHSQPADTSYLQLP 1985
Db 1858 FFPLSSTAIVSPDPENFLCEMERIPFNPV--RSW--LKHSSQAAPPSPFSPDASSPLPMP 1913
QY 1986 KDAPH-----LLQPHSAPTWTIPKLP--PPG-----RSPLAQRPLRRQAAIRTDSDVQG 2034
Db 1914 AEFFHPAVSASQKPEKGTGTGTLPKIALQGSWASLRSPRVNCTLLRQATGSDTSLD---1970
QY 2035 LGSREDLLAEVSGSPPLARAYSWGQSSTQAQQHSHRSKISKHMTPPAPCPGPEPNWG 2094
Db 1971 -----ASPPSSAGSLQITLEDSTLSDSPRRA-----LGPPAPAPGPRAGLS 2012
QY 2095 KGPPETRSLDLDTLSWISGDLPLPPGQEEPPSPRDLKXCYVEAQSCQRRPTSWLDEQ 2154
Db 2013 ---PAARRRLSL-----RGRGLFSLRLRA-----HQ 2036
QY 2155 RRHSIAVCLDSGSPHLGTDPSN---LGQPLGGPGSRPKKLSPPSIT---IDPPESQ 2208
Db 2037 RSHSSGGS-TSPGCTHDSMDPSDEGRGGAGGGAGGSEHSETLSLSLTSLFCPPP---2092
QY 2209 GPRTPPSPGICLRRRAPSSDS---KDPPLASGPPDSMAASPSPKDVLSSGLSSDPADL 2264
Db 2093 ---PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSPSWAAD-----RSKDPFGR 2143
QY 2265 DP 2266
Db 2144 AP 2145

RESULT 8

US-09-935-541-4
; Sequence 4, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-541-4

Query Match 46.1%; Score 5484; DB 9; Length 2188;
Best Local Similarity 51.1%; Pred. No. 0;
Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;

QY	31	RPGPSAEKDPGSADGAEG---	LPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERI	86
Db	25	QPGPRSPSSPPGLEPLDGDADPHVPHDPIAFCLRQTTSPRNWCIKMVCNPFECV	84	
QY	87	SMLVILLNCVTLCMERPCEDIAQDSQRCRIILQAFDDFI	FAFFAVEMVVMVALGIFGKCC	146
Db	85	SMLVILLNCVTLCMQPCDDMDCLSDRCKILQVDDFI	FIFIFAMEMVLKMWALGIFGKCC	144
QY	147	YLGDTWNRDLDFIVTAGMLEYSLDLQNVSESAVRTVR	VLRLPRLAINRVPSMRILVTLILD	206
Db	145	YLGDTWNRDLDFIVMAGMVEYSLDLQNTINLSAIRT	VRVLRPLKAINRVPSMRILVNLILD	204
QY	207	TLPMLGNVLLLCFFVEFIFIGIVGVQLWAGLLRNCFL	PENFSLPLSDVLERYYQTENEDE	266
Db	205	TLPMLGNVLLLCFFVEFIFIGIVGVQLWAGLLRNCFL	EENFTTQGDVALPPYYQPEEDE	264
QY	267	SPFICSQPRENMRSCRSVPTLRGDGGGPPCGL----	DYEAYNSSNTT--CVNWNQ	318
Db	265	MPFICSLSGDNGIMGCHEIPLKEQ---	GRECCLSKDDVYDFGAGRQDLNASGLCVNWNR	321
QY	319	YNTNCSAGEHNPKGAINFDNIGYAWIAIFQVITLEG	WVDIMYFVMDAHSFYNYFILL	378
Db	322	YYNVCRTGSAHFKGAINFDNIGYAWIVFQVITLEG	WVEIMYVMDAHSFYNYFILL	381
QY	379	IIVGSFFMINCLVVIATQFSETKQRESQLMREQVR	FLSNASTLASFSEPGSCYBELLK	438
Db	382	IIVGSFFMINCLVVIATQFSETKQREHRLMLEQR	QRYLS--SSTVASAEPGDCYEEIFQ	440
QY	439	YLVYILRKARRLAQVSRAAGVRVGLLSSPAPLGGQ	ETQPSSSCSRSHRRLSVHHLVHHH	498
Db	441	YVCHILRKAKR-----	RALGLYQALQSRRAQG-----	468
QY	499	HHHHHHVHLNGTLRAPRASPEIQDRDANGSRRLML	PPPSTPALSGAPPGAESVHSFYH	558
Db	469	-----	PEAPA--PAKGP-----	480
QY	559	ADCHLEPVRCAQPPRSPSEASGRVTGSKVYPTVHT	SPPPETLKEKALVEVAASSGPPT	618
Db	481	AK--EPRHYQLCPQHSPLDATHTL--	VQIPATL-----	511
QY	619	LTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSP	CLKADSGACGPDSCPYCAR-----	672
Db	512	-----	ASDPASCPCQCHEDGRRP	529
QY	673	AGAGEVELADREMPDSDSEAVVEFTQDAQHSOLR	DRPHSRRQSLGPDAPSSVL-----	726
Db	530	SGLGSTD--SQEGSGSGSSAGGE--	DEADGDGARSSEDDGASSELGKEEEEBQADGAVWL	586
QY	727	--AFWRLICDTFRKIVDSKYFGRGIMAILVNTLS	MGIEYHEQPEELTNALEISNIVETS	784
Db	587	CGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVS	MGIEHHEQPEELTNILEICNVVETS	646
QY	785	LFALMLLKLIVYGPFGYIKNPYNIFDGVIVVISV	WEIVGQGGGLSVLRTFLMRVLKL	844
Db	647	MFALEMILKLAFLGLFDYLRNPYNIFDSIIIVIS	WEIVGQADGGLSVLRTFRLRLVLKL	706
QY	845	VRFLPALQRLVLMKTMNVATFCMLLMFLIFIFIS	ILGMHLFGCKFASERD-GDTLPDR	903
Db	707	VRFPALRRQLVLMKTMNVATFCMLLMFLIFIFIS	ILGMHLFGCKFSLRTDGTDPDR	766

QY	904	KNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWA	ALYFIALMTFGNVVLFNLLVAIL	963
Db	767	KNFDSLLWAIIVTFQILTQEDWNVLYNGMASTSPW	ASLYFVALMTFGNVVLFNLLVAIL	826
QY	964	VEGFQAEIISKREDASQSLCIQLPVDSQGGDANK	SESEPDFFS-----LDGD	1013
Db	827	VEGFQAE-----	GDANRSYDEDEQSSSIEEFKLOEGLDSS	863
QY	1014	GDRKKCLALVSLGEHPELRKSLPLPIIHTAATP	MSLPSKSTSTGLGEALGPASRRT----	1069
Db	864	GDPKLCPIPMTPNGH-----	LDP-----SLPLGGHLGPAGAAPRLSLQPD	906
QY	1070	-----SSSGSAEPGAAHEMKSPPSARSPHSP	WSAASWTSRRSSRNSLGRAPSLK	1120
Db	907	PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSSY	GPWGRSAASRRSSWN-----SLK	960
QY	1121	RRSPSGERRSLLSGE--GOESQDEEESSEE--	ERASPAGSDH-----RHRG	1162
Db	961	HKPPSAEHESLLSAERGGRVCEVADEGPPRAAP	LHTPHAHHTHGHPLAHRHRHR	1020
QY	1163	SLEREAKSSFDPDLTQVPLGHRHTASGR--	GSASEHQDCNGKSASGRLARALRPDPDPLD	1220
Db	1021	TLSLDNRDSVDLAELVPAVGAHPRAAWRAAGP	APGHEDCNGRMPSIADKDVFTKMGDRGR	1080
QY	1221	GDDADDEGNLSKGERVRAWIRARLPACVLERDS	WSAYIFFPOSRFRLLCHRIITHKMDH	1280
Db	1081	GED-EEEDYTLCFVRKMDIVKPDWCEVRED	WSVYLFSPENRFRVLCQTIIAHKLFY	1139
QY	1281	VVLVIIFLNCITIAMERPKIDPHSAERIFLTLS	NYIFTAVFLAEMTVKVVALGWCFGQA	1340
Db	1140	VVLAFIFLNCITIALERPOIEAGSTERIFLT	VSNIIFTAVFGEMTLKVWSLGLYFGEQA	1199
QY	1341	YLRSSWNVDGLLVLSVIDILVSMVSDSGTKIL	GMRLVRLRLTLRPLRVISRAQGLKL	1400
Db	1200	YLRSSWNVDGFLVFSIIDIIVSLASAGAKIL	GVLRVLRLLTLRPLRVISRAPGLKL	1259
QY	1401	VVETLMSLKPIGNIVVICCAFFIIFGILGVQL	FKGKFFVQCQGEDTRNITNKSQCAEASY	1460
Db	1260	VVETLSSLPKIGNIVLICCAFFIIFGILGVQL	FKGKFFHCLGVDTRNITNRSQCAANY	1319
QY	1461	RWVRHKYFNFDNLGQALMSLVLASKDGWVD	IMYDGLDAVGDQOQPMNHNPMWLLYFISF	1520
Db	1320	RWVHKYFNFDNLGQALMSLVLASKDGWVNI	MYNGLDAVADQOQVPTNHNPMWLLYFISF	1379
QY	1521	LLIVAFFVLMFMFVGVVVENFHKRQHQE	EEEEARRREKRLRLEKRRKAKQRLPYATYC	1580
Db	1380	LLIVSFFVLMFMFVGVVVENFHKRQHQE	EEEEARRREKRLRLEKRRKAKQRLPYATYC	1439
QY	1581	RFRLVHHLCTSHYLDLFTITGVLNVVTMAME	HYQOQILDEALKICNYIFTVIFVLES	1640
Db	1440	HTRLIHSMTCTSHYLDIFITFIICLVNVVT	MSDEHYNQTSLETALKYCNMYFTTVFVLEA	1499
QY	1641	VFKLVAFGRFRFQDRWNQDLAIIVLLSIM	GITLIEEIVNASLPINPTIIRMRVLRIAR	1700
Db	1500	VKLVAFLRFRFQDRWNQDLAIIVLLSV	MGITLIEEINAAALPINPTIIRMRVLRIAR	1559
QY	1701	VKLKMAVGMRALDVTMOALPQVGNLGLL	FMLLFFIFAALGVLEFGLECDETHPCEG	1760
Db	1560	VKLKMATGMRALDVTVQALPQVGNLGLL	FMLLFFIYAALGVLEFGKLVNDENPCEG	1619
QY	1761	LGRHATFRNFGMAFLTLFRVSTGDNWNG	IMKDTLRDC--DQESTCYNTV--ISPIYFVSFV	1817
Db	1620	MSRHATFENFGMAFLTLFQVSTGDNWNG	IMKDTLRDCTHRSCLSSLOQFVSPLFVSFV	1679
QY	1818	LTAQFVLNVNVIIVLMKHLBESNKEAKEE	AELEAELELEM-KTLPSPQHPSPGSPFLWPG	1876
Db	1680	LTAQFVLNVNVIIVLMKHLDDSNKEAQE	ADAEMAHGLGPGPRLPTGSPGA-PG	1738
QY	1877	VEGPD-----	SP-----DSPKPGALH--	1892
Db	1739	RGPGGAGGGDTEGGLCRRCYSPAQENL	WLDVSLLIKDSLEGELTIIDNLSGSIFHHY	1797

QY 1893 --PAA-----HARSAS-----HFSLEHPTMQP-----HPTLP 1918
Db 1798 SSPAGCKKCHDKQEVQLAETEAFSLNSDRSSSILLGDDLSLEDPACPPGRKDSKGELD 1857
QY 1919 GPDLLTVRKSG-----VSRTHSLPN-DSYMCRCGSTAEGPLGHRGWGLPKAQSGSVLSVH 1972
Db 1858 PPEMRVGDLGECFFPLSSTAVSPDPENFLCEMBEIPENPV--RSW--LKHDSSQAPPSP 1913
QY 1973 SQPADTSYIQLPKDAPH-----LLQPHSAPTWTGTPKLPPLPG-----RSPLAORPLRR 2021
Db 1914 FSPDASSPLLPMPAEFFHFAVSAQKPEKGTGTGTLPKIALQGSWASLRSRPNVCTLLR 1973
QY 2022 QAAIRTDSDVQGLGSRREDLLAEVSGPSPPPLARAYSFWGSSTQAAQQHRSRSHKSKHMT 2081
Db 1974 QATGSDTSLD-----ASPSSAGSLQTTLEDLSLTLSDSPRA-----LG 2012
QY 2082 PPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPLPGGQEEPPSPRDLKKCYSEAAQ 2141
Db 2013 PPAPAGPRAGLS---PAARRLSL-----RGRGLFSLRGLRA- 2047
QY 2142 SCQRRPTSWLDEORRHIAVCLDSGSQPHLGTDPN---LGGQPLGGPSRPKKKLSPP 2198
Db 2048 -----HQRSHSSGGS-TSPGCTHDSMDPSDEGRGGAGGGAGSEHSETLSSL 2095
QY 2199 SIT---IDPPESQGRTPPSPGICLRRRAPSSDS---KQPLASGPPDSMAASPSPKKDV 2251
Db 2096 SLTSLFCPPP-----PPPAPGLTPARKFSSTSSLAAPGRPHAAALAHGLARSESWAAD- 2148
QY 2252 LSLSGLSDDPADLDP 2266
Db 2149 -----RSKDPGGRAP 2158
RESULT 9
US-10-425-800-4
; Sequence 4, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-425-800-4

Query Match 46.1%; Score 5484; DB 14; Length 2188;
Best Local Similarity 51.1%; Pred. No. 0;
Matches 1234; Conservative 212; Mismatches 509; Indels 460; Gaps 56;
QY 31 RPPGSAEKDPGSADSEAG---LPYPALAPVVFYFYLSDQSRPRSWCLRTVCNPFERI 86
Db 25 QPGRSPSPSGLEPPLDGADPHVPHDLAPIAFFCLRTTSPRNWCIKMVCNPFECV 84
QY 87 SMLVILLNCVTLMFRPCEDIAQDSQRCRILQAFDDFIFAFFAVEMVVMKVALGIFGKCC 146
Db 85 SMLVILLNCVTLMYQPCDDMDCLSDRCKILQVDDDFIFIFFAMEMVLKMWALGIFGKCC 144
QY 147 YLGDWTNRLDFFIVIAAGMLEYSLDLQNVFSFSAVRTVRLRPLRAINRVPSMRILVTLLED 206
Db 145 YLGDWTNRLDFFIVMAGMVEYSLDLQNLNSAIRTVRLRPLKAINRVPSMRILVNLLED 204
QY 207 TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLPENFSLPLSVDLERYYYQTENEDE 266

Db 205 TLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRNCFLEENFTIQGDVALPPYYQPEEDDE 264
QY 267 SPFICSQPRENGMRSCRSVPTLRGDGGGPPCGL-----DYEAYNSSNTT--CVNWNQ 318
Db 265 MPFICSLSGDNGIMGCHHEIPPLKEQ---GRECLSKDDVDYDFAGRQDLNASGLCVNWR 321
QY 319 YTNCSAGEHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNYFIYFILL 378
Db 322 YNVVCRGTSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYVYVMDAHSFYNYFIYFILL 381
QY 379 IIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLK 438
Db 382 IIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQYLS-SSTVASAEPGDCYEEIFQ 440
QY 439 YLVYILRKAARRLAQVSRAGVRVGLLSPPAPLGGQETQPSSSCSRSHRRLSVHHLVHHH 498
Db 441 YVCHILRKAKR-----RALGLYQALQSRRLQALG----- 468
QY 499 HHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVHSFYH 558
Db 469 -----PEAPA--PAKPGP-----H 480
QY 559 ADCHLEPVRCQAPPPRSPSEASGRITVGSKVYPIVHTSPPTLKEKALVEVAASSGPPT 618
Db 481 AK---EPRHYQLCPQHSPLDAPHTL-----VQPIPATL----- 511
QY 619 LTSINIPPGPYSSMHKILETQSTGACQSSCKISSPCLKADGACGPDSCPYCAR----- 672
Db 512 -----ASDPASCCQCHEDGRRP 529
QY 673 AGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHRRRQSRSLGDAEPSSVL----- 726
Db 530 SGLGSTD-SQEGSGSGSSAGGE--DEADGDGARSSSEDGASSELGKEEEEEQADGA VWL 586
QY 727 --AFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISNIVFTS 784
Db 587 CGDVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNIILEICNVVFTS 646
QY 785 LFALEMLLKLIVGPFYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFLMRVLKL 844
Db 647 MFALEMTILKLAAGLFDYLRPNYPNIFDSIIIVISWEIVQADGGLSVLRTFLRLVLKL 706
QY 845 VRFLPALQQLVLMKTMONVATFCMLLMLEFIFISILGMHLFGCKFAASERD-GDTLPDR 903
Db 707 VRFPALRRQLVLMKTMNDVATFCMLLMLEFIFISILGMHIFGCKFSRLTDTGDTVPDR 766
QY 904 KNFDSLILWAIWTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYLVFNLLVAIL 963
Db 767 KNFDSLILWAIWTVFQILTQEDWNVLYNGMASTSPWASLYFVALMTFGNYLVFNLLVAIL 826
QY 964 VEGFOAEEISKREDASQLSCIQLPVDSSQGDANKSESEPDPFSPS-----LDGD 1013
Db 827 VEGFOAE-----GDANRSYDEDSQSSNIEEFDKLQEGLDSS 863
QY 1014 GDRKKCLALVSLGHPPELKRSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRT---- 1069
Db 864 GDPKLCPIPMTE NGH-----LDP-----SLPLGGHLGPAGAAGPAPRLSLOPD 906
QY 1070 -----SSGSAEPGAAHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLK 1120
Db 907 PMLVALGSRKSSVMSLGRMSYDQRLSSSRSSYYGPGWGRSAWASRRSSWN-----SLK 960
QY 1121 RRSPPSGERRSLSGE--GQESQDEEESSEE--ERASPGSDH-----RHRG 1162
Db 961 HKPPSAEHESLLSABERGSGARVCEVAADGPPRAAPLHTPHAHHTHGHPLAHRHRHRR 1020
QY 1163 SLEREAKSSFDLPDTLQVPGLHRTASGR--GSASEHQDCNGKSASGRALARALRPPDPPLD 1220
Db 1021 TSLDNRDSVDLAELVPAVGAHPRAAWRAAGPAGPHEDCNGRMPSIAKDVFTKMGDRGDR 1080
QY 1221 GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFLLCHRIITHKMFHDH 1280
Db 1081 GED-EEEDYTLCFRVRKMDIVKPKDWCEVEDWSVYLFSPENRFRVLCQTIIAHKLFDY 1139

Db 505 -----ISAILASD-----PSSCPHCQHEA 523

Qy 673 ----AGAGEVELADREMPDSDSEAVYEFQTDAQHSDLRDPHSRRQRSLSGPDAPSSVLA- 727

Db 524 GRRPSGLSTD-SQEGSGSGGSAAEANGDG---LQSEDDGVSSDLGKEEEDGAAR 578

Qy 728 ----FWRLICDTFRKIVDSKYFGGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFT 783

Db 579 LCGDVWRETRKKLRIGIVDSKYFNRGIMMAILVNTVSMGIEHHEQPEELTNILEICNVVFT 638

Qy 784 SLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLK 843

Db 639 SMFALEMILKLAAGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLLRVLK 698

Qy 844 LVRFPLALORQLVVLKMTMDNVATFCMLMLFIFIFISILGMHLFGCKFASERD-GDTLPD 902

Db 699 LVRFMPALRRQLVVLKMTMDNVATFCMLMLFIFIFISILGMHIFGCKFSRLRTDGTVPD 758

Qy 903 RKNFDSLLWAIIVTVFQILTQEDWNKVLYNGMASTSSWAALFYIALMTFGNYVLENLLVAI 962

Db 759 RKNFDSLLWAIIVTVFQILTQEDWNVLYNGMASTTPWASLYFVALMTFGNYVLENLLVAI 818

Qy 963 LVEGFQAEIISKREDASGQLSCIQLPVDSQGGDANKSESPDFFSPS-----LDG 1012

Db 819 LVEGFQAE-----GDANRSCDEDDQSSNLEEFDKLPEGLDN 855

Qy 1013 DGRKXKCLALVSLGEHPELRKSLPLPLIHTAATPMSLPKSTSTGLGEALGPA-SRRTSS 1071

Db 856 SRDLKLCPIPMTPNGH-----LDP-----SLP-----LGAHLGPAGMTAP 892

Qy 1072 SGSAEPG-----AAHEMKSPPSARSSPHSPWSAASSWTSRERSRNSL 1113

Db 893 RLSLQDPDVLVALDSRKSSVMSLGRMSYDQRLSSSRSSSYGPGWRSGTWSRSSWN-- 950

Qy 1114 GRAPSLKRSPSGERRSLLSGEQESQDEE-ESSEEE---RASPAQSDH----- 1158

Db 951 ----SLKHKPPSAEHESLLSGEGGSCVRACEGAREEAPTRTAPLHAPHAHHGPHLA 1006

Qy 1159 ----RHRCGLEREAKSSFDLPDTLQVPGLHRTAS--GRGSASEHQDCNGKSASGRLARAL 1212

Db 1007 HRHRHRTLSLDRDSDVLGELVPVVGAAHRAAWRGAGQAGHEDCNGRMPNIAKDVF 1066

Qy 1213 RPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRI 1272

Db 1067 KMDDRRDRGED-EEEDYTLCFVRKMDIVYKPDWCVEVDWSVYLFSPENKFRILCQTI 1125

Qy 1273 ITHKMFHDVVLVIFLNCITIAMERPDKIDPHSAERIFLTLNSYIFTAVFLAEMTVKVVAL 1332

Db 1126 IAHKLFDVVVLAFIFLNCITIALERPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVS 1185

Qy 1333 GWCFGEOAYLRSSWNVLGGLVLISVIDILVSMVSDSGTKILGMLRVLRLRLRPLRVI 1392

Db 1186 GLYFGEQAYLRSSWNVLGGLVFLVFSIIDIVSVASAGGAKILGLVRLVRLRLRPLRVI 1245

Qy 1393 SRAOGLKVVTETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNK 1452

Db 1246 SRAPGLKVVTETLISSLKPIGNIVLICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNR 1305

Qy 1453 SDCAEASRWRVRHKYNFNDLGOALMSLFLVASKDGVVDIMYDGLDVGVDQQPIMNHNPW 1512

Db 1306 SDCVAANYRWVHHKYNFNDLGOALMSLFLVASKDGVWNIMYNGLDDAVADQQPVTNHNPW 1365

Qy 1513 MLLYFTSFLLIIVAFFVLNMFVGVVVENFHKCRQHQEERREARRREEKRLRLEKKRKAQC 1572

Db 1366 MLLYFTSFLLIIVFFVLNMFVGVVVENFHKCRQHQEERREARRREEKRLRLEKKRKAQR 1425

Qy 1573 KPYSDYSRFRLLVHLCTSHYLDLFTIGVIGLVNVTMAMEHYQQPQILDEALKICNYIF 1632

Db 1426 LPYYATYCPRLLIHSMCTSHYLDLFTFIICLVNVTMSLEHYNQPTSLETALKYCNMYF 1485

Qy 1633 TVIFVLESVFKLVAFGFRFFQDRWNQDLDAIVLLSIMGITLEEIEVNASLPINPTIIRI 1692

Db 1486 TTVFVLEAVLKLVAFGLRRFFKDRWNQDLDAIVLLSVNGITLEEIEINAALPINPTIIRI 1545

Qy 1693 MRVLRIRARVLKLLKMAVGMRALLDVTMOALPOVGNLGLLPMLLFFIFAALGVELFGDLEC 1752

Db 1546 MRVLRIRARVLKLLKMATGMRALLDVTVOALPOVGNLGLLPMLLFFIYAALGVELFGKLV 1605

Qy 1753 DETHPC EGLGRHATFRNFGMAFLTLFRVSTGDNWNGMKDTLRDC-DQESTCYNTV--IS 1809

Db 1606 NDENPC EGMRSRHATFENFGMAFLTLFQVSTGDNWNGIMKDTLRDCTHDERTCCLSSQLFVS 1665

Qy 1810 PIYFVSFVLTAQFVLNVVTVIAVLMKHLEESNKEAKEAELEAELELEM-KTSLSPQHSPL 1868

Db 1666 PLYFVSFVLTAQFVLINVVAVLMKHLDDSKEAQEDAEMDAEIELEMAHGLGPCP---- 1721

Qy 1869 GSPFLWPGVEGPDSPDSPKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLLTV--- 1925

Db 1722 -----GPCPG-----PCPCPCPCAGPRLPTSSPG 1747

Qy 1926 ---RXSGVSRTHSLPNDSYMCRH 1945

Db 1748 APGRGSGGAGAGG-DTESHLGRH 1769

RESULT 11

US-10-425-800-5

; Sequence 5, Application US/10425800

; Publication No. US20030180886A1

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

; APPLICANT: McGivern, Joseph G.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/10/425,800

; CURRENT FILING DATE: 2003-04-29

; PRIOR APPLICATION NUMBER: US/09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 1835

; TYPE: PRT

; ORGANISM: Rattus sp.

US-10-425-800-5

Query Match 45.1%; Score 5366; DB 14; Length 1835;

Best Local Similarity 56.8%; Pred. No. 0;

Matches 1138; Conservative 183; Mismatches 346; Indels 336; Gaps 38;

Qy 27 GAGGRPGSAEKDPGSADSAEG---LPYPALAPVVFYVLSQDSRPRSCLRTVCNPM 82

Db 19 GITEQGPSPSPSPPPGLEELEGNTPDVPHPDAPVAFCLRTQTSRPNWCIMKVCNPM 78

Qy 83 FERISMLVILLNCVTILGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIF 142

Db 79 FECVSMVLVILLNCVTILGMYPQDDMECLSDRCKILQVFDDEFIFFFAMEMVLMVALGIF 138

Qy 143 GKCKYLGDWTNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVT 202

Db 139 GKCKYLGDWTNRLDFFIVMAGNVEYSLDLQNLINLSAIRTVRVLRLKAINRVPSMRILVN 198

Qy 203 LLLDTLPMLGNVLLLCFFVFFIFIGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERYQTE 262

Db 199 LLLDTLPMLGNVLLLCFFVFFIFIGIVGVQLWAGLLRNRCFLEENFTIQGDVALPPYQPE 258

Qy 263 NEDESFFICSQPRENGMRSCRSVPTLRDGGGGPPCGL-----DYEAYNSSNTT--CV 314

Db 259 EDDMEFFICSLTGDNGIMGCHIEIPLKEQ---GRECCLSKDDVYDFGAGRODLNASGLCV 315

Qy 315 NWNQYVYTNCSAGEHNPFGKAINFDNIGYAWIAIFQVITILEGWVDIMYFVMDAHSFYNFYI 374

Db 316 NWNRYNVVCRGTGNANPHKAINFDNIGYAGIVIFQVITILEGWVEIMYVYVMDAHSFYNFYI 375

Qy 375 FILLIIVGSFFMINCLVVIATQFSETKQRESQLMRQVRFLSNASTILASFSEPGSCYE 434

QY 140 GIFGKCYLGDWTNRLLDFFIIVLAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRI 199
Db 184 GIFGKCYLGDWTNRLLDFFIIVMAG-----NINLSAIRTVRVLRPLKAINRVPSMRI 234
QY 200 LVTLLDTPMLGNVLLLCFFVFFIFIGVQVWAGLLRNRCFLPENESLPLSVDLERY 259
Db 235 LVNLLDTPMLGNVLLLCFFVFFIFIGIIGVQVWAGLLRNRCFLEENFTIQGDVALPPY 294
QY 260 QTENEDSEPFICQPRENGMRSCRSVPTLRDGGGGPPCGL-----DYEAVNSSNTT- 312
Db 295 QPEEDDEMPFICSLSGDNGIMGCHEIPLKEQ---GRECLS KDDVYDFGAGRQDLNASG 351
QY 313 -CVNWNQYVTCNSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYN 371
Db 352 LCVNWNRYNVVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYYVMDAHSFYN 411
QY 372 FIYFILLII----- 380
Db 412 FIYFILLIISELHLVMPDCSFSAQSPKQCQDGLPGVAAESLLLRDSSSSVITDEAAAA 471
QY 381 ----- 380
Db 472 ENLLAGTSKGDES YLLRLAGSQVHSQAQMLGRGLGPESLETGEEPHSWSPRATRWDPQ 531
QY 381 -----VGSEFFMINCLVVIATQFSETKQESQOLMREQVRFLSNASTLAS 425
Db 532 CQPQPLPHFMQAQVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVAS 590
QY 426 FSEPGSCYBELLKYLVIYLKKAARLAQVSRAAGVRVGLLSSPAPLGGQETQPSSSCSRS 485
Db 591 YAEPGDCYEEIFQYVCHILRKAKR-----RALGLYQALQSRQALGPEAPAPAKP- 640
QY 486 HRRLSVHLVHHHHHHHHYHLGNCTLRAPRASPEIQDRDANGSRRLMLPPSPALSGA 545
Db 641 -----GPHAKEPRHYPLTVWESILGRQAEECTLRAA-----AHPSSGAS 679
QY 546 PPG-GAESVHSFYHADCHLEPVRCOAPPPRSPSEASGRTVSGSKVYPTVHTSPPETLKE 604
Db 680 HPGVGSEEA-----PELC---PQHSPLDATPHTL-----VQPIPATL-- 713
QY 605 KALVEAASSGPPTLTSLNIPPGPYSSMHKLLLETQSTGACQSSCKISSPCLKADSGACGP 664
Db 714 -----ASDP 717
QY 665 DSCPYCAR-----AGAGEVELADREMPDSDSEAVYFTQDAQHSDLRDPHSRQRSLGP 718
Db 718 ASCPCCQHEDGRRPSGLGSTD-SQEGSGSGSSAGGE--DEADGDGARSSSEDGASSELGX 774
QY 719 DAEPSSVL-----AFWRLICDTFRKIVDSKYFGRGIMTAILVNTLSMGIEVHEQPE- 769
Db 775 EEEEEQADGAVWLCDGVWRETRAKLRGIVDSKYFNRGIMMAILVNTVSMGIEHHEQASA 834
QY 770 -----ELTNALE-----ISNIV----- 781
Db 835 AQPGRACRGQNPDLCMTLKAPCLCHNVFSPGQGVLSHPVTPPHTAPWRMETGKQHGCE 894
QY 782 -----FTSLFALEM LKLLVYGPEGYIKNPYNIFDGVTVIVISVWEIVGQGGGLSVLRT 835
Db 895 EGPQRSSDMFALEMILKLAAGLFDYLRNPYNIFDS-IVIISIWEIVGQADGGLSVLRT 954
QY 836 FRLMRVLKVRFLPALORQLVLMKTMNDNVATFCMLMLFIFIFSILGMHLFGCKFASER 895
Db 955 FRLLRVLKVRFPALRRQLVLMKTMNDNVATFCMLMLFIFIFSILGMHIFGCKFSLRT 1014
QY 896 D-GDTLPDRKNFDSLLWAIIVTVFQILTQEDWNKVLYNGMASTSSWAALFYIALMTFNGYV 954
Db 1015 DTGDTVDRKNFDSLLWAIIVTVFQILTQEDWNVLYNGMASTSPWASLYFVALMTFNGYV 1074
QY 955 LFNLLVAILVEGFQAE-EISKREDA-----SGQLSCIQLP 988
Db 1075 LFNLLVAILVEGFQAEVTVVLAEEAPPQGLRKTGRGRGLDGGGLQFKLLAGNLS-LKEG 1133
QY 989 VDSQGGDANKSESEPFFSPS-----LDGDGRKKCLALVSLGELHPELRKSLLP 1038

Db 1134 VADEVGDANRSYDEQDQSSSNIEEFFDKLQEGLDSSGDKLCPIMPMPNGH-----LDP 1186
QY 1039 LIIHTAATPMSLPKSTSTGLGEALGPA-----SRRTS----- 1070
Db 1187 -----SLPLGGHLGPAGAAGPAPRLSLQDPDMLVALGSRKSSVMSLGRMSYDQRS 1236
QY 1071 -----SSGSAEPGAAHEMKSP-----PSARSSPHSPWSAASWTSRRSS 1109
Db 1237 LVGGLRATAGVQAAGHLVPQWVCLWGADPNGNSFQSSSRSSYYGPGWGRSAAWASRRSS 1296
QY 1110 RNSLGRAPSLKRRSPSGERRSLLSGE-GQESQDEESSEE--ERASPAGSDH----- 1158
Db 1297 WN-----SLKHKPPSAEHESLLSAERGGGARVCEVAADGPPRAAPLHTPHAHVHHGP 1350
QY 1159 -----RHRGSLEREAKSSFDLPDTLQVPLHRTASGR--GSASEHQDCNGKSASGRLA 1209
Db 1351 HLAHRHRHRTLSLDNRDSVDLAELVPAGAHPRAPRAAGPAPGHEDCNGRMPSIAKD 1410
QY 1210 RALRPDDPPLDGDADD-----EGNLSKGERVRAWIRARLPACYLERDSWSAYIFP 1260
Db 1411 VFTKMGDRGDRGEDEEIDYVSGGGAEGDLTLCFRVRKMDIVKPDWCEVREDWSVYIFS 1470
QY 1261 PQSRFR-----LLC-----HRIITHKMFHDHVLVIIFLNCITIAE 1296
Db 1471 PENRLRDLGWVSLECCQKVGLVWVWYQRRQRQTTIAHKLFDYVVLAFIFLNCITIALE 1530
QY 1297 RPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVL DGLLVLI 1356
Db 1531 RPQIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVSLGLYFGEQAYLRSSWNVL DGFV 1590
QY 1357 SVIDILVSMVSDSGTKILGMLRVLRLRLTLRPLRVISRAQGLKLVETLMSLKPIGNIV 1416
Db 1591 SIIDIVVSLASAGGAKILGVLRLRLTLRPLRVISRAPGLKLVETLISSLKPIGNIV 1650
QY 1417 VICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASYRWRHKYNFDNLGQAL 1476
Db 1651 LICCAFFIIFGILGVQLFKGKFYHCLGVDTNRNITNRSDCMAANYRWWHHKYNFDNLGQAL 1710
QY 1477 MSLFVLASKDGWVDIMYDGLDAVGVDQOQPIMNHNPMWMLLYFISFLLIVAFFVLNMFVG 1536
Db 1711 MSLFVLASKDGWVIMYNGLDAAVADQOQVTNHNPMWMLLYFISFLLIVSFFVLNMFVG 1770
QY 1537 VENFHCRQHOEEEEARRREKRLRRLEKKRRKAQCKPYSDYSRFRLLVHHLCTSHYLD 1596
Db 1771 VENFHCRQHOEAEARRREKRLRRLEKKRRKAQRLPYATYCHTRLLIHSMTCTSHYLD 1830
QY 1597 LFTGVIGLNVVVTMAMEHYQQP 1618
Db 1831 IFITFICLNVVVTMSLEHYNQP 1852

RESULT 13

US-10-369-493-6836
; Sequence 6836, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; LENGTH: 1657
; TYPE: PRT

; ORGANISM: Caenorhabditis elegans									
US-10-369-493-6836									
Query Match 29.9%; Score 3564.5; DB 14; Length 1657;									
Best Local Similarity 42.2%; Pred. No. 1.5e-215;									
Matches 822; Conservative 231; Mismatches 430; Indels 465; Gaps 50;									
QY	15	QPRSPMRLNDSGAGRPG-----PGSAEKDPG-----SADSEA	48						
Db	56	QSQSTRRHEDVEALGSIIEGSKETQLSEHGRLASSEASPSRWEGRQIEWGNEEQIEES	115						
QY	49	EGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTLGMRPCED-I	107						
Db	116	E-LPYPGFAEPALRCFYQAPPPRKWALQVMSPWFDRTIMAVIMINCVTLGMYRPCEDGP	174						
QY	108	ACDSQRCRILQAFDDFIAPFAFVEMVVMVALGIFGKKCYLGDWTNRLDFFIVIAQMLEY	167						
Db	175	DCDTRCQILDIIIDNCIFVYFAPFEMVIKIMALGFYGAAYMSDTWNRLDFFIVMAGIAEF	234						
QY	168	SLDLQ---NVFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFI	224						
Db	235	VLHEYLGGINLTAIRTVRVLRPLRAVNRIPSMRILVNLTLTLPMLGNVLLLCFFVFFI	294						
QY	225	FGIVGVLWAGLLNRNCF--LPENFS-----LPLSVDLERYQOTENEDESFPICSPREN	277						
Db	295	FGIVGVLWAGLLNRNRCVNLPKTISENQSALENNVVKLTRFYIPE-DTSLEYICSPDAN	353						
QY	278	GMRSCRVPTRLRGDGGGPPCGILDYEAYNSSNTTCVMNQYTYNCSAG-----	326						
Db	354	GLHTCSNLPPTYVD--GVKCNLTLDYDKVTNDSCINWNIYYNECQVNIYPSLMTIAIS	410						
QY	327	-----EHNPPFKGAINFDNIGYAWIAIFQVITLEGVVDIMYFVMDAHSFYNIYFILLII	380						
Db	411	CFIKVMQRNPFQGSVSFDNIGFAVVAIFLVISLEGWTDIMYVQDAHSFVNNWIFVLLIV	470						
QY	381	VGSFMINLCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPG-----S	431						
Db	471	IGAFMINLCLVVIATQFAETKRRETERMLQERKMILNRDSISCTGSEIGGASSKEEGDT	530						
QY	432	CYEELLKYLVIYILKAAARLQAQVRAAGVRVGLLSSPAPLGGQETQPSSSCSRSHRLSV	491						
Db	531	VYAAFVRFIGHTFRR-TKRAAKKKYTAYMEE-----	560						
QY	492	HHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAE	551						
Db	561	-----RAERKSSERQOR-----RKSLLDDMAT--LS-----	584						
QY	552	SVHSFYHADCHLEPVRCQAPPPSPSEASGRTVSGVKYPTVHTSPPPETLKEKALVEVA	611						
Db	585	-----RIEKAEDF--	593						
QY	612	ASSGPPTLSLNIPPGPYSSMHKLLLETQSTGACQSSCKI-SSPCLKADSGACGPDSCPYC	670						
Db	594	--EDETTITREN-----GDDQIEQNGDGVRIKRVKIEEPEKIKIGN-----GNSNGPHY	640						
QY	671	ARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSGLPDAEPSSVLAFWR	730						
Db	641	KHSSSDE-----ESDEDGEEDQVYDGBEAKKS-----TPSKL--WW-	675						
QY	731	LICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQBELTNALEISNIVTSLFALEM	790						
Db	676	-FREKIQFVICDHFTRGILVAILVNTLSMGVEYHQQPEILTIVILEYSLNFFTFALFALEM	734						
QY	791	LLKLLVYGPGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTFRMLRVLKLVRFLPA	850						
Db	735	LLKIIASGLFGYLADGNLFDGGGIVALSLELFOEGKGGGLSVLRTFRLLRILKLVRFMPA	794						
QY	851	LQRLVLMKTMNDNVATFCMLLMLEFIFISILGMHLFGCKFASERD---GDTLP--DRKN	905						
Db	795	LRYLQVLMRLTMDNVTVFGLLVLFIFIFISILGMNLFQCKFCKVEEKFLGGLAKKCKRN	854						
QY	906	FDSLLWAVTVFQILTQEDWNKVLNMGMASTSSWAALYFTALMTFGNYVLFNLVAILVE	965						

Db	855	FDILLWALITVFQILTQEDWNMVLFNMGMAQTNPWAALYFVALMTFGNYVLFNLVAILVE	914
QY	966	GFOAEIISKREDASGLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSL	1025
Db	915	GFQE---SKEEE-----KFQLEEDARKQAVEEEDERKRELELI--	949
QY	1026	GEHPELRKSLLPPLIIHTAATPMSLPSKSTSTGLGEALGPASRRRTSSSGSAEPGAHEMKS	1085
Db	950	-----IAKTTSPAFNNGVAPA-----ECTQRPSSPEESPS	980
QY	1086	PFSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSG-----ERRSLLSGEQESQ	1140
Db	981	PRLLSANYH-----PSPERKHSANLDAIIDKRLVL-----	1010
QY	1141	DEESSEERASAPGSDHHRGSLEREAKSSFDPDQLQVPLGHLRTASGRGSAHEHQDCN	1200
Db	1011	--RNSAPFDR-SPV-SEGRDSDRLNRHA--SLVLPVANGVP-----YRRQRVH	1052
QY	1201	GKSASGRLARALRPDDPLDGDADDDEGNLSKGE-RVRAWIRARL-PACYLERDSWSAYI	1258
Db	1053	SWKASQELKQAL-----AEEE--KRNEAKQNTFVRKLLKKTCLHNRTEFSLFL	1098
QY	1259	FPQSRFRLLCHRIITHKMPDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1318
Db	1099	MGPKNPLRIKCLQTTQKKWFDYTLVFFIGINCITIAMERPSIPPPDSFERQLHISGYIFT	1158
QY	1319	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVSMVSDSGTKILGMLR	1378
Db	1159	VIFTGEMMMK-----	1168
QY	1379	VLRLTLRLPLRVISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILGVQLFKGF	1438
Db	1169	-----VSHRIPTLKPICNIVLICCTFFIIFGILGVQLFKGMM	1205
QY	1439	FVCGEDTRNITNKSDCAEASYR--WVRHKYNFQNLQALMSLFLVASKDGWVDIMYDGL	1496
Db	1206	YHCIGPEVGNVTTKADCIIE-DYRNKWNHRYNFDNLQALMSLFLVSSKDGWVSIMYQGI	1264
QY	1497	DAVGVDQQPIMNHNPMMLLYFISFELLIVAFFVLNMFVGVVVENFHKRCRQHEEEARRRE	1556
Db	1265	DAVGVDVQPIENYNEWMIYFISFLLLVGVFFVLNMFVGVVVENFHKKEALEKEMREKEK	1324
QY	1557	EKRLRLEK-----KRRKAQC-----KPYYSYDSYRFRLLVHHL	1590
Db	1325	EKRLKRLKQKQFEESMAGKRNRIWAGSAIKSIFSVERNYPYHYDYGHLRFLHGIV	1384
QY	1591	TSHYLDLFIITGVIGLVNVTNAMEHYQQOQIILDEALKICNYIFTVIFVLESVFKLVAFGR	1650
Db	1385	TSKYFDLAIAAVIGINVISMAEFYMMPMGLKYVLKALNYFFTAVFTLEAAMKLIALGFK	1444
QY	1651	RFFQDRWNQLDAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIRVLLKLMKMAVG	1710
Db	1445	RFFIEKWNRLDMFIVILSIAGIIFEEFEA-LELPIINPTIIRVMRVLRIRVLLKLMKMAK	1503
QY	1711	MRALDVTVMQALPQVGNLGLLPMLLFFIFAALGVLELFGDLECDETHPCGELGRHATFRNF	1770
Db	1504	IRSLDVTVGEALPQVGNLGLSIFLLFFIFAALGVLELFGKLECEDHPDGLGEHAHFKNF	1563
QY	1771	GMAFLTFRVSTGDNWNGIMKDTLR-DCD-----QESTCYNTVISPIYFVSFVLTAQFVL	1824
Db	1564	GMAFLTFRVSTGDNWNGIMKDALRDDCDSSDHCECTCCVDPILAPCFFVIFVLISQFVL	1623
QY	1825	VNVVAVLMKHLSESNKEAKEAELEAE	1852
Db	1624	VNVVAVLMKHLSESN---KRDAEGPAE	1648

RESULT 14
US-10-627-370-2
; Sequence 2, Application US/10627370
; Publication No. US20040081988A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jason M.

Db 812 HLDRLVVELGRDGARGPVGGKARPEAAABEGVDPPRRHHHRDKDKTPAAGDQDRAEA 871

QY 1074 -----SAEPGA-----AHEMKSPPSARS-----SPH-----SPWSAASSW 1103

Db 872 PKAESGEPGAREERPRPHRSHSKEAAGPEARSERGRGPGEGRRHRRGSPEEAERE 931

QY 1104 TSR-RSSRNLGRAPSLKRRSPSGERRSLLSGEQESQDEESSEE-----ERASP- 1153

Db 932 PRRHRAHRH---QDPSEKACAGERRARHRRGGPRAGPREAESGEEPARRHRRHKAQPA 988

QY 1154 -----AGSDHHRHGRSLEREAKSSFDLPDTLQVPLGHLRTASGRG 1191

Db 989 HEAVEKETTEKEATEKEAEIIVEADKEXELRNHQPREPHCDLETSGTIVGPMHTLPSTCL 1048

QY 1192 SASEHQDCNGKSASGRILARLPDDP-----PLDGDADDEGNL-----SKGE 1234

Db 1049 QKVEEQPEDADNQNVTRMGSPQPPDNTIIVHVPMLTGPLGEATVVPNGVDLESQAEGK 1108

QY 1235 R-----VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIF 1287

Db 1109 KEVEADDVNRSGPRPIVPS-----SMFCLSPNTLLRRFCHYIVTMYFEFVILVIA 1161

QY 1288 LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWN 1347

Db 1162 LSSIALAEDP-VRTDSPRNALKYLDYIFTGVFTFEMVTKMIDLGLLLHHPGAYFRDLWN 1220

QY 1348 VLDGLLVLSVIDI-LVSMVSDSGTKILGMLRVLRLRLRPLRVLRSRAOGLKLVVETLM 1406

Db 1221 ILDFIVVSGALVAFASFVSGSGKGDINTIKSLRVLRLRPLRPLKTIKRLPKLKAEDCVV 1280

QY 1407 SSLKPIGNIUVVICCAFFIIFGILGVOLFPGKFFVCQGE-----DTRN--ITNKSDCAEA 1458

Db 1281 NSLKNVLNILLVYMLFMFIFAVIAVOLFPGKFFCYCTDESKELERDCRGQYLDYEKEVEA 1340

QY 1459 SYR-WVRHKYNFDNLGOALMSFLVLASKDGVVDIMYDGLDAVGVDQOQIMNHNPMWMLLYF 1517

Db 1341 QPROWKKYDFHYDNVLWALLTLFTVSTGEGWPMVLKHSVDATYEEQGPSPGYRMELSIYF 1400

QY 1518 ISFLLIVAFVFLNMFVGVVVENFHKCRQHOOEEEEARRREKRLRLEKKRKA-----QC 1572

Db 1401 VVYFVVFVFVFVNI FVALIIITF-----QEQGDKVMSE-----CSLEKNERACIDFAISA 1450

QY 1573 KPY--YSDYSR--FRLLVHHLCTSHYLDLPITGVIGLVNVVTMAMEHYQQOQILDEALKIC 1628

Db 1451 KPLTRYMPQNRQSFQYKTTWTVVSPPFYFIMAMIALNTVVLMMKFYDAPYELMLKCL 1510

QY 1629 NYIFTVIFLESVFKLVAFGRFRFFQDRWNQLDLAIVLLSIMGITLEEI-EVNASILPINP 1687

Db 1511 NIVFTSMFSMECVLKIIAFGVNLNFRDAWNVDFVTVLGSITDILVTEIAETN-----NF 1565

QY 1688 TIIRIMRVLRIARVLKLLKMAVGMRALLDTVMQALPQVGNLGLLFLMLLFFIFAALGVLELF 1747

Db 1566 INLSFLRLFPRAARLKLIRQGYTIRILLWTVFQSFKALPVVCLLIAMLFFIYAIIGMQVF 1625

QY 1748 GLECEDETHPCGLGRHATFRNFGMAFLTTLFRVSTGDNWNGIMKDTLRD--CDQE--STC 1803

Db 1626 GNIALDDD---TSINRHNNTFELQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE 1682

QY 1804 YNTVISPIYFVSFVLTAQFVLNVVVIIVLM-----KHLEE-----1838

Db 1683 CGSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDEFIRVWAEYDP 1742

QY 1839 -----1838

Db 1743 AACGRISYNDMFEMLKHMSPLGLGKKCPARVAYKRLVRNMNPI SNEDMTVHFTSTIMAL 1802

QY 1839 -----SNKEAKEEAEEAELEEMKTLSPQHSPLGSPFLWPVGVEGPDSPDP 1886

Db 1803 IRTALEIKLAPAGTKQHQCDAELRKEISVWVANL-PQKTLDLLVP-----PHKPDEN 1853

QY 1887 KPGALHPA-----AHARSASHFSLEHPTM-----QPHPTLPGPD 1921

Db 1854 TVGKVYAALMIFDFYKQNKTTTRDQMOPAGGLSQMGPSVLFHPLKATLEQTQPAVLRGAR 1913

Search completed: November 18, 2004, 13:59:31
Job time : 210.672 secs

QY 1922 LLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYI 1981

Db 1914 VFLRQKSSSTLSN-----GGAIQNQESGIKESV-----SWG 1944

QY 1982 LQLPKDAPHLLQP-----HSAPTWTGTIPKLPPPGRSPLAQPLRRQAAIR-----TDS 2029

Db 1945 TQRTQDAPHEARPPLERGHSTEI-----PVGRSGALAVDVQMOSITRRGPDGEQPG 1996

QY 2030 LDVQGLGSRDLLAEVSGP---SPPLARAYSFWQSQSTQAQQHRSRSHSKISKHMTPPAPC 2086

Db 1997 LESQGRAASMPRLAAETQPVTDASPMKRSI-----STLAQRPGRGTHLCST---TPDRPP 2047

QY 2087 PG-----PEPNWKGPPPETRSSLELDTLSWISGDLPLPPGGQEEPPSP 2129

Db 2048 PSQASSHHHHRRCHRRDRKQSRLEKGP---SLSADMDGAPSSAVGGLPPG--EGPTGC 2102

QY 2130 RDLKKCYVSEAQSCQRR-PTSWLDEQRRHSIAVSCLDG-----SQPHLG 2173

Db 2103 RRERERRQERGRSQERRQPPSSSSSEKQRF---YSCDRFGGREGPPKPKPSLSHPTSPTAG 2159

QY 2174 TDP-----SNLGGQPL-----GGPGRSRPKKKLSP-PSITI-----DPPESQG 2209

Db 2160 QEPGPHPOGSGSVNGSPILLSTSGASTPGRGRRQLPQTPLTPRPSITYKKTANSSPIHFAG 2219

QY 2210 PRT--PP-SPG-----ICLRRRAPSSDSKDPLASGPPDSMAASPSPKKDVLSLSGL 2257

Db 2220 AQTSLPAFSPGRLSRGLSEHNALLQRDPLS---QPLAPG-----SRI 2258

QY 2258 SSDP 2261

Db 2259 GSDP 2262

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:14:21 ; Search time 50.2671 Seconds
(without alignments)
4337.375 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEDGAGAEESGQPRSF.....PKKDVLSLSGLSSDPADLDP 2266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	10945	91.9	2254	2 T09053	low voltage-activa
2	3564.5	29.9	1657	2 T15838	hypothetical prote
3	1746.5	14.7	2339	2 A42566	omega-conotoxin-se
4	1741	14.6	2237	2 T45115	N-type calcium cha
5	1711	14.4	2336	2 A45386	omega-conotoxin-se
6	1706	14.3	2288	2 S41080	calcium channel al
7	1697	14.3	2259	2 S29236	calcium channel pr
8	1689	14.2	1810	2 T31092	probable voltage-g
9	1681	14.1	2178	2 S29237	calcium channel pr
10	1681	14.1	2272	2 C54972	voltage-dependent
11	1665	14.0	2270	2 A54972	voltage-dependent
12	1664.5	14.0	1891	2 T43262	calcium channel al
13	1663.5	14.0	2251	2 B54972	voltage-dependent
14	1656	13.9	2223	2 A47447	calcium channel pr
15	1651.5	13.9	2222	2 A37490	voltage-dependent
16	1633	13.7	1911	2 T43048	calcium channel al
17	1632	13.7	1873	2 A30063	dihydropyridine re
18	1626	13.7	1993	2 T30902	sodium channel SCA
19	1625.5	13.7	1852	2 A37860	calcium channel pr
20	1612	13.5	2143	2 JH0427	voltage-dependent
21	1602.5	13.5	2139	2 A44467	voltage-dependent
22	1597.5	13.4	1559	2 T30535	calcium channel al
23	1596.5	13.4	2166	2 S11339	calcium channel pr
24	1591	13.4	2019	2 A33996	sodium channel pro
25	1590	13.4	1783	2 T37258	probable voltage-d
26	1586	13.3	2016	2 A38195	sodium channel pro
27	1583.5	13.3	1873	2 A55645	calcium channel, v
28	1583	13.3	1977	2 S54771	sodium channel alp
29	1581.5	13.3	2171	2 S05054	calcium channel al

30	1578	13.3	1917	2 C88728	protein C48A7.1 [i
31	1573.5	13.2	1983	2 A60054	sodium channel pro
32	1572.5	13.2	2212	2 A41098	calcium channel pr
33	1568.5	13.2	1687	2 S41742	calcium channel al
34	1566.5	13.2	2203	2 T42742	voltage-dependent
35	1565.5	13.2	1951	2 S00320	sodium channel pro
36	1564.5	13.1	2181	2 A38198	calcium channel al
37	1561	13.1	2326	2 B47447	calcium channel pr
38	1560.5	13.1	1610	2 A46227	voltage-dependent
39	1557.5	13.1	2161	2 JH0564	calcium channel al
40	1555	13.1	2220	2 A45290	calcium channel pr
41	1554	13.1	2262	2 T30890	calcium channel al
42	1553.5	13.1	2005	2 A46269	sodium channel alp
43	1550	13.0	1957	2 S68453	sodium channel pro
44	1549.5	13.0	2009	2 A25019	sodium channel pro
45	1549	13.0	1646	2 JH0422	voltage-dependent

ALIGNMENTS

RESULT 1
T09053
low voltage-activated, T-type calcium channel alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09053
R;Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox
Nature 391, 896, 1998
A;Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium
A;Reference number: Z16538; MUID:98154730; PMID:9495342
A;Accession: T09053
A;Status: preliminary; translated from GB/EMBL/DBRJ
A;Molecule type: mRNA
A;Residues: 1-2254 <PER>
A;Cross-references: UNIPROT:O54898; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Map position: 17
A;Note: CACNA1G
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: calcium channel; voltage-gated ion channel

Query Match		91.9%;	Score 10945;	DB 2;	Length 2254;
Best Local Similarity		92.5%;	Pred. No. 0;		
Matches 2107;		Conservative	34;	Mismatches 101;	Indels 36; Gaps 6;
QY	1	MDEEDGAGAEESGQPRSFMRINDLSGAGGRPGSGAEKDPGSADSEAEGLPYALAPVV	60		
Db	1	MDEEDGAGAEESGQPRSFQNLNDSGAGGRQPGSGTEKDPGSADSEAEGLPYALAPVV	60		
QY	61	FFYLSQDSRPRSWCLRTVCNPPFERISMLVILLNCVTILGMFRPCEDIACDSQRILQAF	120		
Db	61	FFYLSQDSRPRSWCLRTVCNPPFERVSMVLVILLNCVTILGMFRPCEDIACDSQRILQAF	120		
QY	121	DDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR	180		
Db	121	DDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVR	180		
QY	181	TVRLRPLRAINRVPSMRILVTLLDTPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR	240		
Db	181	TVRLRPLRAINRVPSMRILVTLLDTPMLGNVLLCFFVFFIFGIVGVQLWAGLLRNR	240		
QY	241	CFLPENFSLPSVDLERYVOTENEDESPFICSQPRENGMRSRCSVPTLRDGGGPPPCGL	300		
Db	241	CFLPENFSLPSVDLEPYVOTENEDESPFICSQPRENGMRSRCSVPTLRGEGGGPPCSL	300		
QY	301	DYEAYNSSNTTCVNMNQYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM	360		
Db	301	DYETYNSSNTTCVNMNQYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM	360		
QY	361	YFVMDAHSFYNFIFYILLIIVGSFFMINCLVVIATQPSQKRESQLMREQVRFLSNA	420		

Db 361 YFVMDAHSFYFIYFILLIIVGSPFMINCLVVIATOFSETKQRESQLMREQVRFLSNA 420

QY 421 STLASFSEPGSCYEELLKYLIVYLKKAARLAQVSRAGVRVGLLSSPAPLGQETQPSS 480

Db 421 STLASFSEPGSCYEELLKYLIVYLKKAARLAQVSRAGLSSPVARSGQEPQPSG 480

QY 481 SCRSRRLSVHHLVHHHHHHHHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTP 540

Db 481 SCTRSRRLSVHHLVHHHHHHHHLGNGTLRVPRASPEIQDRDANGSRRLMLPPSTP 540

QY 541 ALSGAPPGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSKVYPTVHTSPPE 600

Db 541 TPSGGPRGAESVHSFYHADCHLEPVRCAQPPRCPSEASGRTVGSKVYPTVHTSPPE 600

QY 601 TLKEKALVEVAASSGPTLTLSLNIPPGYSSMHKLTQSTGACQSSCKISSPCLKADSG 660

Db 601 ILKDKALVEVAPSPGPTLTSTFNIPPGPFSSMHKLTQSTGACHSSCKISSPCKADSG 660

QY 661 ACGPDCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS-RRQRS LGPD 719

Db 661 ACGPDCPCYARTGAGEPESADHVPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS LGPD 720

QY 720 AEPSSVLAFWRLLICDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 779

Db 721 AEPSSVLAFWRLLICDTRFKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN 780

QY 780 IVFTSLFALEMLLKLIVYGPEGIKNPNIFDGVIVVISVWEIVGQGGGLSVLRTFRLM 839

Db 781 IVFTSLFALEMLLKLIVYGPEGIKNPNIFDGVIVVISVWEIVGQGGGLSVLRTFRLM 840

QY 840 RVLKLVRELPALQRLVLMKTMNDNVATFCMLLMLFIFIFSILGMHLFGCKFAERDGD 899

Db 841 RVLKLVRELPALQRLVLMKTMNDNVATFCMLLMLFIFIFSILGMHLFGCKFAERDGD 900

QY 900 LPDRKNFDSLLWAVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 959

Db 901 LPDRKNFDSLLWAVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL 960

QY 960 VAILVEGFAEEISKREDASGQLSCIQLPVDSQGGDANKSESEPFFSPSLDGDGRKKC 1019

Db 961 VAILVEGFAE-----GDATAKSESEPFFSPSLDGDGRKKR 997

QY 1020 LALVSLGEHPPELRKSLPPLIITHAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGA 1079

Db 998 LALVALGEHAELRKSLPPLIITHAATPMHPKSSSTGVGEALGSGRRRTSSSGSAEPGA 1057

QY 1080 A-HEMKPPSPARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1138

Db 1058 AHHEMKPPSPARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE 1117

QY 1139 SQDEEESSEERASAPAGSDHHRHGSLEREAKSSFDPLDTLOVPGHLRTASGRGSAEHQD 1198

Db 1118 SQDEEESSEEDRASAPAGSDHHRHGSLEREAKSSFDPLDTLOVPGHLRTASGRGSAEHQD 1177

QY 1199 CNGKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYI 1258

Db 1178 CNGKSASGRLARLTLDPPQLDGDDEGNLSKGERIQAWVRSLPACCRERDSWSAYI 1237

QY 1259 FPQSRFLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1318

Db 1238 FPQSRFLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT 1297

QY 1319 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGGLLVLSVIDILVSMVSDSGTKILGMLR 1378

Db 1298 AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGGLLVLSVIDILVSMVSDSGTKILGMLR 1357

QY 1379 VLRLRLTLRLRVISRAOGLKLVVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1438

Db 1358 VLRLRLTLRLRVISRAOGLKLVVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKGKF 1417

QY 1439 FVCQGEDTRNITNKSDCAEASRVRHKYNFDNLGQALMSLFLVASKDGVMDYDGLDA 1498

Db 1418 FVCQGEDTRNITNKSDCAEASRVRHKYNFDNLGQALMSLFLVASKDGVMDYDGLDA 1477

QY 1499 VGVDQOPIMNHNPMWLLYFTSFLLIIVAFFVLNMFVGVVVENFHKRQHQEERARRREK 1558

Db 1478 VGVDQOPIMNHNPMWLLYFTSFLLIIVAFFVLNMFVGVVVENFHKRQHQEERARRREK 1537

QY 1559 RLRRLEKKRR-----KAQCKPYYSYDSRFRLLVHHLCTSHYLDLFTITVIGLNVVTMA 1611

Db 1538 RLRRLEKKRRSKEQMAEAQCKPYYSYDSRFRLLVHHLCTSHYLDLFTITVIGLNVVTMA 1597

QY 1612 MEHYQOPILDEALKICNYITFTVIFVLESVEFKLVAFGFRFFQDRWNQLDLAIVLLSIMG 1671

Db 1598 MEHYQOPILDEALKICNYITFTVIFVESVEFKLVAFGFRFFQDRWNQLDLAIVLLSIMG 1657

QY 1672 ITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDITVMOALPQVGNLGLL 1731

Db 1658 ITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDITVMOALPQVGNLGLL 1717

QY 1732 FMLLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMK 1791

Db 1718 FMLLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMK 1777

QY 1792 DTLRCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVAVLMKHLEESNKEAKEAELEA 1851

Db 1778 DTLRCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVAVLMKHLEESNKEAKEAELEA 1837

QY 1852 ELELEMKTLSPPHSPGLSPFWGVEGPDSPDKPKALHPAAHARSASHFSLEHPTMQ 1911

Db 1838 ELELEMKTLSPPHSPGLSPFWGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMV 1897

QY 1912 PHPTLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRGWGLPKAQSGSV 1968

Db 1898 PHPEEVVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNSTAESRSLGHRGWGLPKAQSGSI 1957

QY 1969 LSVHSQPADTSYILQLPKDAPHLLQPHSAPTWTGTPKLPPGRSPLAQRPLRQAARTD 2028

Db 1958 LSVHSQPADTSCILQLPKDVHLLQPHGAPTWGAIPKLPPGRSPLAQRPLRQAARTD 2017

QY 2029 SLDVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSSTAQQHRSRSHSKISKHMTTPAPCPG 2088

Db 2018 SLDVQGLGSRREDLLSEVSGSPCLTRSSSFWGGSSIQVQORSGIOKSVKHRLPAPCPG 2077

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QY 2209 GPRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPCKDVLSLSGLSSDPADLDP 2266

Db 2197 GSRPPCPGVCLRRRAPASDSKDPSSVSSPLDSTAASPCKDVLTLGLSSDPTDMDP 2254

RESULT 2

T15838

hypothetical protein C54D2.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000

C;Accession: T15838

R;Minx, P.

submitted to the EMBL Data Library, October 1995

A;Description: The sequence of C. elegans cosmid C54D2.

A;Reference number: Z18415

A;Accession: T15838

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1657 <MIN>

A;Cross-references: EMBL:U37548; NID:g1017804; PID:g1017809; PIDN:AAA79201.1; CESP:C54D

C;Genetics:

A;Gene: CESP:C54D2.5

A;Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; 334/2; 370/2; 439/3; 470/3; 51

C;Superfamily: sodium channel protein

Query Match		29.9%;	Score 3564.5;	DB 2;	Length 1657;
Best Local Similarity		42.2%;	Pred. No. 6.5e-210;		
Matches 822;		Conservative 231;	Mismatches 430;	Indels 465;	Gaps 50;
QY	15	QPRSFMRNLDSGAGRPG-----PGSAEKDPG-----SADSEA	48		
Db	56	QSQSTRRHEDVEALGSIEGSKETQLSEHGRLASSEASPSRWEGRQIEWGNEEQIEEES	115		
QY	49	EGLPYPALAPVVFYLSQDSRPRSMCLRTVCNPWFERISMLVILLNCVTGLMFRPCED-I	107		
Db	116	E-LPYPGFAEPALRCFYQARPPRKWALQVMWSPWFDRTITMAVIMINCVTLGMWRPCEDGP	174		
QY	108	ACDSQRCRIIQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDWTNRLDFFIVIAGMLEY	167		
Db	175	DCDTRYCQILDIIDNCIFVYFAFEMVIKIMALGFYGPAAVMSDTWNRLDFFIVMAGIAEF	234		
QY	168	SLDLQ---NVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDITLPLMGNVLLLCFFVFFI	224		
Db	235	VLHEYLGGINLTARTVRVLRPLRAVNRIPSMRILVNLLDITLPLMGNVLLLCFFVFFI	294		
QY	225	FGIVGVQLWAGLLNRCF--LPENFS-----LPLSVDLERYIQTENEDESPFCISQPREN	277		
Db	295	FGIVGVQLWAGLLNRRCVINLPKTISENQSALENNVVKLTRYIPE-DTSLEYICSQPDAN	353		
QY	278	GMRSCRVPITLRGDGGGPPCGLDYEAYNSSNTTCVNMNQYVYTNCSAG-----	326		
Db	354	GLHTCSNLPPYTVD---GVKCNLTLDYDKVTNDSCINWNIIYNECQVNIYPSLMTIAIS	410		
QY	327	-----EHNPFKGAINFDNIGVAMIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLII	380		
Db	411	CFIKVMQRNPFQGSVDFNIGFAWVAIFLVISLEGWTDIMYVQDAHSFVNNIYFVLLIV	470		
QY	381	VGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPG-----S	431		
Db	471	IGAFFMINCLVVIATQFAETKRRETERMLQERKMLNRDSISCTGSEIGGASSKEEGDT	530		
QY	432	CYEELLKYLVIILKAARRLAQVSRAGVRVGLLSPAPLGGQETQPSSCSRSHRRLSV	491		
Db	531	VYAAVRFIGHTFRR-TKRAAKKITYAYMEE-----	560		
QY	492	HHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAE	551		
Db	561	-----RAERKSSERQOR-----RKSKLDDMAT--LS-----	584		
QY	552	SVHSFYHADCHLEPVRQAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVA	611		
Db	585	-----RIEKAEDE--	593		
QY	612	ASSGPPTLSLNIPPGPYSSMHKLLLETQSTGACQSSCKI-SSPCLKADSGACGPDSCPYC	670		
Db	594	--EDETTITREN-----GDDQIEQNGDGVRIKRVKIEEPEKIKIGN---GNSNGPHY	640		
QY	671	ARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSGLGPDAPSPSVLAFWR	730		
Db	641	KHSSSDE-----ESDEDEGEDQVYDGEAAKKS-----TPSKL--WW--	675		
QY	731	LICDTRKIVDSKYFGRGIMIAILVNTLSMGIEVHEQPEELTNALEISNIVFTSLFALEM	790		
Db	676	-FREKIQKFVICDHFTRGILVAILVNTLSMGVEYHQOPEILTVILEYSNLFTTALFALEM	734		
QY	791	LKLIVYGPFGYIKNPYNIPDGVIIVISVWEIVGQGGGLSVLRTFRMLRVLKLVRFLPA	850		
Db	735	LXIIASGLFGYLADGFLNDFDGGIIVALSVLFLFQEGKGLSVLRTFRLLRILKLVRFMPA	794		
QY	851	LQRQLVVLMTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD--GDTLP--DRKN	905		
Db	795	LRYQLVVMRLTMDNVTFPGLLVLFIFIFSILGMNLFGCKFKCKVEEKLGLLAKKCERN	854		
QY	906	FDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVE	965		
Db	855	FDTLWALITVFQILTQEDWNVWLFNGMAQINPWAALYFVALMTFGNYVLFNLLVAILVE	914		

QY	966	GFOAEEISKREDASQQLSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGDRKKCLALVSL	1025
Db	915	GFQE---SKEEE-----KRQLEEDARKQAVEEEDERKRELELI--	949
QY	1026	GEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSAEPGAAHMKS	1085
Db	950	-----IAKTSPAFNNGVAPA-----ECTCQRPSSPEEPS	980
QY	1086	PPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSG-----ERRSLLSGEQESQ	1140
Db	981	PRLLSANYH-----PSPERKHSANLDAIIDKRLVL-----	1010
QY	1141	DEESESBEERASPAGSDHRHRGSLEREAKSSFDLPTLQVPLHRTASGRGSASEHQDCN	1200
Db	1011	--RNSAPFDR-SPV-SEGRDDSRNLNRHA--SLVLPVANGVP-----YRRQRVH	1052
QY	1201	GKSASGRLARALRPDDPPLDGGDDADDEGNLSKGE-RVRAWIRARL-PACYLERDSWSAYI	1258
Db	1053	SWKASQELKQAL-----AEEE--KRNEAKQNTFVRKLLKKTCLHNRTEFSLFL	1098
QY	1259	FPPQSRERLLCHRIITHKMFHVVLVIIPLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1318
Db	1099	MGPKNPLRIKCLQTQTKKWEDTVLFFIGINCITLAMERPSSIPDSFERQFLHISGYIFT	1158
QY	1319	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDDLGLVLISVIDILVSMVSDSGTKILGMLR	1378
Db	1159	VIFTGEMMMK-----	1168
QY	1379	VLRLRLTLRPLRVISRAQGLKLVVETLMSLSLKPIGNIVVICCAFFIIFGILGVOLFKGKF	1438
Db	1169	-----VSHRIPTLKPIGNIVLICCTFFIIFGILGVOLFKGMM	1205
QY	1439	FVCOGEDTRNITNKSDCAEASYSR--WVRHKYNFDMNLQALMSLFLVASKDGWVDIMYDGL	1496
Db	1206	YHCIGPEVGNVTTKADCIE--DYRNKWNVHRYNFDMNLQALMSLFLVSSKDGWVSIMYQGI	1264
QY	1497	DAVGVDQOQPIMHNPNMLLYFISFLLIVAFFVLNNFVGVVVENFHKCRHQHEEEAARRRE	1556
Db	1265	DAVGVDVQPIENYNENWMIYFISFLLLVGFFVLNNFVGVVVENFHKCKEALEKEMREKEK	1324
QY	1557	EKRLRRLEK-----KRRKAQC-----KPYYSYDSYRFRLLVHHLC	1590
Db	1325	EXRLKRLKROKFEESMAGRKKNRIVWAGSAIKSIFSVERNYPYHYDGHTRFLHGIV	1384
QY	1591	TSHYLDLFTITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGR	1650
Db	1385	TSKYFDLAIAAVIGINVISMAFEYMMMPMGLKYVLKALNYFFTAVFTLEAAMKLIJALGFK	1444
QY	1651	RFFQDRWNQLDLAIVLLSIMGITLEEIEVNASIPINPTIIRIMRVLRIARVLKLLKMAVG	1710
Db	1445	RFFIEKNRLDMFIVILSIAGIIFEEFEA-LBELPINPTIIRVMRVLRIARVLKLLKMAKG	1503
QY	1711	MRALLDVTMOALPQVGNLGLLFFMLFFIFAALGVVELFGDLECDETHPCGELGRHATFRNF	1770
Db	1504	IRSLDVTVEALPQVGNLGSLLFFLLFFIFAALGVVELFGKLECSDEHPCDGLGEHAHFKNF	1563
QY	1771	GMAFLTFRVSTGDNWNGIMKDTLR-DCD-----QESTCYNTVISPIYFVSFVLTAQFVL	1824
Db	1564	GMAFLTFRATGDNWNGIMKDALRDDCDSSDHCTNCCVDPILAPCFFVIFVLISQFVL	1623
QY	1825	VNVVIAVLMKHLEESNKEAKEAEAELEAE	1852
Db	1624	VNVVAVLMKHLEESN---KRDAEGPAE	1648

RESULT 3
A42566

omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively splice
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
C;Accession: A42566
R;Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McCu
Science 257, 389-395, 1992

A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type
A;Reference number: A42566; MUID:92335886; PMID:1321501
A;Accession: A42566
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2339 <WIL>
A;Experimental source: IMR32, hippocampus
A;Note: sequence extracted from NCBI backbone (NCBIP:109168)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match		14.7%;	Score	1746.5;	DB	2;	Length	2339;
Best Local Similarity		24.2%;	Pred.	No. 2.2e-98;				
Matches		641;	Conservative	361;	Mismatches	823;	Indels	819; Gaps
		86;						
QY	27	GAGRPGGSAEKDPGSADSEAEGLPYPALAPVF	-----FYLSDSRP	70				
Db	25	GAGGAGGPGGLQPGQVLYKQSIARARTMALYNFIPVKQNCFTVNRSLSLFVSEDNVV	84					
QY	71	RSWCLRTVCNPWFERRISMLVILLNCVTILGMFRPCEDIACDSQRCRILQAFDD	---FIFAF	127				
Db	85	RKYAKRITTEWPPFEYMLATIIANCIVLAL	---EQHLPDGDKTPMSERLDDTEPYFIGI	140				
QY	128	FAVEMVVKMVALG-IFGKKCYLGDWTNRLDFFIVTAGMLEYS	---LDLQNVSPSAVRTVR	183				
Db	141	FCPEAGIKIIALGFVHRGYSYLRNGWNVMDFVVVLTCILATAGTDFDLR	-----TLRAVR	195				
QY	184	VLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLCPFFVFFIFGIVGVQLWAGLLRNCFL	243					
Db	196	VLRPLKLVSGIPSLQVVLKSIMKAMVPLLQIGLLLFALLMFAIIGLEFYMGKFHKA	CF- 254					
QY	244	PENFSLPLSDLERYYYQTENEDESPFCISQPRENGMRSCRSVPTLRGDGGGPPCGLDYE	303					
Db	255	-----PNSDAAE	-----PV-----GDFPCQKEAP	273				
QY	304	AYNSSNTTCVNNQYYTNCSEAHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIMYFV	363					
Db	274	ARLCEGTEC---REYWP	-----GPNFGITNFDNLFALITVFQCITMEGWDILYNT	323				
QY	364	MD-AHSEFYNYFIILLIIVGSPFMNLCVVIATQFSETKQRES	-----QLMREQRVRF	416				
Db	324	NDAAGNTWNWLYFIPLIIIGSFMLNLVLGVLGSEFAKERERVENRRAFLKLRQQQIE	- 382					
QY	417	LSNASTLASFSFEPGSCYEBELKVLVYLKRAARRLAQVSRAGVRVGLLSSPAPLGQET	476					
Db	383	-----RELNGYLEWIFKAEVMLAEEDRNA	-----EEK	410				
QY	477	QPSSSCSRSHRRRLSVHHLVHHHHHHHHYHLNGTILRAPASPEIQDRDANGRRRLMLPP	536					
Db	411	SPLDVLKRAATKKSNDLIH	-----AEEGEDRFAD	440				
QY	537	PSTPALSGAPPGAESVHSFYHADCHLEPVRCQAPPSPSEASGRTVGSKVYPTVHTS	596					
Db	441	-----	-----	440				
QY	597	PPPETLKEKALVEVAASSGPPPTLTSLNIPPGPYSSMHKLELTQSTGACQSSCKISSPCLK	656					
Db	441	-----	-----LCAVGSPFAR	450				
QY	657	ADSGACGDPSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS	716					
Db	451	ASLSKSGKTESSSYFR	-----KEKMR	473				
QY	717	GPDAEPSSVLAFAWRLLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNAL	776					
Db	474	-----FIRRMVKAQSPYVWVLCVVALNLCVAMVHYNQPRRLTILY	515					
QY	777	ISNIVFTSLFALEMLLKLIVYGPFGYTKNPYNIFDGVIVVISVWEIVG	---QQGG---GLS	831				
Db	516	FAEFVFLGLFLTEMSLKMYGLGPRSYFRSSFNCFDFGVIIVGSFEVWVAIAIKPGGSFGIS	575					
QY	832	VLRTFRLMRVLKLVRFPLPALQRLVVLMTKMDNVATFCMLLMFLFIFSI	GMHLFGCKF	891				
Db	576	VLRAIRLLRIKVKYSSLRNLVSVSLNSMKSIIISLLFLFLFVVFALLGMQLFGGQF	635					

QY	892	ASERDGDTLPRKPNFDSLLWAIIVTVFQILTQEDWNKVLYNGM	-----ASTSSWAALYFIA	946				
Db	636	NFQDETPT---TNPDTPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFFIV	691					
QY	947	LMTFGNYVLNLLVAILVEGF-QAAEISK	---REDASGQ	986				
Db	692	LTLFGNYTLLNVFLAIVDNLANAQELTKDEEMEEAANKALOKAKAEVAVSPMSAAN	751					
QY	987	LPVDSQGGDANKSESEPDFFSPSLDGDGRKKCLALVSLGE	-----HPELRK	1033				
Db	752	ISIAARQONSAKARSVMQEQRASQLRLQNLRASCEALYSEMDPEERLRFATRHLRPMKT	811					
QY	1034	SLLPPLIIHTAATPMSLP	---KSTSTGLGHALGPASR	1073				
Db	812	HLDRLVLVVELGRDGAEGPVGGKARPEAAEAPEGVDPPRRHRRHRDKDKTPEAGDQDRAEA	871					
QY	1074	---SAEPGA	-----AHMKSPPSARS	1103				
Db	872	PKAESGEPGAREERPRPHRSHSKEAAGPPPEARSEGRGPGEGRRHRRHRRGSP	EEAERE 931					
QY	1104	TSR-RSSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSE	-----ERASP-	1153				
Db	932	PRRRAHRH---QDPSKECAGAKGERRARRHRRGGFRAGPREAESGEEPARHRAHKAQPA	988					
QY	1154	-----AGSDHRRHRSLEAKSFDLPD	TLQVPLHRTASGRG	1191				
Db	989	HEAVEKETTEKEATEKEAIVEADKEKELRNHQPREPHCDLETS	GTIVVGMHTLPSTCL	1048				
QY	1192	SASBHQDCNGKSASGRLARALRPDDP	-----PLDGDADDEGNL	1235				
Db	1049	QKVEEQPEDADNQNRNVTMGSPDPDPNTIVHIPVMLTGPLGEATVPVPSGNVDLESQAEQK	1108					
QY	1236	-----VRAWIRARLPACYLERSWSAYIFPPQSRFRLLCHRIITHKMFDPHVVLVIF	1287					
Db	1109	KEVEADDVMSRGPPIVPYS	-----SMFCLSPTNLLRRFCHYIVTMYFEVVLVWIA	1161				
QY	1288	LNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN	1347					
Db	1162	LSSIALAAEDP-VRTDSPRNALKYLDYIFTGVFTFEMVIKIDGLLLHGPAYFRDLWN	1220					
QY	1348	VLDGLLVLSVIDILVSMV-SDSGTKILMLRLVRLRLTLRLPLRVISRAQGLKLVVETLM	1406					
Db	1221	ILD---FIVVSGALVAFAPSGSGKGDINTIKSLRVLRLPLKTIKRLPLKKA	VDCV 1276					
QY	1407	SSLKPIGNIVVICAFIIFIGILGVQLFKGKFFVCCQE	-----DTRN--ITNKSDCAEA	1458				
Db	1277	NSLKNVLNLIIVYMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCRGGYLDYKEEVEA	1336					
QY	1459	SYR-WVRHKYNFDNLGQALMSLFVLASKDGVVDIMVDGLDAGVDQOPIMNHNPMWLLYF	1517					
Db	1337	QPRQWKYDFHYDNVLMWALLTLFTVSTGEGMPVMLKHSVDATYEEQGPSGYRMELSIFY	1396					
QY	1518	ISFLLIIVAPFVLMFVGVVVENFHKCRQHQQEERREKRLRLEKRRKA	-----QC	1572				
Db	1397	VVYFVVPFFVNFIVALIITF	-----QEQGDKVMSE	1446				
QY	1573	KPY--YSDYSR--FRLLVHHLCTSHVLDLFTITVIGLVNVTMAMEHYQQPQILDEALKIC	1628					
Db	1447	KPLTRYMPQNRQSFQYKTTWTFVVSPPFEYFIMAMIALNTVVLMMKFYDAPYEYELMLKCL	1506					
QY	1629	NYIFTVIFVLESVKLVAFGFRFFQDRWNQDLAIIVLLSIMGITLEEI-EVNASLPINP	1687					
Db	1507	NIVFTSMFSMECVLKIIAFGVNLNPFDAWNVDFVTVLGSITDILVTEIAETN	-----NF	1561				
QY	1688	TIIRIMRVLRIARVLKLLKMAVGMRALDVTMOALPQVGNLGLLFFMLFFIFAALGVVELF	1747					
Db	1562	INLSFLRFPRAARLIKLLRQGYTIRILLWTQVQSFKALPYVCLLIAMFFIYAIIGMQVF	1621					
QY	1748	GDLECEDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRD	--CDQE--STC	1803				
Db	1622	GNIALDDD---TSINRHNFRFTLQALMLLFRSATGEAWHEIMLSCLSNQACDEQANATE	1678					

QY 1804 YNTVISPIYFVSFVLTAFQVVLNVVIAVLM-----KHLDE----- 1838
Db 1679 CGSDFAYFYFVSFTFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHLDEFIRVWAEYDP 1738
QY 1839 ----- 1838
Db 1739 AACGRISYNDMEMLKHMSPPLGLGKKCPARVAYKRLVRMNPISNEDMTVHTSTLMAL 1798
QY 1839 -----SNKEAKEAEAELEEMKTLSPQPHSPGLSPFLPWPGEVGPDSPPSP 1886
Db 1799 IRTALEIKLAPACTKQHCDAELRKEISVVWANL-PQKTLDLLVP-----PHKPEDEM 1849
QY 1887 KPGALHPA-----AHARSASHFSLEHPTM-----QPHPTELPGPD 1921
Db 1850 TVGKYYAALMIFDYKQNKTTTRDQMQAAPGGLSQMGVPVSLFHLKATLEQTQPAVLRGAR 1909
QY 1922 LLTVRKSGVSRTHSLPNDSYMCRHGSTABGPLGHRGWGLPKAQSGSVLSVHSQPADTSYI 1981
Db 1910 VFLRQKSSSTLSN-----GGAIQNOESGIKESV-----SWQ 1940
QY 1982 LQLPKDAPHLLQPHSAPTWTGTPKLPPPGRSPLAQRPLRRQAIRTDSLDVQLGSRE-- 2039
Db 1941 TQRTQDAPHEAR-----PPLERGHSTEIPVGRSGALAVD-VQMQSITRRQPD 1986
QY 2040 -----DLLAEVSGSPPLARAYSFWGQSSTQAQHQHSRSHSKISK-----HM---TPPAPC 2086
Db 1987 QEPQPGLESQORAASMPRLAAET---QPVTDASPMKRSISITLAQRPRGTHLCSTTPDRPP 2043
QY 2087 PG-----PEPNWGKGPETRRSSLELDTLSWISGDLLPPGGQEEPPSP 2129
Db 2044 PSQASSHHHHRCHRRRRDRKQRSLEKGP---SLSADMDGAPSSAVGGLPPG--EQPTQC 2098
QY 2130 RDLKKCYSEVAQSCQRR-PTSWLDEQRRHSIAVSCLDG-----SQPHLG 2173
Db 2099 RRERRRQERGRSQERRRQPSSSSSEKQRF---YSCDRFGRGEPKPKPSLSHPTSPTAG 2155
QY 2174 TDP-----SNLGGQPL-----GQPGSR---PKKILSP-PSITIDPPES-----Q 2208
Db 2156 QEPGPHPOGSGSVNGSPLLSTSGASTPGRGQRRQLPQTPLTPRPSITYKTANSSPIHFAQ 2215
QY 2209 GPRTPP--SPG-----ICLRRRAPSSDSKDPGLASGPPDSMAASPSKDVLSLGL 2257
Db 2216 AQTSLPAFSPGRLSRGLSEHNALLQRDPLS---QPLAPG-----SRI 2254
QY 2258 SSDP 2261
Db 2255 GSDP 2258

RESULT 4
T45115
N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human
C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T45115
R:Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McQ
Science 257, 389-395, 1992
A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-type
A:Reference number: A42566; MUID:92335886; PMID:1321501
A:Accession: T45115
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2237 <WIL>
A:Cross-references: UNIPROT:Q00975; EMBL:M94173; NID:g179759; PIDN:AAA51898.1; PID:g1797
A:Experimental source: cell line IMR32; neuroblastoma
C:Genetics:
A>Note: CCHL1A2
C:Function:
A:Description: calcium influx
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.6%; Score 1741; DB 2; Length 2237;
Best Local Similarity 24.1%; Pred. No. 4.6e-98;

Matches 629; Conservative 361; Mismatches 836; Indels 780; Gaps 80;
QY 27 GAGRPGPGSAEKDPGSDADSEAEGLPYPALAPVVF-----FYLSDSRP 70
Db 25 GAGGAGGPGGLQPGQORVLYKQSIQARTMALYNPIPVKQNCFTVNRSLFVSEDNVV 84
QY 71 RSWCLRTVCNPFERISMLVILLNCVTILGMFRPCEDIAQDSQRILQAFDD---FIFAF 127
Db 85 KYAKRITETWPPPEYMILATIIANCIVLAL---EQHLPDGDKTPMSERLDDTEPYFIGI 140
QY 128 FAVEMVVMVALG-IFGKKCYLGDWTNRDLDFIIVAGMLEYS---LDLQNVFSAVRTVR 183
Db 141 FCFEAGIKIIALGFVFHKGSYLRNGWNVMDVVVLTGILATAGTDFDLR-----TLRAVR 195
QY 184 VLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLCCFFVFFIFGIVGVQLWAGLLRNRQPL 243
Db 196 VLRPLKLVSGTIPSLQVVLKSIKAMVPLLQIGLLFFAILMFAIIGLEFYMGKFHKACF- 254
QY 244 PENFSLPLSVDLERYYYQTENEDESPFICSQPRENGMRSCRSVPTLRGDDGGGPPCGLDYE 303
Db 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273
QY 304 AYNSSNTTCVNWNQYYTNCISAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFV 363
Db 274 ARLCEGDTEC---REYWP-----GPNFGITNFDNILFAITLVFQCITMEGTDILYNT 323
QY 364 MD-AHSFYNFIYFILLIIVGSPFMINCLVVIATQFSETKQRES-----QLMREQRVRF 416
Db 324 NDAAGNTWNWLYFIPLIIIGSFFMLNLVLGVLGSEFAKERVENRRRAFLKLRQQQIE- 382
QY 417 LSNASTLASFPSEPGSCYEELLKYLVLKKAARRLAQVSRAGVRVGLLSSPAPLGGQET 476
Db 383 -----RELNGYLEWIFKAEVMLAEEDRNA-----EEK 410
QY 477 QPSSCSRSRHRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPP 536
Db 411 SPLDVLKRAATKKSRLDLI-----AEGEDRFAD----- 440
QY 537 PSTPALSGAPPGGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKVYPTVHTS 596
Db 441 ----- 440
QY 597 PPPETLKEKALVEVAASSGPPILTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLK 656
Db 441 -----LCAVGSPPAR 450
QY 657 ADGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQSL 716
Db 451 ASLKSCKTESSESYFRR-----KEMFRF----- 473
QY 717 GPDAEPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPELTNALE 776
Db 474 -----FIRMVKAQSFYVWVLCVVALNTLCVAMVHYNQPRRLTTLY 515
QY 777 ISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIQFQVIVVISVWEIVGQ-----QGGGLS 831
Db 516 FAEFVLGLFLTEMSLKMVGLGPRSYFRSSFCDFGVIVGVSFVFWAAIKPGSSFGIS 575
QY 832 VLRTEFLMRVLKLVRFPLALQRLVLMKTMNDNVATFCMLLMLFIFIFSILGMHLFGCKF 891
Db 576 VLRALRLRIFKVTKYWSSLRNLVSVLLNSMKSIISLLFLFLFIVVFALLGMQLFGGQF 635
QY 892 ASERDGDTLPRKNFDSLWAIWTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFIA 946
Db 636 NFQDETPT---TNFDTFPAAILTVFQILTGEDWNAVMYHGIESQGGVSKGMFSSFYFIV 691
QY 947 LMTFGNYVLNLLVAILVEGF-QAEEISK---REDASGQ-----LSCIQ 986
Db 692 LTLFGNYTLNVLFLAIVDNLANAQELTKDEEEMEEAANQKALQKAKEVAEVSPPMSAAN 751
QY 987 LPVDSQGGDANKSESEPDFFSPSLDGDGDRKCKCLALVSLGE-----HPELRK 1033
Db 752 ISIAARQONSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLRFATTHLRPDMKT 811

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QY 1034 SLPPPLIHTAATPMSLP-----KSTSTGLGEALGPASR-----RTSSG----- 1073
Db 812 HLDRELVVELGRDGARGPVGKARPEAAAEPEGVDPFRHHRDKDKTPAAGDQDRAEA 871
QY 1074 ----SAPPGA-----AHMKSPPSARS-----SPH-----SPWSAASSW 1103
Db 872 PKAESGPGAREERPRPHRSHKXAAGPPPEARSEGRGPGPEGGRHRRRGSPEEAAERE 931
QY 1104 TSR-RSSNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEESSEE-----ERASP- 1153
Db 932 PRHRAHRH---QDPKCECAGKGERRARHRRGGPRAGPREAESGEEPARRHRAHKAQPA 988
QY 1154 -----AGSDHRHGSLEAREAKSFDLPDTLQVPGHLHTASGRG 1191
Db 989 HEAVEKETEKATEKEAEIWEADKEKELRNHQPREPHCDLETSGTVTVGPMHTLPSTCL 1048
QY 1192 SASEHQCNCKSASGRLARALRPDDP-----PLDGGDDADDEGNL-----SKGE 1234
Db 1049 QKVEEQPEDADNQNRNVRMRGSPQPPDPNTIVHIPVMLTGPLGEATVVPVSGNVDLBSQAEGK 1108
QY 1235 R-----VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVVLIIF 1287
Db 1109 KEVEADDVMRSGPRPIVPYS-----SMFCLSPTNLLRRFCHYIVTMYFEVVILVIA 1161
QY 1288 LNCITIAMBRPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWN 1347
Db 1162 LSSIALAAEDP-VRTDSPRNNAKYLDYIFTGVFTFEMVIKMDLGLLLHPGAYFRDLWN 1220
QY 1348 VLDGLLVLIISVIDILVSMV-SDSGTKILGMLRVLRLLRLRLRPLRVISRAQGLKLVVETLM 1406
Db 1221 ILD-----FIVVSGALVAFAGSGKGDINTIKSLRVLRVLRPLKTIKRLPKLKAVIDCVV 1276
QY 1407 SSLKPIGNIVVICCAFFIIFGILGVQLPKGKFFVCQGE-----DTRN--ITNKSDCAEA 1458
Db 1277 NSLKNVLNIIIVMLFMFIFAVIAVQLFKGKFFYCTDESKELERDCRGQYLDYEKEVEA 1336
QY 1459 SYR-WVRHKYNFDNLGQALMSLVFLASKDGWVDIMYDGLDVGVDQQPIMNHNPMWMLLYF 1517
Db 1337 QPROWKYDFHYDNVNLWALLTLFTVSTGEGWPMVLKHSVDAITYEEQGSPSPGYRMEISIFY 1396
QY 1518 ISFLLIYAFFVLNMFVGVVVENFHKCRHQHEEEARRREKRLRRLEKKRKA-----QC 1572
Db 1397 VVYFVVFVFFVFVIFVALIITF-----QEGDKVMSE-----CSLEKNERACIDFAISA 1446
QY 1573 KPY--YSDYSR--FRLLVHHLCTSHYLDLFTITGVIGLVNVTVMAMEHYQQPQILDEALKIC 1628
Db 1447 KPLTRYMPQNRQSFQYKTWTFTVVSPPFEYFIMAMIALNTVVLNMMKFYDAPYEYELMLKCL 1506
QY 1629 NYIFTVIFVLESYFKLVAFGRFRFFQDRWNQDLAIIVLLSIMGITLEEI-EVNASLPINP 1687
Db 1507 NIVFTSMFMECVLKIIAFGVNLNFRDANWVDFVTVLGSITDILVTEIAETN-----NF 1561
QY 1688 TIIRIMRVLRIRVLKLLKMAVGMRALDITVMQALPOVGNLGLLFMLLFFIFAALGVLELF 1747
Db 1562 INLSFLRLFRAARLLKLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVF 1621
QY 1748 GDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDTLRD--CDQE--STC 1803
Db 1622 GNIALDDD--TSINRHNFRFTFLQALMLLRSATGEAWHEIMLSCLSNQACDEQANATE 1678
QY 1804 YNTVISPIYFVSFVLTAQFVLNVVIAVLM-----KHLEE----- 1838
Db 1679 CGSDFAFYFYVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGPHHLDEFIRVWAEYDP 1738
QY 1839 ----- 1838
Db 1739 AACGRISYNDMFEMLKHMSPPPLGLGKKCPARVAYKRLVRNMNMPISNEDMTVHTSTLMAL 1798
QY 1839 -----SNKEAKEAEAELEAEELEMKTLSPQHPSPGSPFPLWPGVEGPDSPDSP 1886
Db 1799 IRTALEIKLAPAGTKQHQCDAELRKEISVVWANL-PQKTLDLLVP-----PHKPDDEM 1849
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QY 1887 KPGALHPA-----AHARSASHFSLEHPTM-----QHPHTELPSPD 1921
Db 1850 TVGKYVAAALMIFDYKQNKTRDQMQQAPGGLSQMGVSLFHPLKATLEQTQPAVLRGAR 1909
QY 1922 LLTVRKSGVSRTHSLPNDSYMCRHGSTAEGLPHRGWGLPKAQSGSVLSVHSQPADTSYI 1981
Db 1910 VFLRKSKSTLSN-----GGAIQNQESGIKESV-----SWG 1940
QY 1982 LQLPKDAPHLLQP-----HSAPTWTGTIPKLPBPPGRSPLAQRLRRQAAIR-----TDS 2029
Db 1941 TQRTQDAPHEARPPLERGHSTEI-----PVGRSGALAVDVQMOSITRRGPDGEPQPG 1992
QY 2030 LDVQGLGSRDALLAEVSGP---SPPLARAYFWGQSSTQAQQHSHRSKISKHMTPTTAPC 2086
Db 1993 LESQGRAASMPRLAAETQPVTTDASP MKRSI-----STLAQRPGRGTHLCST---TPDRPP 2043
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Db 2044 PSQASSHHHHRCHRRRRDRKORSLEKGP---SLSADMDGAPSSAVGGLPPG--EGPTGC 2098
QY 2130 RDLKKCYVEAQSCQRR-PTSWLDEQRRHSIAVSCLDGS-----QPHLGTDPNS--LG 2180
Db 2099 RRERERRQERGRSQERRQPSSSSSEKQRF---YSCDRFGGREPPKPKPSLSHPTSTAG 2155
QY 2181 GQPLGGPSRPPKKLSPPSITIDPPESQGPRTPPSP-----GIC 2219
Db 2156 QEP--GHPQAGSAVGFPNTT--PCCRETSPASWPPLALELALTLTWGSVWTVRPLSTPC 2211
QY 2220 LRRRAPSSDSKDPGLASGPPDSMAASP 2245
Db 2212 LRTRSLSRRLWPPTRAAPPGLPTCPP 2237
RESULT 5
A45386
omega-conotoxin-sensitive calcium channel alpha-1 subunit rbB-I - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45386
R;Dubel, S.J.; Starr, T.V.; Hell, J.; Ahljanian, M.K.; Enyeart, J.J.; Catterall, W.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5058-5062, 1992
A;Title: Molecular cloning of the alpha-1 subunit of an omega-conotoxin-sensitive calc
A;Reference number: A45386; MUID:92279265; PMID:1317580
A;Accession: A45386
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2336 <DUB>
A;Cross-references: UNIPROT:O89089
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:104355)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
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Best Local Similarity 24.0%; Pred. No. 3.3e-96;
Matches 644; Conservative 365; Mismatches 810; Indels 860; Gaps 93;
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Db 25 GAGGAGGPGQGGLPPGQORVLYKQSIQAQARTMALYNPIPVKQNCFTVNRSLFVFSEDNVV 84
QY 71 RSWCLRTVCNPFERISMLVILLNCVTLGMFRPCEDIACDSQRCLIQAFDD---FIFAF 127
Db 85 RKYAKRITETWPPPEYMLATIIANCIVLAL-----EQHLPDGDKTPMSERLDDTEPYFIGI 140
QY 128 FAVEMVVKMVALG-IFGKKCYLGDVTNRLDFFIVIAGMLEYS---LDLQNVSFSAVRTVR 183
Db 141 FCPEAGIKIIALGPFVFKGSLRNGWNVDMFVVVLTEILATAGTDFDLR-----TLRAVR 195
QY 184 VLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIGIVGVLWAGLLNRCEL 243
Db 196 VLRPLKLVSGIPSLQVVLKSIKMAVPLLIQIGLLFFAILMFAIGLEFYMGKFKACF- 254
QY 244 PENFSLPLSVDLERYYYQTENEDESPFICSPRENGMRSCRSVPTLRGDDGGGPPCGLDYE 303
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Db 255 -----PNSTDAE-----PV-----GDFPCGKEAP 273

QY 304 AYNSSNTTCVNWNOYYTNC SAGEHNPFGAINFDNIGYAWTAIFQVITLEGWVDIMYFV 363

Db 274 ARLCSDTEC-----REYWP-----GNFGITNFDNILFAILTVFQCITMEGWTIDLYNT 323

QY 364 MD-AHSFYNFIFILLIIVGSEFFMINLCLVVIATQFSETKQRES-----QLMREQRVRF 416

Db 324 NDAAGNTWNWLYFIPLIIGSFFMLNLVLGVLGSEFAKERVENRRAFLNVRROQQIE- 382

QY 417 LSNASTLASFBPGSCYEELLKYLVIYLRKAARRLAQVSRAGVRVGLLSSPAPLGGQET 476

Db 383 -----RELNGYLEWIFKAEVVM LAEEDKNA-----EEK 410

QY 477 QP-SSSCSRSHRRLSVHHLVHHHHHHHHVHLGNGTLRAPRASPEIQDRDANGSRRLMLP 535

Db 411 SPLDAVLKRAATKKSRNDLIH-----AEEGEDR----- 438

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Db 439 ----- 438

QY 596 SPPPETLKEALVEVAASSGPPTLTSLNIPPGPYSSMHKLLTQSTGACQSSCKISSPCL 655

Db 439 -----FVDLCAAGSPFARASL-----KSGKTESS----- 462

QY 656 KADSGACGSDSCPYCARAGAGEVELADREMPDSDSEAVVEFTQDAQHSDLRDPHSRRQRS 715

Db 463 -----SYFRR-----KEMFRF----- 474

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Db 475 -----LIRRMVKAQSFYVWVLCVVALNTLCVAMVHYNQORLTAL 515

QY 776 EISNIVFTSLFALEMLLKLIVGPGFYIKNPYNIFDGVIVVISVWEIVGQ-----QGGGL 830

Db 516 YFAEFVFLGLFLTEMSLKMVGLGPRSYFRSSFCDFGVIVGSIFEVVWAAIKPGTSFGI 575

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Db 576 SVLRALRLRIRFKVTKYWNSLRNLVSVLLNSMKSIISLLFLFLFIVVFALLGMQLFGGQ 635

QY 891 FASERDGDTLPDRKNFDSLWAIWTVTFQILTQEDWNKVLYNGM-----ASTSSWAALYFI 945

Db 636 FNFQDETPT-----TNFDTFPAAILTVFQILTGEDWNVAVMYHGIESQGVSKGMFSSFYFI 691

QY 946 ALMTFGNYVLFNLLVAILVEGF-QAEEISK-----REDASGQ-----LSCI 985

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QY 986 QLPVDSQGGDANKSESEPDPFSPSLDGDGRKKCLALVSLGE-----HPELR 1032

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QY 1033 KSLLPPLIIH-----TAATP----- 1047

Db 812 THMDRPLVVEPGRDGLRGPAGNKSKEGTEATEGADPPRRHRRDRDKTSASTPAGGEQ 871

QY 1048 --MSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAHEMKSPPSARSSPHSPWSAASWTS 1105

Db 872 DRIDCPKAESTETGAREERARPRRSHSKEA-PGADTQVRCERSRRHRRGSPPEATEREP 930

QY 1106 RR-----SSRNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEERAS PAG 1155

Db 931 RRHRAHRHAQDSSKEGEGTAPVL---VPKGERRARHRGPRTGPRETENSEEPT R----- 982

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QY 1236 -----VRAMIRARLPACYLERDSWSAYI--FPPQSRFRLL 1268

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QY 1269 CHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVK 1328

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Db 1200 MIDLGLLHPGAYFRDLWNILDFIVVSGALVAFAFSSFMGSGKGDINTIKSLRVLRVL R 1259

QY 1388 PLRVISRAOGLKLVVETLMSCLKPIGNIIVVICCAFFIIFGILGVQLFKGKFFVCCQGE--- 1444

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QY 1445 ---DTRN---ITNKSDCAEAS YR-WVRHKYNFDNLGOALMSLFLVASKDGWVDIMVDGLDA 1498

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QY 1499 VGVDQQQPIMNHNPMWLLYFISLILIVAFFVLNMFVGVVVENFHKCRQHOOEEEEARRREEK 1558

Db 1380 TYEEQGPSPGFRMELSI FYVYVYVVFVFFVFVNI FVALIITF-----QEQQDKVMSE-- 1431

QY 1559 RLRLLEKKRRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTITGVIGLNVVT 1609

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QY 1610 MAMEHYQQQILDEALKICNVIFTVIFVLESVFELVAFGFRFFQDRWNQLDLAIVLSI 1669

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QY 1670 MGITLEIEVNASLPINPTIIRIMRVLRIARVLKLLKXAVGMRAALLDTVMQALPOVGNLG 1729

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Db 1604 LLIAMLFFIYAIIGMVQFVGNIALDDG---TSINRHNNFRTFLOALMLLFRSATGEAWHEI 1660

QY 1790 MKDTL--RD CD--QESTCYNTVISPIYFVSFVLTAQFVLNVVVI AVL M----- 1833

Db 1661 MLSCIGNRACDPHANASEC-GSDFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEBYLTRDSS 1719

QY 1834 ---KHLEE----- 1838

Db 1720 ILGPHHLDEFIRVWAEYDPAACGRISYNDMFEMLKHMSPPGLGKKCPARVAYKRLVRMN 1779

QY 1839 ---SNKE-----AKEBAEAEAELEMEKTL---SPQPHSPL 1868

Db 1780 MPISNEDMTVHFTSTLMALIRTALEIKLAPAGIKQHQCDAELRKEISSVWANLPQKTLDL 1839

QY 1869 GSPFLWPVGEGPDS PDKPGALHPA-----AHARSASH-----FSLEH 1907

Db 1840 LVP-----PHKPD EMTVGKVYAALMIFDFYKQNKTTTRDQTHOAPGGLSQMGFVSLFH 1891

QY 1908 PTM----QPHPTELPGDPLLTVRKSGVSRTHSLPNDSYMCRHGSTATG PLGHRGWGLPKA 1963

Db 1892 PLKATLEQTQPAVLRGARVFLRQKSAT---SLSNGGAIQTQESGIKESL---SWG TQT 1944

QY 1964 QSGSVLSVHSQPADTSYILQLPKDAPHLLQ-----PHSAPTWG-----TI 2003

Db 1945 Q--DVLYEARAPLERGHS AEIPVGPQPGALAVDVQMNM TLRGPDGEFPQGL ESQGRAASM 2002

QY 2004 PKL-----PPPGRSP-----LAQRPLRQAAIRTDSLDVQGLSGREDLLAEVSGPSP 2051

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QY 2169 -----QPHLGTDP-----SNLGGQPL-----GGPGSRPKKLS 2196
Db 2134 EPPQKPSLSSHPISPTAALPQPHPGQSGSVNGSPLMSTGASTPGRGRRQLPQTPLT 2193
QY 2197 P-PSITIDPPES-----QGPRTTP--SPG-----ICLRRAPSSDSKDPLASGPP 2238
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QY 2239 -----DSMAASPSKDVLSL-----SGLSS 2259
Db 2251 IGSDPYLQRLDSEASAHNLPEDTLTFEEAVATNSGRSS 2289

RESULT 6
S41080
calcium channel alpha-1 chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S41080
R:Coppola, T.; Waldmann, R.; Borsetto, M.; Heurteaux, C.; Romey, G.; Mattei, M.G.; Lazdu
FEBS Lett. 338, 1-5, 1994
A:Title: Molecular cloning of a murine N-type calcium channel alpha-1 subunit. Evidence
A:Reference number: S41080; MUID:94139884; PMID:8307146
A:Accession: S41080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2288 <COP>
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.3%; Score 1706; DB 2; Length 2288;
Best Local Similarity 24.5%; Pred. No. 6.6e-96;
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QY 71 RSWCLRTVCNPFERISMLVILLNCVTLGMFPCEDIAQSCQRCRILQAFDD---FIFAF 127
Db 85 RYAKRITWPPPEYMITATIIANCIIVLAL---EQHLPDGKTPMSERLDDTEPYFIGI 140
QY 128 FAVEMVVMVALG-IFGKCYLGDWTNRDLDFIVIAQMLEYS---LDLQNVSFSAVTRV 183
Db 141 FCFEAGIKTIAGLGFVHKGSYLRNGWNVDFVVVLTGILATAGTDFDLR-----TLRAVR 195
QY 184 VLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCLF 243
Db 196 VLRPLKLVSGIPSLQWLKSIKAMVPLLIQIGLLFFAILMFGIIGLEFYMGKFKACF- 254
QY 244 PENFSLPLVDLERYYYQTENEDESPFICSPRENGMRSCRSVPTRLGDDGGGPPCCGLDYE 303
Db 255 -----PNSTDTE-----PV-----GDFPCGKDDP 273
QY 304 AYNSSNTTCVNNQYYTNCSEAGHNPFKAINFDNIGYAWIALFQVITLEGWVDIMYFV 363
Db 274 ARQCDGDETC---REYWP-----GPNFGITNFDNIFAILTFVQCITMEGTIDILYNT 323
QY 364 MD-AHSFYNYFIYELLIIIVGSFFMINCLVVIATQFSETKQES-----QLMREQRVRF 416
Db 324 NDAAGNTWNWLYFIFLIIGSFFMLNLVLGVLGSEFAKERERVENRFAFLKLRQOQIE- 382
QY 417 LSNASTLASFSEPGSCYEELLYLVILKAAARLAQVSRAAGVRVGLLSSPAPLGQET 476
Db 383 -----RELNGYLEWIFKAEVVMLEEDKNA-----EEK 410
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Db 411 SPLDLKRAATKKSRLNLIH----- 430

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Db 474 -----FIRMVKAQSFYVVVLCVVALNTLCVAMVHYNQORLTTALY 515
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QY 832 VLRTFRLMRVLKVRFLPALQRLVVLMTKMDNVATFCMLLMFLFIFISILGMHLFGCKF 891
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QY 892 ASERDGTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLNNGM-----ASTSSWAALYFIA 946
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QY 947 LMTFGNYVLFNLLVAILVEGF-QAEEISK-----REDASGQ-----LSCIQ 986
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QY 1111 NSL-----GRAPSLKRRSPSGERRSLLSGE---GOESQDEESSEERASPGSDHHRG 1162
Db 931 HAQDSSKEGTVPVL---VPKGERARHGRPTGPREAENNEEPTRRHRA-----RHK- 979
QY 1163 SLEREAKSPDLPDPTLQVPLGHLRTASGRGSAHEQDCNGKSASGRALARALRPPDDPLD- 1220
Db 980 -----VPPTLQPP---EREAEEKSNPVEGD-----KETRNHQKPEPHCDLE 1018
QY 1221 -----GDDADDEGNLSK-----GE 1234
Db 1019 AIAVTDVGLHMLPSTCLQKVDEQPEDADNQNVTRMGSPQSDPSTTVHVPVTLTGPGGE 1078
QY 1235 R-----VRAWIRARLPACYLERDSWSAYIFPPQSRFRLLC 1269
Db 1079 TPVVPNGNMNLEQAEGKKEAEADDVLRGRPRPIVPS-----SMFCLSPTNLFRFC 1131
QY 1270 HRIITHKMFHDHVVLIIFLNCITIAMBRPKIDPHSAERIFLTSNYIFTAVFLAEMTVKV 1329
Db 1132 HYIVTMYLEWVILVIALSSIALAAEDP-VRTDSFRNNALEYMDYIFTGVTCCEMVIKM 1190
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Db 1191 IDLGLLLHPGAYFRDLWNILD---FIVVSGALVAFAFSGSKGDKDINTIKSLRVLRLRTP 1246
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Db 156 IAKGLVMEHAYLRDPWNWLDVWVILGVYTLVPNVANL--SGIRIFRVLRALTRTISAVE 213

QY 196 SMRILVTLTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNRCFLPENFSLPLSVDL 255

Db 214 GLKTMVNALLKSMKMLSDVILITTFCLCFALVGMQLFVGS LRKNCVCLKPPLNTTIDYDS 273

QY 256 ---ERYYQOTENEDES PFICSQPRENMRSCRSVPTLRGDGGGPPCGLDYEAYNSSSNT 311

Db 274 FVTNESHWHHPDTPITC-----GNSTSAGPCPLNY----- 306

QY 312 TCNVNWNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYN 371

Db 307 TCL-----ANIG-NNPNYGYTNLDNFGWAVITAFQLVTLDYWENVYNYVLSSMGSWY 357

QY 372 FIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLAS-FSEPG 430

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QY 551 ESVHSFYHADCHLEPVRCQAPPPRSPSEASGRVTGSGKVYPTVHTSPPPETLK--EKALV 608

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QY 609 EVAASSGPPTLTSLNIPPGPYSSMHKLLLETQSTGACOSSCKISSPCLKADSGACGPDSCP 668

Db 535 K-----TLDVKSSFRLKLSAISEQSSTGDVDNNENINN-----TQPQKSVS 575

QY 669 YCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAPESPVL-- 726

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QY 786 FALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWE-----IVGQGGGSLSVLRTFRLMR 840

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Db 988 GRQD-HGTS-----DPPDPP-----MTEVDECCPWCNMKMTGCGCITR--W 1024

QY 1255 SAYI-FPPQSRFRLLCHRIIITHKMFHDVVLVIIFLNCITIAME-----RPKIDPHSAER 1307

Db 1025 KASDGYRSWRNLRLAVKKFVEHKYFEBWTILAIIMASSIALTFEDINLPSRPKL-----K 1078

QY 1308 IFLTLSNYIFTAVFLAEMTVKVVVALGMCFGEQAYLRSSWNVLJGLLVLISVIDILVSMVS 1367

Db 1079 EYLQYLNITFAVTFSIEFLCLKVLG-----GVWSYFRNCWNCLDVLIVFVPV-----SSVIA 1130

QY 1368 DSGTK--ILGMLRVLRLRLRPLRVISRAQGLKLAVVETIMSSLKPIGNIVVICCAFFII 1425

Db 1131 DSSNQDSSLSLSRLRTLRLRPLRAISRWEGMRVVVNSLLFAIPGIGNVLLVCMVFWLI 1190

QY 1426 FGILGVQLFKGKFFVCQGEDTRN-----ITNKSDCABASVWRVHRKYNFEDNLGQALMSLF 1480

Db 1191 FSIIMGVOFFGGRFFKCVDDNNKELPLISIVQNRSECIQKGYRWVNSDINFDSLNGFMALF 1250

QY 1481 VLASKDGVVDIMYDGLDAVGVDQOQIMNHNPMWMLLYFISFLLIIVAFFVLNMFVGVVVENF 1540

Db 1251 QVATFEGWIEVMRDAVDAREVDQOQSDGYNFESAYAYFVVFIIVGSFFTLNLFIGVIIDNF 1310

QY 1541 HKCRQHQEE-----EEARRREEKRLRR--LEKRRKAQCKPYYSYDSRRELLVHHLCT 1591

Db 1311 NRLKQYEDFGALDVLTPSQRAWFGTIRKAATKKPKKVISRPENS-----FMAWLFDVIH 1366

QY 1592 SHYLDLFTITGVLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGERR 1651

Db 1367 SSRFETLIMFFICLNILNMIIQHYGQKPAVEQALMINLVFTGLFTLEAILRIVVLRL-H 1425

QY 1652 FFQDRWNQLDLAILLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLMKMAVGM 1711

Db 1426 YFREPNVNFDFVIVVLSILGIILEHLEYELFITSPFF---VARVFRIGRLRIFYKGAKGI 1482

QY 1712 RALLDTVMQALPOVGNLGLLFWLLFFIFAALGVLELFGDLECDETHPCGELGRHATERNFG 1771

Db 1483 RRLLFALIISLPALLNIGALLFLIMFIYAIIGMSSFGYVK-----KTGALDSVVNFETFG 1537

QY 1772 MAFLTFRVSTGDNWNGIMKDTL---RDCDQE-----STCYNTVISPIYFVSFVLTAQF 1822

Db 1538 NSMLLFLRLSTSAGWNVDVLKPLLKPPDCDKKLWCIPNGNCSTPWLAVVYFTTILFTFL 1597

QY 1823 VLVNVVIAVLMKHLEESNKEAKEAELEAELEEMKTLSPQSPHSPLGSPFLWPVGVEGPD 1882

Db 1598 TIINMYIAIILENLQAH-EQEEVGVTDDDLDMFY-----YHWERFD---- 1638

QY 1883 PDSPKPGALHPAAHARSASHF--SLEHPTMQPHPTELPGPDLLTVRKSGVSRTHSLPND 1940

Db 1639 -----PGATQYIPHS-ALSDFVDGLDHLPLRIPQPNKFACINLNIPIKQG-DRVHCFDVMQ 1691

QY 1941 YMCRH--GSTAEGPLHGRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLOPHSAP 1998

Db 1692 ALVRRVLGDIEEDGLG-----SSSV-----AYTLMKSKMEQHCHI----- 1725

QY 1999 TWGTIPKLPPPGRSPLAQRPLRRQAAIRTD 2030

Db 1726 --STFPK---RHRTKTESTTLKRTQEVRAATI 1752

RESULT 9

S29237

calcium channel protein BII-2, brain - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S29237

R;Niidome, T.; Kim, M.S.; Friedrich, T.; Mori, Y.

FEBS Lett. 308, 7-13, 1992

A;Title: Molecular cloning and characterization of a novel calcium channel from rabbit brain

A;Reference number: S29236; MUID:92354772; PMID:1379552

A;Accession: S29237

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2178 <Nil>

Db 1717 EYLTRDSSILGPHHLDHFVRVWAEYDRAACGRHITYEMYELTLM-----SPPLGLG 1768

QY 1877 VEGPDSPPSPKPGALHFAAARSASHFSLEHPTMQPHTLPGLPDLTLVRKSGVSRTHSL 1936

Db 1769 KRCPSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD-----IKIAKGGADRQQL- 1821

QY 1937 PNDSYMCRHGSTAEGPLGRGWGL-----PKAOSGSVLSVHQSOPADTSYI----- 1981

Db 1822 --DSELQKETLAIWPHLSQKMLDLLVPMPKASDLTVGKIYAAMIMDYKQSKVKKQRRQ 1879

QY 1982 LQLPKDAP--HELLOPHSAP-----TWGTIPKLP--PPGRSPLAQRPRLRQAARTDSDLV 2032

Db 1880 LEEQKNAPMFQRMFPSSLPQEIIANAKALPCLPQPPA----- 1917

QY 2033 QGLGSREDLLAEVSGSPPLARAYSFWGQSSTQAQOHSRSHSKISKHMTTPAP-----C 2086

Db 1918 -GLGGRSGCPA-----MSPLSPQIFQLTC 1940

QY 2087 PGPEPNWKGPPETRSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCYSAEQSCQRR 2146

Db 1941 MDPADDDGQF-QEQRSLVVTD-----PGSMRRSFSTIRD--KRS 1976

QY 2147 PTSWLDE-----QRRHSIAVSC-----LDGSGPHLGTDPNSLGGQPLGG 2186

Db 1977 SSSWLEEFMERSSDNTYKSRRRSYHSSIRLSAHLNSDSGHK----SDTHRSSGGERG- 2031

QY 2187 PGSRPKKLSPPSITIDPPESQG-----PRTPPSPGICLRRRAPSSDSKDPLAS 2235

Db 2032 -RSKEREHLLSADVSRCSSEERGAQADWDSPERHPSRSPSEG---RSQSPSRQGTGSLSE 2087

QY 2236 GPPDSMAASPSPKK 2249

Db 2088 SSIPSVSDTSTPRQ 2101

RESULT 10

C54972

voltage-dependent calcium channel alpha 1E - mouse

C:Species: Mus musculus (house mouse)

C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004

C:Accession: C54972

R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil J. Biol. Chem. 269, 22347-22357, 1994

A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel

A;Reference number: A54972; MUID:94350992; PMID:8071363

A;Accession: C54972

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: mRNA

A;Residues: 1-2272 <WIL>

A;Cross-references: UNIPROT:Q61290; GB:L29346; NID:g522330; PIDN:AAA59206.1; PID:g522331

A;Note: authors translated the codon AGG for residue 788 as Lys, and CCT for residue 886

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.1%; Score 1681; DB 2; Length 2272;

Best Local Similarity 23.7%; Pred. No. 2.2e-94;

Matches 607; Conservative 375; Mismatches 844; Indels 740; Gaps 82;

QY 30 GRPGGSAEKDPGSADSAEGLPYPALAPV----- 60

Db 11 GRPGSGDGDSD--QSRNRQGTVPASGPAAYKQSKAQARTMALYNPIVRQNCFTVN 67

QY 61 --FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLMFR--PCEDIACDSQRCRI 116

Db 68 RSLFIFGEDNIVRKYAKKLIDWPFPFEYMIATIANCIVLALEQHLPEDDKTPMSRR--- 124

QY 117 LQAFDDFIFAFFAVEMVVMQVALG-IFGKKCVLGDWTNRLDFFIVTAGMLEYSLDLQN-- 173

Db 125 LEKTEPYFIGFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVVLSGILATAGTHFNTH 184

QY 174 VSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIQVQVLW 233

Db 185 VDLRALRAVRVLRPLKIVSGIPSLQIVLKSIMKAMVPLLQIGLLFFAILMFAIIGLEFY 244

QY 234 AGLLRNRCFLPENESLPLSVDLERYYYQTENEDESPFICSQPRENGMRCRSVPTLRGDGG 293

Db 245 SGKLHRCACFMNNGIL-----EGFDP-----PHPCGVQGC----- 274

QY 294 GGPPCGLDYEAYNSSNTTCVNWNQYYTNCAGEHNPFKGAINFNIGYAWIAIFQVITL 353

Db 275 ---PAG--YE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITM 309

QY 354 EGWVDIMYFVMDA-HSFYNFYIFILLIIVGSEFFMINCLVVIATQFSETKQRESQLMREQ 412

Db 310 EGWTTVLYNTDAGATWNWLYFIPLIIGSFFVLNLVGLSGEFAKERERV-----EN 364

QY 413 RVRFLSNASTLASFSEPGSCYBEELKVLVYLKAAARRLAQVSRAGVRVGLLSSPAPLG 472

Db 365 RRAFMK-----LRRQQOI----- 377

QY 473 GQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLNGTTLRAPRASPEIQDRDANGSRRL 532

Db 378 -----ERELNGYRAW 387

QY 533 MLPPPSTPALSAPPGGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVSGKVYPT 592

Db 388 I----- 388

QY 593 VHTSPPPETLKEKALVEAASSGPPTLTSLNIPPGPVSSMHKLLLETQSTGACQSSCKISS 652

Db 389 -----DKAEVMLAEENKNSGTSALEVLRRTATIKRSRTTEAMTRDSSDEHCVIDISSVT 441

QY 653 PCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRR 712

Db 442 PLARASIKSTKVDGASY-----FRHKE----- 463

QY 713 QRSGLPDAEPSSVLAFWRLLICTFRKIVDSKYFGRGIMAILVNTLSMGIEVHEQPELT 772

Db 464 -----RLLRISIRHMVKSQVFIWLVSVVALNTACTVAIVHNNQPQWL 506

QY 773 NALETSNIIVFTSLFALEMLLKLIVYGPFGYIKNPYNIPODGVIVVISVWEIVGQ-----QG 827

Db 507 HLLYYAEFLFLGLFLLLEMSLKMVGMPRLYFHSSFCDFGVTVGSIFFVWAIFFRPGTS 566

QY 828 GGLSVLRTFRLMRVLKVRFLPALQRLVLMKTMNDNVATFCMLLMLFIFIFSILGMHLF 887

Db 567 FGISVLRALRLLRIFKITKYWASLRNLVSLMSSMKSIISLLFLFLFVIVFALLGMQLF 626

QY 888 GCKFASERDGTLPDRKNFDSLWAIIVTVFQILTQEDWNKVLYNGM-----ASTSSWAAL 942

Db 627 GGRF-NFNDG---TPSANPDTFPAAIMTVFQILTGEDWNEVMYNGIRSQGGVSSGMWSAI 682

QY 943 YFIALMTFGNYVLNLLVAILVEGF-QAAEISK----REDASGQLSCTQLPVDSQGGDAN 997

Db 683 YFIVTLFGNYTLLNVLFLAIVDNLANAQELTKDEQEEEAFAFNQKHALQAKEV----- 736

QY 998 KSESEPDFFSPLDGDGRKKCLAL-----VSLGE 1027

Db 737 SPMSAPNM--PSIERDRRRHHMSMWEPSSHLRERRRRHHMSVWEQTSQLRRHMQMSS 794

QY 1028 HPELRKSLLPPLIHTAATPMS--LPKSTSTGL-----GEALGPA-----SRRTSSS 1072

Db 795 QEALNKEEAPPMPNPLNPLNPLNAHPSLYRRPRPIEGLALGLGLEKCEERISRG 854

QY 1073 GSAE-----PGAHEMKSPPS-ARSSPHSPWSAASSWTS----- 1105

Db 855 GSLKGDIGLTSALDNQRSPLSLGKREP--PWLPRSCHGNCDPQQEAGGETVTVTFEDR 912

QY 1106 ---RRSSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEESSEERASAPAGSDHRHRG 1162

Db 913 ARHRQSQRSSRRHVRVTEGKDSASASRS-RSASQERSLDEGVSVGEKEHEPHSHRSKE 971

QY 1163 SLEREAKSSFDL--PDTLQVP---GL-----HRTASGRGSASEHQDCNGK 1202

Db 972 PTIHEERTQDLRRTNSLMVPRGSLVGCALDEAETPLVQPQPELEVGDAAALTEQEAEGS 1031

QY 1203 SAS-----GRLARALRPD-----DPPLD----- 1220

Db 1032 SEQALLGDVQLDVGRGISQSEPDLSMTANMDKATTESTSVTVAIPDVPDPLVDSTVVNIS 1091
QY 1221 -----GDDADDEGNLSKGER-----VRAWIRARLPACYLERDSWSAYIFPPQSR 1264
Db 1092 NKTDGEASPLKEAETKEEEEEVEKKKKQKKEKRETGKAMVPHS-----SMFIFSTTNP 1144
QY 1265 FRLLCHRIITHKMFHVVLVILFNCITIAMERP KIDPHSAERIFLTLSNYIFTAVFLAE 1324
Db 1145 IRRACHYIVNLRYPFEMCILLVIAASSIALAEDPVLNTERNKV-LRYFDYVFTGVFTPE 1203
QY 1325 MTVKVVALGWCFGQAVLRSSWNVL DGLLVLSVIDI-LVSMVSDSGTKILGMLRLVRL 1383
Db 1204 MVIKMIDQGLILQDGSYFRDLWNILDFVVVVGALVAFALANALGNTKGRDIKTIKSLRVL 1263
QY 1384 RTLRPLRVISRAOGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVC-- 1441
Db 1264 RVLRLPKTIKRLPKLKA VDFCVVTS LKNVFNILIVYKLFMFIFAVIAQLFKGKFFYCTD 1323
QY 1442 QGEDTRN-----ITNKSDCAEASYSR-WVRHKYNFDNLGQALMSLVFASKDGVVDIMYD 1494
Db 1324 SSKDTEKECIGNYVDHEKNRMEVKGREWKREHFHYDNIWALLTLFTVSTGEGWPQVLQH 1383
QY 1495 GLDAVGVDQOPIMNHNPMWMLLYFISFLLI VAFVLMFVGWVVENFHKCRQHQEEEEARR 1554
Db 1384 SVDVTEEDRGPSRSNRMEMSIFVYVVFVFPFFFNIFVALIITF-----QEQGDKM 1436
QY 1555 REEKLRLRLEKKRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTITGVIGL 1605
Db 1437 MEE---CSLEKNERACIDFAISAKPLTRYMPQNRHTFYRVWHFVWSPSFYEITAMIAL 1493
QY 1606 NVVTWAMEHYQOQOILDEALKICNYIFTVIFVLESVKLVAFGRFFQDRWNQDLAIV 1665
Db 1494 NTVVLMWKYITAPCTYELALKYLNIAFTMVFSLECVLKVAFGFLNYFRDWTNIFDITV 1553
QY 1666 LLSIMGITLEEIEVNASLPINPTIRIMRVLRIARVLKLLKMAVGMRALLDVTMQALPOV 1725
Db 1554 IGSITEIILTDSKLVNTSGFNMSFLKLFR--ARLKLRLQGYTIRILLTWFVQSFKAL 1610
QY 1726 GNLGLLFMLFFIFAALGVELFGDLECD-ETHPCGELGRHATFRNFGMAFLTFRVSTGD 1784
Db 1611 PYVCLLIAMFFIYAIIGMQVFGNIKLDDESH---INRHNFRSFFGSLMLFRSATGE 1666
QY 1785 NWNGIMKDTL--RDCDQESTC-----YNTVISPIYFVSFVLTAQFVLNVNVI AVL M 1833
Db 1667 AWQEIMLSCLGEKCEPDTTAPSGQNESERCGTDLAYVYFVSFIFFCSFLMLNLFVAVIM 1726
QY 1834 KHLEESNKEAK-----EEAELEALE-----LEMKTLSQPSPHSPGLSPFL 1873
Db 1727 DNFEYLTRDSSILGPHHLDEFVRVWAEYDRAACGRIHYTEMYEMTLM-----SPPL 1778
QY 1874 WPGVEGPDSPDPKPGALHPAAHARSASHFSLEHPTMQPHPTLPGLD LTVRKSGVSRK 1933
Db 1779 GLGKRCPSKVAYKRLVLNMMPVAEDMTVHFT--STLMALIR TALD-----IKIAGGADRQ 1832
QY 1934 HSLPNDSYMCRHGSTAEGPLGHRGWGL-----PKAQSGSVLSVHSQPADTSYI----- 1981
Db 1833 QL---DSELQKETLAIWPHLSOKMLDLLVPMFKASDLTVGKIYAAAMIMDYKQSKVKKQ 1889
QY 1982 ---LQLPKDAP--HLLQPHSAP-----TWGTIPKLPP-----PGRSPLAQRP 2019
Db 1890 RQOLEEQKNAPMFORMEPSSLPQEI IANAKALPYLQDPVSGLSGRSGYPSMSPLSPQEI 1949
QY 2020 -----RRQAAIRTDSDLVQGLGSR-----EDLLAEVSGPSPPLA 2053
Db 1950 FQIACWDPADGQFQEQQSLVVTDPSSMRRSFSTIRDKRSNSSLWLEEFSMERSSENTYKS 2009
QY 2054 RAYSWGQSSTQAQQH-----SRSHSKISKHMTTP----- 2083
Db 2010 RRRSY--HSSLRLSAHRLNSDSGHKSDTHRSGGREGRSKERKHLSPDVSRCNSEERGT 2067
QY 2084 -APCGPEPNWGKPPETRS-----SLE-----LDTELSWISGDLPPGGQEEP 2126

Db 2068 QADWESPERRQSRSPSEGRSQTPNRQGTGSLSESSIPSISDTSTPRRRRQLPP-----VP 2123
QY 2127 PSPRDLKKCYSEVAQSCQRRPTSWLDEQRRHSIAVCLDSGSQLHGTDPNSNLGGQPLGG 2186
Db 2124 PKPRPLLSYSSL-----MRHTGGISPPPDGSE-----GGSPLAS 2157
QY 2187 PGRSRPKK-LSPPSITIDPPESQGRPTP---PSPGICLRRRAPSD 2228
Db 2158 QALESNSACLTESSNSLHPQOQHPSQHYISEPYLALHEDSHASD 2203
RESULT 11
A54972
voltage-dependent calcium channel alpha 1E-3 - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accession: A54972
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mi
J. Biol. Chem. 269, 22347-22357, 1994
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A;Reference number: A54972; MUID:94350992; PMID:8071363
A;Accession: A54972
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2270 <WIL>
A;Cross-references: UNIPROT:Q15878; GB:L29385; NID:g495869; PIDN:AAA59205.1; PID:g49587
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
Query Match 14.0%; Score 1665; DB 2; Length 2270;
Best Local Similarity 24.2%; Pred. No. 2.1e-93;
Matches 620; Conservative 386; Mismatches 814; Indels 744; Gaps 90;
QY 31 RPPGSAEKDPGSADSEAEGLPYPALA-----PV----- 59
Db 11 RPPSGDSD---QSRNRQGTVPASGQAAAYKQTKAQRARTMALYNPIPVQRNCFTVNR 67
QY 60 VFFYLSQDSRPSRWCLRTVCNPFERISMLVILLNCVTLGMFR--PCEDIACDQRCL 117
Db 68 SLFIFGEDNIVRKYAKKLIDWPFFEYMI LATI IANCIVLALAEQHLPEDDKTPMSRR---L 124
QY 118 QAFDDFTAFPAFAVEMVVMVALG-IFGKKCYLGDTWNRLDFFVIAGMLEYSLDLQN--V 174
Db 125 EKTEPYFICFCFEAGIKIVALGFIFHKGSYLRNGWNVMDFIVLSGILATAGTHFNTHV 184
QY 175 SFSAVRTVRVLRPLRAINRVPNMRILVTLLD TPLMGNVLLLCFFVFFIFGIVGVQLWA 234
Db 185 DLRTLRAVRVLRPLKLVSGIPSLQIVLSIMKAMVPLQLGILLFFAILMFAIIGLEFYS 244
QY 235 GLLNRNCFLENFSLPLSVDLERYYTENEDESPFICSPQRENMRSCRVP TLRGDGGG 294
Db 245 GKLHRACFMNNSGIL-----EGFDP-----PHECGVQGC----- 273
QY 295 GPPCGLDYEAYNSSNTTCVNMNQYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLE 354
Db 274 --PAG--YE-----CKDW-----IGPNDGITQFDNILFAVLT V FQCITME 309
QY 355 GWVDIMYFVMDA-HSFYNFYIFILLIIVGSFFEMINLCVVIATQFSETKORES-----Q 407
Db 310 GWTTVLYNTNDALGATWNWLYFIPLIIGSFFVLNLVGLVLSGFEFAKERERVENRRAFMK 369
QY 408 LMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYLIRKAARLQAQVSRAAGVRVGLLS 467
Db 370 LRRQQQIE-----RELNGYRAWIDKAEVVMLEAKENKNAG----- 403
QY 468 PAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLNGT LRAPRASPEIQDRDAN 527
Db 404 -----TSALEVLRRATI-----KRSRTAMTRDS- 427
QY 528 GSRRLMLPPPSTPALSGAPPGAESVHSFYHADCHLEPVRQAPPPRSPSEASGRVTGSG 587
Db 428 -----SDEH----- 431
QY 588 KVYPTVHTSPPETLKEKALVEAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSS 647

Db 432 -----CVDI 435

QY 648 CKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRD 707

Db 436 SSVGTPLARASIKSAKVDGSY-----FRKE--- 462

QY 708 PHRRQRSGLGPDAPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQ 767

Db 463 -----RLRISRHMVKSQVFYWIVLSLVALNTACVAIVHNQ 500

QY 768 PEELTNALEISNIVFTSLFALEMLLKLVYGPFGYIKPNYNIFDGVIVWISVWEIVGQ-- 825

Db 501 POWLTHLLYYAEELFLGLFLEMSLKMVGMPRLYFHSSFCNCFDGVTVGSI FEVVNAIF 560

QY 826 ---QGGGLSVLRTFRMLRVLKLVRFLPALQRLVWLKMTMDNVATFCMLLMLFIFISIL 882

Db 561 RPGTSFGISVLRALRLRIFKITKYWASLRNLVWSLSSMKSTISLLFLFLFIVVFALL 620

QY 883 GMHLFGCKFASERDGDTLPDCKNFEDSLIWAIVTVFQILTQEDWNKVLYNGM-----ASTS 937

Db 621 GMQLFGGRF-NFNDG---TPSANFDTPPAIMTVFQILTGEDWNEVMYNGIRSQGVSSG 676

QY 938 SWAALYFIALMTFGNYVLNLLVAILVEGF-QAEEISK----REDASQOLSCIQLPVDSQ 992

Db 677 MWSAIYFIVLTILFGNYTLLNVFLAIVDNLANAQELTKDEQEEEAFAFNKHALQKAKEV- 735

QY 993 GGDANKSESEPDFFSPSLDGDGRKKCLAL-----VSLGEH--PELRKS 1034

Db 736 -----SPMSAPNM--PSIERDRRRRHMSMWEPRSSHLRERRRRHHMSVWEQRTSQLRKH 788

QY 1035 L-----LPPLIHTAATPM-----SLPKSTSTGLGEALGPA-----SR 1067

Db 789 MQMSSQBALNREBAPTMNPPLNPLNPLNPLNAHPSLYRRPRAIEGLALGLALEKFEE 848

QY 1068 RTSSGS-----AEPGAHEMKSPPSARSSPHSPWSA----- 1099

Db 849 RISRGGSLKGDGDRSSALDNQRTPLSLGQREPPWLARPCHGNCDPTQOEAGSGEAVVTF 908

QY 1100 ---ASSWTSRRSRNSLGR-----APSLKRRSPSGHRRSL---LSGEGQESQD----- 1141

Db 909 EDRARHQSQRRSRHRRVRTECKESSASRSRSASQERSLDEAMPTGEKDHELRGNHGA 968

QY 1142 EESSEERASPAGSDHRRHRSGLERAKSSF-----DLPDTLQVPGLHRTASGRGSAS 1194

Db 969 KEPTIQEERA---QDLRRTNSLMVSRGSLAGGLDEADTPLVLPHPELE---VGKHVV 1021

QY 1195 EHQCNGKSAS-----GRLARALRPD-----DPPL 1219

Db 1022 TEQEPGSSSEQALLGNVQDMGRVISQSEPDLSGITANTDKATTESTSVTVAI PDVDPLV 1081

QY 1220 DG-----DDADDEGNLSKGERVRAWIRARLPACYLERDSWSA 1256

Db 1082 DSTVVHISNKTDGEASPLKEABEIREDEEEVEKKQKKEK-RETGKAMVPHS-----SM 1133

QY 1257 YIFPPQSRFRLLCHRIITHKMFHDHVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYI 1316

Db 1134 FIFSTNPIRRACHYI VNLRYFEMCILLVIAASSIALAAEDPVLTSERNKV-LRYFDYV 1192

QY 1317 FTAVFLAEMTVKVALGWCFGEQAYLRSSMNVL DGLLVLSVIDI-LVSMVSDSGTKILG 1375

Db 1193 FTGVFTFEMVIKIDQGLILQDGSYFRDLWNILDFVVVVGALVAFALANALGNTKGRDIK 1252

QY 1376 MLRVLLRLTLRPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFIGILGVQLFK 1435

Db 1253 TIKSLRVLRVLRPLKTIKRLPKLKA VDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFK 1312

QY 1436 GKFFVC--QGEDTRN-----ITNKSDCAEASYSR-WVRHKYNFDNLQALMSLFLVASKD 1486

Db 1313 GKFFYCTDSSKDTKEKICIGNYVDHEKNKMEVKGREWKREHFHYDNIWALLTLFTVSTGE 1372

QY 1487 GWVDIMYDGLDAVGVDQQPIMNHNPMWLLYFISFLIVAFFVLNMFVGVVVENFHKCRQH 1546

Db 1373 GWPQVLQHSVDVTEEDRGPSRSNRMEMSIFVVVYFVVFVFFVFVFIIVALIITF----- 1426

QY 1547 QEEEEARRREEKRLRLEKKRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDL 1597

Db 1427 -QEQDKMEE--CSLEKNERACIDFAISAKPLTRYMPQNRHTFOYRVWHFVVSFSFEY 1482

QY 1598 FITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVEKLVAFGFRFFQDRW 1657

Db 1483 TIMAMIALNTVVLMMKY SAPCTYELALKVNLINIAFTMVFSLECVLKVIAFGFLNYFRDTW 1542

QY 1658 NQLDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDT 1717

Db 1543 NIFDFITVIGSITEIILTDSKLVNTSGFNMSFLKLFR---ARLIKLRQGYTIRILLWT 1599

QY 1718 VMQALPOVGNLGLLFMLLFFIFAALGVELFGDLECD-ETHPCBGLGRHATERNFGMAFLT 1776

Db 1600 FVQSFKALPYVCLLIAMLFFIYAIIGMQVFGNIKLEDESH---INRHNNFRSFFGSLML 1655

QY 1777 LFRVSTGDNWNGIMKDTL--RDCQESTC-----YNTVISPIYFVSFVLTAQFVLV 1825

Db 1656 LFRSATGEAWQEI MSLC LGEKCEPDTTAPSGQENENERCGTDLAYVYFVSFIFFCSFLML 1715

QY 1826 NVVIAVLKMLEESNKEAK-----EEAELEAELE-----LEMKTLSPQH 1865

Db 1716 NLFVAVIMDNFEYLTRDSSILGPHHLDEFVRVWAEYDRAACGRIHYTEMYEMLTLM--- 1771

QY 1866 SPLGSPFLWPGEVGPDS PDKPGALHPAAHARSASHFSLEHPTMQPHPTELPGPDLITV 1925

Db 1772 ----SPPLGLGKRCPSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD----IKI 1821

QY 1926 RKS GVSRTSLPND SYMCRHGSTAEGPLHGRWG L-----PKAQSGSVLSVHSQPADTSYI 1981

Db 1822 AKGGADRQQL---DSELQKETLAIWPHLSOKMLDLLVMPKASDLTVGKIYAAMIMDY 1878

QY 1982 -----LQLPKDAP--HLLQPHSAP-----TWGTIPKLPP-----PGR 2011

Db 1879 KQSKVKKQKQOQLEEQKNAPMFQRMESPSSLPOEIIANAKALPYLQQDPVSGLSGRSGYPSM 1938

QY 2012 SPLAQRP LRRQA AIRTDSL DVQGLSREDLLAEVSGPSPP LARAYS----- 2057

Db 1939 SPLSPQDIFQLACM--DPADDGQFQERQSLV--VTDPS-SMRRSFSTIRKRSNSSLWLEE 1993

QY 2058 FWQSSTQAQQHSRSHSKISHMTPPAPCPGPEPNWGKPPETRSSLELDT-ELSWISG- 2115

Db 1994 FMSERSSENTYKSRRRS-----YHSSLRLSAHRLNSDSGH 2028

QY 2116 --DLLPPGGQEEPPSPR-----DLKKCVSVEAQSCORRPTSWLDEQRRHSIAVSC LDS 2166

Db 2029 KSDTHPSGGRERRRSKERKHLSPDVSRCNSEE---RGTDADWESERRQRSRSPS--EG 2082

QY 2167 GSQPHLGTDP SNLGGQPLGGPSRPKKLSPPSITIDPPES--QGPRTPPSPGICLR--- 2221

Db 2083 RSQ-----TPNR-----QGTGSLSESSIPSVSDTSTPRRSRRQLPPVPPKPRPLLSYSS 2131

QY 2222 --RRAPS-----SDSKDPLASGPPD SMAA-----SPSPKK 2249

Db 2132 LIRHAGSISPPADGSEEGSPLTSQALESNNAWLTESTSNSPHPQQ 2175

RESULT 12

T43262

calcium channel alpha-1 chain, L-type - Stylophora pistillata

C;Species: Stylophora pistillata

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T43262

R;Zoccola, D.; Tambutte, E.; Senegas-Balas, F.; Michiels, J.F.; Failla, J.P.; Jaubert, J.

Gene 227, 157-167, 1999

A;Title: Cloning of a calcium channel alpha1 subunit from the reef-building coral, Stylophora pistillata

A;Reference number: Z22375; MUID:99148007; PMID:10023047

A;Accession: T43262

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1891 <ZOC>

A;Cross-references: UNIPROT:O97017; EMBL:U64465; NID:G4204977; PID:G4204978; PIDN:AAD114

C;Genetics:

A;Gene: CACHL

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.0%; Score 1664.5; DB 2; Length 1891;
Best Local Similarity 25.2%; Pred. No. 1.8e-93;
Matches 486; Conservative 316; Mismatches 510; Indels 617; Gaps 55;

QY	11	BESGQPRSMRLND-----LSGAGRPGPGSAEKDPSADSEAEGLPYP	54
Db	2	EQNGYPRANFTQGSKIFWPNGTDLMTQTRARLNGHGKYAKSVAAKROKKSNTVR--PKR	59
QY	55	ALAPVVFYLSQDSRPRSWCLRTVCNPW--FERISMLVILLNCVTGLGMRPCEDIACDSQ	112
Db	60	AL-----LCLSLGNPIRSAAINLV--EWKPFVDMILITIFANCAALAAFEPLPE--KDSS	110
QY	113	RCRILQAFDDFIF-AFFAVEMVVMVALG-IFGKKCYLGDWNRLLDFFIVLAG-----MLE	166
Db	111	BINDNLEVAEYVFLAVFTMEAVLKIIAYGFLFHGAYLRNGWNILDFVIVVVGATILVK	170
QY	167	YSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLCFFVFFIFG	226
Db	171	ATLSSGSFDVKALRAFRVLRPLRLVSGVPSLQVVLNSIIKALIPLFHIALLVFVVIYA	230
QY	227	IVGVQLWAGLLRNRCFLPENFSLPLSVLDLRYRYQTENEDESPFICSQPRENMRSCRVP	286
Db	231	IIGVELFMGRLHKTGY--DNVT-----GAESF-----EHPHPCS-----	262
QY	287	TLRGDGGGPPCGLDYEAVNSSNTTCVWNQYYTNCAGEHNPFKGAINFNIGYAWIA	346
Db	263	-----SGSSGFQC-----DKAAGV-----CEGWKGNHGIITNFDNIGLACMT	301
QY	347	IFQVITLEGWVDIMYFVMDA-HSFYNFIYFILLIIVGSFFMINCLVVIATQFSETKQR-	404
Db	302	VFQCITLEGWTDVLYWINDAVGNSWPVYFVTLIWSGFFVLNLVLGVLGSEFAKEKARR	361
QY	405	-----ESQLMREQR-----VRFLSNASTLASFSEPCSCYBELLKYLVIILRKAARRL	451
Db	362	QKSGEFQKREKQVEDAYNGYLDWTITQAEIDEGDSESGDES-----KASKKT	411
QY	452	AQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVHLLVHHHHHHHHVHLNGT	511
Db	412	S--SRQS-----RTEDIEMIDRNERQDSI-----SQHDTHEY-----	441
QY	512	LRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGAESVHSFYHADCHLEPVCQAP	571
Db	442	-----	441
QY	572	PPRSPSEASGRTVSGKVYPTVHTSPPPETLKEKALVEAASSGPPTLTSLNIPPGPYSS	631
Db	442	-----	441
QY	632	MHKLEQTQSTGACQSSCKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDE	691
Db	442	-----GWCHNEKKV-----	450
QY	692	AVYEFTQDAQHSDLRDPHSRRQRSRQSLGPDABPSSVLAFWRLICDTRKIVDSKYFGRGIMI	751
Db	451	-----LKKWHHRRTQTEL-----RKAVKTOAFYWIIVIV	477
QY	752	AIVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVYGPFGYIKNPYNIFD	811
Db	478	VVFLNSLTALAHYDQPDWLTCKFLDIANKLFLGIFTIEMIVKMYCLGFHGYFASLFRNF	537
QY	812	GVIVV-----ISVWEIVGQGGGLSVLRTFRIMRVLKLVRFLPALQRLVLMKTMNVA	866
Db	538	CLVVISSLLELAITEALKQPPIGISVLRCIRLIRIFKVTRYWSSLSNLVASLLNSMRSIA	597
QY	867	TFCMLIMLFIFIFSLGMLFGCKFASERDGDTPDRKNFDSLLWAIWTVFQILTQEDWN	926
Db	598	GLLLLLSLFMLICSLGMLGQIFGGKF--NTDDDEIP-RSNFDSFWRALITVFQILTGEDWN	654

RESULT 13

B54972

voltage-dependent calcium channel alpha 1E-1 - human

C;Species: Homo sapiens (man)

QY	927	KVLYNGMAS-----TSSWAALYFIALMTFGNYVLFNLVAILVEGF-----QAEE	971
Db	655	AVMYDGIRAWGIGEGGSAIAILYFIFLVVGNVILLNVFLAIAVDNLADAENLTEMEEE	714
QY	972	ISKREDASQSLSCIQL--PVDSQGDANKSESEPDFFSPSLDGDGRKKCLALVSLGEHP	1029
Db	715	KKKKKEKAREKEALKMGKSVDSQG-----RIDQDG-----	744
QY	1030	ELRKSLLPPLIIHTAA--TPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAAHEMKSPP	1087
Db	745	---AIVPN--HSSASRSNVTLDKST-----QELHSTGT-----	772
QY	1088	SARSSPHSPWSAASWTSSRRNSLGRAPSLKRRSPSGERRSLLSCEG---QESQDEEE	1144
Db	773	-----LNGNGVARTASHDDVE	788
QY	1145	SSEERASPAGSDHRHGRSLEREAKSSFDPDLPTLQVPLHRTASGRGSAHEHQCNGKSA	1204
Db	789	AQSTDISEIVGS-----KSAVSNNNESASASS	815
QY	1205	SCRALARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSR	1264
Db	816	SDIDRAPMPPEAL-----FIFSPNTI	838
QY	1265	FRLLCHRIITHKMFHVVVLIIFLNCITTIAMERPKIDPHSAERIFLTLNSYIFTAVFLAE	1324
Db	839	FRVVCYKIATNTYFVNFILCLIIIVSSILLAAEDP-LNASAKRNQVNLNFDYFTSVFTFE	897
QY	1325	MTVKVVALGWCFCGEQAYLRSSWNVLGLLVLISVIDILVSMVSDSGTKILGMLRVLRLLR	1384
Db	898	ILVKFISYGLILHKGSFCRSFAFNLLDLLVVSVSVISLSL-----TSQFSVVRIILRVLR	951
QY	1385	TLRPLRVISRAOGLKLVVETIMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGE	1444
Db	952	VLRLRAINRAKGLKHVVQSVFVAVKTIIGNIKLVMLFQFLFAVIGVQLFKGTFESCND	1011
QY	1445	DTRNITNKSDCAEASY-----RWVRHKVNFNDLQALMSFLVASKDGM	1488
Db	1012	---KILTABEC-QGNYIDFKGPLSNPVVKERWRHRHDNFEDNVGNAMLTLFTVMTFEGW	1067
QY	1489	VDIMYDGLDAGVDQOPIMHNHPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHOE	1548
Db	1068	PGILENSIDSTEVDKGPNNRNPWVAIYIYIIIIIAFEMVNIIVGVFVITF-----	1119
QY	1549	EEEARREKRLRRLEKKRKA-----QCKPY--YSDYSRFRLLVHHLCTSHYLDLITG	1601
Db	1120	--QSEGREEFKGCELDKNQRCQCTEFALKAKPLKRYIPENLQFHIWVVTSSQAFVYLIFA	1177
QY	1602	VIGLNVVTNAMEHYQQPQILDEALKICNYIFTVIFVLESVPKLVAFGFRFFQDRWNQLD	1661
Db	1178	FIVCNTVVLMMQYQEPKLYTRVLDGFNIGTAVFLECEILKLIAPKPKNYFTDRWNLF	1237
QY	1662	LAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMRALDVTM--	1719
Db	1238	FIIVVGSIIIDITMNEVSSEQMFAFG-----FFRLFRALRLVKLLNQSGIKTLLWTFIKS	1292
QY	1720	-QALPQVGNLGLLFWLLFFIFAALGVLELFGDLECDETHPECEGLGRHATFRNFGMAFLTIF	1778
Db	1293	FOALPYV---ALLIVMMFFIYAVIGMQMFGRIANSND---TAINRNNNFQTFPPQSLMVL	1346
QY	1779	RVSTGDNWNGIM-KDTLRD---CDQE-----STCYNTVISPIYFVSFVLTAQFVLNVV	1828
Db	1347	RSATGENWQQIMLACTHRDDVKCDQNADPPQPSGLCGSDFAFYFVFSYFISCSFLIINLF	1406
QY	1829	IAVLMKHLE	1837
Db	1407	VAVIMDNFD	1415

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
C;Accession: B54972
R;Williams, M.E.; Marubio, L.M.; Deal, C.R.; Hans, M.; Brust, P.F.; Philipson, L.H.; Mil
J. Biol. Chem. 269, 22347-22357, 1994
A;Title: Structure and functional characterization of neuronal alpha-1E calcium channel
A;Reference number: A54972; MUID:94350992; PMID:8071363
A;Accession: B54972
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-2251 <WIL>
A;Cross-references: GB:L29384; NID:G495867; PIDN:AAA59204.1; PID:G495868
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 14.0%; Score 1663.5; DB 2; Length 2251;
Best Local Similarity 24.2%; Pred. No. 2.6e-93;
Matches 617; Conservative 383; Mismatches 815; Indels 735; Gaps 89;

QY 31 RPGPSAEKDPGSADSEAEGLPYPALA-----PV----- 59
Db 11 RPGSDDGSD---QSRNRQGTVPASGQAAAYKQTKAQRARTMALYNPIPVQRNCFTVNR 67

QY 60 VFFYLSQDSRPRSCLRTVCNPFERISMLVILLNCVTLMGER--PCEDIACDSQRCRIL 117
Db 68 SLFIFGEDNIVRKYAKKLIDWPPPEYMTILATIANCIVLALEQHLPEDDKTPMSRR---L 124

QY 118 QAFDDFIFAFFAEMVMVKVALG-IPGKKCYLGDTWNRLDFFVIAGMLEYSLDLQN--V 174
Db 125 EKTEPYFIFGFCFEAGIKIVALGFIFHKGYLNRGNWVMDPIVVLSGILATAGTHFNTHV 184

QY 175 SFSAVRTVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWA 234
Db 185 DLRTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLFFAILMFAIIGLEFYS 244

QY 235 GLLRNRCPLENFSLPLSVDLERYQOTENEDESPFICSPRENGMRSCRSPVTLRGDGGG 294
Db 245 GKLHRACFMNNSGIL-----EGFDP-----PHPCGVQGC----- 273

QY 295 GPCCGLDYEAYNSSNTTCVWNWQYYTNCSSAGEHNPFKGAINEDNIGYAWIAIFQVITLE 354
Db 274 --PAG--YE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITME 309

QY 355 GWVDIMYFVMDA-HSFYNFIYFILLIIVGSFFMINCLVVIATQFSETKQRES-----Q 407
Db 310 GWTTVLYNTNDALGATWNWLYFIPLIIGSFFVLNLVGLVSGEFAKERERVENRRAFMK 369

QY 408 LMREQVRVFLSNASTLASFSEPGSCYEELKYLVLIRKAARRLAQVRAAGVRVGLLSS 467
Db 370 LRRQQQIE-----RELNGYRAWIDKAEVMLAEENKNAG----- 403

QY 468 PAPLGGQETQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLNGTTLRAPASPEIQDRDAN 527
Db 404 -----TSALEVLRRTATI-----KRSRTEAMTRDS- 427

QY 528 GSRRLMLPPSTPALSGAPPGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSG 587
Db 428 -----SDEH----- 431

QY 588 KVPYTVHTSPPPETLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKILETQSTGACQSS 647
Db 432 -----CVDI 435

QY 648 CKISSPCLKADSGACGPDSCPYCARAGAGEVELADREMPDSDSEAVYFTQDAQHSLRD 707
Db 436 SSVGTPLARASIKSAKVDGVSY-----FRHKE--- 462

QY 708 PHRRQRSGLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQ 767
Db 463 -----RLLRISIRHMVKSQVFYWIVLSLVALNTACVAIVHQN 500

QY 768 PEELTNALEISNIVFTSLFALEMLLVGPPGYIKNPYNIFDGVIVVSWVEIVGQ-- 825
Db 501 PQWLTHLLYYAEFLGLFLLEMSLKMVGMPRLYFHSSFNCFDGVTVGSIFEVVWAIF 560

QY 826 ---QGGGLSVLRTFLMRVLKLVRFPLPALORQLVVLVLMKTMNDVNATFCMLLMFLFIFISIL 882
Db 561 RPTSGISVLRALRLRIFIKITKYWASLRLNVVSLMSSMKSIISLLFLFLFIVV FALL 620

QY 883 GMHLFGCKFASERDGTLPDRKNFDSLWAIWTVVFQILTQEDWNKVLYNGM-----ASTS 937
Db 621 GMQLFGGRF-NFNDG---TPSANFDTFPAAIMTVFQILTGEDWNWVWYNGIRSQGGVSSG 676

QY 938 SWAALYFIALMTFNGYVLFNLLVAILVEGF-QAEEISK---REDASQOLSCIQLPVDSQ 992
Db 677 MWSAIYFIVLTLPFGNYTLNVLFLAIAVDNLANAQELTKDEQEEEAFAFNQKHALQAKEV- 735

QY 993 GGDANKSESEPDPFSPSLDGDGDRKKCLAL-----VSLGEHPERK----- 1033
Db 736 -----SPMSAPNM--PSIERERRRRHHMSVWEQRTSQLRKEMQSSQEALNREEAPT MNP 788

QY 1034 -----SLLPPLIIHTAATPMSLPKSTSTGLGEALGPA-----SRTSSSGS-----AE 1076
Db 789 LNPLNPLSSLNPLNAHP-----SLYRRPRAIEGLALGLALEKFEERISRGGSLKGDGDG 843

QY 1077 PGAAHEMKSPPSARSPPHSPWSA-----ASSWTSRRSSR 1110
Db 844 RSSALDNORTPLSLGQREPPWLRPCHGNCDPTQOEAGGAEAVVTFEDRARHRQSRSR 903

QY 1111 NSLGR-----APSLKRRSPSGERRSL---LSGEGEQSD-----EESSESEERASPA G 1155
Db 904 HRRVRTEGESSSASRSRSASQBSLDEAMPTEGEKDHELGNHGAKEPTIOEERA---- 959

QY 1156 SDHRHRGSLEREAKSSF-----DLPDTLQVPLHRTASGRGSASEHQDCNGKSAS--- 1205
Db 960 QDLRRTNLSLMVSRGSLAGGLDEADTPLVLPHPELE---VGKHVVLTQEPEGSSEQALL 1016

QY 1206 -----GRLARALRPD-----DPPLDG----- 1221
Db 1017 GNVQLDMGRVISQSEPDLSCTANTDKATTESTSVTVAIPDVPDPLVDSTVVHISNKTDGE 1076

QY 1222 -----DDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCH 1270
Db 1077 ASPLKEAEREDEEEVEKKQKKEK-RETGKAMVPHS-----SMFISTTNPIRRACH 1128

QY 1271 RIITHKMFHDHVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVELAEMTVKVW 1330
Db 1129 YIVNLRIFYEMCILLVIAASSIALAAEDPVLNTSERNKV-LRYFDYVFTGVFTFEMVIKMI 1187

QY 1331 ALGWCFFGEQAYLRSSWNVLDGLLVLSVIDI-LVSMVSDSGTKILGMLRVLRLTLRPL 1389
Db 1188 DQGLILQDGSYFRDLWNILDVWVVGALVAFALANALGNTKGRDIKTKSLRVLRLRPL 1247

QY 1390 RVISRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFFVC--QGEDTR 1447
Db 1248 KTIKRLPKLKAVFDCVVTSLKNVFNILIVKLFMFIFAVIAVQLFKGKFFYCTDSSKOTE 1307

QY 1448 N-----ITNKSDCAEASYR-WVRHKYNFDNLGQALMSFLVLASKDGWVDIMYDGLDAVG 1500
Db 1308 KECIGNYVDHEKNKMEVKGREWKRRHEFHVDNIIWALLTLFTVSTGEGWFPQVLQHSVDVTE 1367

QY 1501 VDQQPIMHNHPWMLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRQHQEEEEARRREEKRL 1560
Db 1368 EDRGPSRSNRMEMSIFYVVYFVVPFFFFVIFVALIITF-----QEQQDKMEE--- 1417

QY 1561 RRLEKKRRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTIGVIGNVVTMA 1611
Db 1418 CSLEKNERACIDFAISAKPLTRYMPQNRRHTFQYRVWHFVVSFVSPSEYTIMAMIALNTVVL M 1477

QY 1612 MEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFRFFQDRWNQOLDLAIVLLSIMG 1671
Db 1478 MKYYSAPCTVELALKYLNIAFTMVFSLECVLKVIAFGFLNYFRDTWNIFDFITVIGSITE 1537

QY 1672 ITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRAALLDTVMQALPQVGNLGLL 1731
Db 1538 IILTDSKLVNTSGFNMSFLKLFRA---ARLIKLLRQGYTTRILLWTVFVQSFKALPYVCLL 1594

QY 1732 FMLLFFIFAALGVLEFGDLECD-BTHPCEGLGRHATFRNFGMAFLTFLFRVSTGDNWNGIM 1790

Db 1595 IAMLFFIYAIIGQVFGNIKLDDESH-----INRHNFRSFFGSLMLLFRSATGEAWQELM 1650
QY 1791 KDTL--RDCQDQESTC-----YNTVISPIYFVSFVLTAQFVLNVNVIIVLAKHLEES 1839
Db 1651 LSCLGKGECPDITAPSGQENERCGLDLAYVYFVSFFFCFSFLMLNLFVAVIMDNFEYL 1710
QY 1840 NKEAK-----EAELEAELE-----LEMKTLSPQHSPLGSPFLWPVGVEG 1879
Db 1711 TRDSSILGPHLDEFVRVWAEYDRAACGRHYHTEMYLEMTLM-----SPLGLGKRC 1762
QY 1880 PDSPDPKPGKALHPAAHARSASHPSLEHPTMQPHPTLPGPDLLTVRKSGVSRTHSLPND 1939
Db 1763 PSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD---IKIAGGADRQOL---D 1813
QY 1940 SYMCRHGSTAEGPLGHRGWL-----PKAQSGSVLSVHSPADTSYI-----LQL 1984
Db 1814 SELQKETLAIWPHLSQKMLDLLVPMPKASDLTVGKIYAAMMIMDYKQSKVKKQROQLEE 1873
QY 1985 PKDAP--HLLQPHSAP-----TWGTIPKLPP-----PGRSPLAQRPRLRQAAI 2025
Db 1874 QKNAPMFQRMESPSSLQEIITANAKALPYLQDQPVSGLSGRSGYPMSPLSPQDIFQLACM 1933
QY 2026 RTDSLQVQGLGSRDILLAEVSGSPPLARAYS-----FWGQSSTQAAQOHSR 2071
Db 1934 --DPADDDQGFQERQSLV--VTDPSS--SMRRSFSFTIRDKRSNSWLEEFMSERSSENTYKSR 1988
QY 2072 SHSKISKHMTTPAPCPGPEPNWGKPPETRRSSLELDT-ELSWISG---DLLPPGGQEEPP 2127
Db 1989 RRS-----YHSSLRLSAHRLNSDSGHKSDTHPSGGRERR 2023
QY 2128 SPR-----DLKKYSVEAQCORRPTSWLDEQRHSIAVCLDSGSOHLGTDPSNLG 2180
Db 2024 SKERHLLSPDVSRCNSEE-----RGTQADWESPERRQSRSPS--EGRSQ-----TPNR-- 2070
QY 2181 GQPLGGSRPKKLSPPSITIDPPES--QGRTPPSPGICLR-----RRAPS----- 2226
Db 2071 ---QGTGSLSESSIPSVSDTSTPRRSRQLPVPVPPKPRPLLSYSSLIRHAGSISPPADG 2126
QY 2227 SDSKDPLASGPPDSMAA-----SPSPKK 2249
Db 2127 SEEGSPLTSQALESNNAWLTSSNSPHPQQ 2156

RESULT 14
A47447
calcium channel protein alpha-1 chain (variant doe-1) - electric ray (Discopyge ommata)
C;Species: Discopyge ommata
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Accession: A47447
R;Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
A;Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray Discopyge ommata
A;Reference number: A47447; MUID:93248175; PMID:7683405
A;Accession: A47447
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-2223 <HOR>
A;Cross-references: UNIPROT:P56699
A;Note: sequence extracted from NCBI backbone (NCBIP:130671)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 13.9%; Score 1656; DB 2; Length 2223;
Best Local Similarity 24.2%; Pred. No. 7.3e-93;
Matches 595; Conservative 385; Mismatches 811; Indels 668; Gaps 89;

QY 35 GSAEKDPGSADSEAGLPPAL---APV-----VFFYLSQDSRPRSWCLRTVCNPW 82
Db 44 GAAQGSAGFKQTRAQARTMALYNPIPVVRHNLCTANRSLFLFGEDNIVRKSAARRVIEWPP 103
QY 83 FERISMLVILLNCVTLMFR--PCEDIAQDSQRILQAFDDFIFAFVAVEMVVMVALG 140
Db 104 FEYMILATIANCVVLALEQHLPNGD---KTPMAKSLEQTEPYFIGIFCFEAGIKIVALG 160

QY 141 -IFGKCYLGDTWNLDDFFIVIAGLEYSLDLQNVFSFSAVTVRVLRPLRLRAINRVPMRI 199
Db 161 FVFHKGSLRNGWNVMDFIIVLSGLL--ATAATHFNLRTLRAVRVLRPLKLVSGIPSLQI 218
QY 200 LVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLERY 259
Db 219 VLKSIKAMVPLLOIGLILFFAILMFAIGLEFYFGKLRHRTCYTDDAAAEELDLOF--- 274
QY 260 QTENEDESPFCSPRENGMRSCRSVPILRGDGGGPPCGGLDYEAYNSSNTTTCVNMNQY 319
Db 275 -----PCGTQEPTRCPNGTVCYSW--- 294
QY 320 YTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDA-HSFYFIYFILL 378
Db 295 -----IGPNDGITQFDNIFALLTVFOCIITMEGWTILYNTDDALGAMWNWLYFIPL 346
QY 379 IIVGSFFMINCLVVIATQFSETKQRES-----QLMREQVRVRLSNASTLASFSEPGSC 432
Db 347 IIGSFFVLNLVGLSGEFAKERERVENRRSFLKLRRQQIE----- 389
QY 433 YBELLKYLVIILKAAARLAQVSRAGVRVGLLSSPAPLGGQETQPSSSCSRSHRRLSVH 492
Db 390 -RELNGYRAWIDKAEVLMLEENKNAKESAL----- 420
QY 493 HLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGAES 552
Db 421 -----HVLRRATIKKGR----- 432
QY 553 VHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPETLKEKALVEVAA 612
Db 433 -----MEMIQTES-----SEDQYTEISS 450
QY 613 SSGPPLTSLNIPPGPYSSMHKLELTQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR 672
Db 451 VGSPLARASI-----KSTKLLEGSS----- 470
QY 673 AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHRRQRSLGPDAPSSVLAFWRLI 732
Db 471 -----YFRRKE-----RML 479
QY 733 CDTFRKIYDSKYFGRGIMIALVNTLSMGIEYHEQPELTNALEISNIVTSLFALEMLL 792
Db 480 RISIRHVMVKSHAFYIWLGLVALNTVCVAVVHYDQPLWLSNFLYAEFTFLGLFSSEMFL 539
QY 793 KLLVYGPFGYIKNPYNIFDGVIVVISVWEIV-----GQGGGLSVLRTFLRMVRLKLVRF 847
Db 540 KMYGCGPLYPHSSFCDFCGVIGSIFDVVWTTIIRPFSFGISVLRALRLRIFKITKY 599
QY 848 LPALQRLVVLKMTMDNVATFCMLLMFLFIFISILGHLFGCKEASERDGTLPDRKNFD 907
Db 600 WASLRNLVLSMSSMKSIISLLFLFLFVIVFALLGMQLFGQPFEE--GTPP--TNFD 655
QY 908 SLLWAIIVTFQILTOEDWNKVLVNGVAS-----TSSWAALYFIALMTFGNYVFLNLLVAI 962
Db 656 TFPAAIITVFQILTGEDWNEVMYNGIKSGGVNSGMWSSVYFVLTFLFGNYTLLNVELAI 715
QY 963 LVEGF-QAEEISK---REDASGQLSCIQ-----LPVDSQGGDANKSE----- 1000
Db 716 AVDNLANAQELTKBEQEEEAINKHALQKAKEVSPMSAPGPSTEREFRRHKMSIWEA 775
QY 1001 -----SEPDPFFSPSLDG-DGDRKK-----CLALVSLGEHPELRKSLLDPL 1039
Db 776 RTSQLRRRMQMSREALFTDALQGLEGRYRRHRSRIFEAEHLRLAEQAAESHQLEGEV 835
QY 1040 IIHTAATPMSLPKSTSTGLGEALGPAGNRSTS-----SSCSAEPGAHEMKSPPSA 1089
Db 836 GRREAFKRSRLNS-----WQAPGPDKSSSIKVNQEQGRALGRSVEAGASFRMAEPIRA 890
QY 1090 RSSPHSPW-----SAASSWTSRRSSRNSLGR-APSLKRRSPG---ERRSLLSGEGQ 1137
Db 891 RRRYRSLYKEAKMGLSESAETSLRRPGKNKEGRLLQLQCEQESGQLTQTPVMDAQGQ 950

QY 1138 ES-----QDEESSEEBERASPAGSDHRRHGRSLERE-----AKSFDLPD----- 1176
Db 951 MKAFSWQGEPHSSMTPTPDVTD-PSGGNLEKESGRTPENGKERSANTSEQVNEQSNWL 1009
QY 1177 TLQV-----PGLHRTASGRGSASEHQ-----DCNGKSASGLRALARPDDPPLD-- 1220
Db 1010 NLQLNQATPGDRELTTGTRDTKQDKTQEQTEIDVDCEN-----TETPMDSL 1056
QY 1221 ---GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFFPQSRFRLLCHRIITHKM 1277
Db 1057 VTPGNAYSSSSVKEDEKKS---KAIIPYT-----SMFLFRKTNPIRRVCHFIYNLRY 1106
QY 1278 FDHVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGCFCG 1337
Db 1107 FEMCILLVIAASSVALAEDP-IHKDSARNQVLRIFYDYFTGVTTFEMVIKIDIGLVFH 1165
QY 1338 EQAYLRSSWNVLGLLVLISVIDI-LVSMVSDSGTKILGMLRVLRLLRTLRLPLRVISRAQ 1396
Db 1166 EGSYFRDVWNILDFIVVSGALVAFATNLIGSSGKDINTIKSLRVLRVLRPLKTKRLP 1225
QY 1397 GLKLVEITLMSLSKPIGNIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDDCA 1456
Db 1226 KLKAVFDCVVTSLKNVFNILIVYKLFMFIFAVIAVQLFKGKFFYC--TDSSKMT-KQDC- 1281
QY 1457 EASYRWVRHK-----YNFDNLGQALMSFLVASKDGWVDIMYDGLDAVGVDQQ 1504
Db 1282 RGQFVLRQRTKLSIENGNTTTFHYDNVVMWALLTLFTVSTGEGWPQVLQHSVDTEADQG 1341
QY 1505 PIMNINPWMLLYFISFLLIVAFFVLNMFGVVVENFHKCRQHOOEEEEARRRERKRLRLE 1564
Db 1342 PIPGNRMEMSIYIVYFVVPFFVNFVALIITF-----QEQGDKMLEES---SLE 1391
QY 1565 KKRKA-----QCKPY--YSDYSR--FRLLVHHLCTSHYLDLFTITGVIGLNVVTNAMEHY 1615
Db 1392 KNERACIDFAISAKPLTRYMPQNRQTQYRVWQFVSPSFEYTILTMIALNTVVLMMKHH 1451
QY 1616 QQPQILDEALKICNIYIFTVIFVLESVKLVAFGRFRFFQDRWNQLDLAIVLLSIMGITLE 1675
Db 1452 SPPPGFASVLKLMNIAFTITFTLECILKIIAFGLNLYFRDSWNVDFVTVVGSISEIIVT 1511
QY 1676 EIE--VNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALDVTVMQALPQVGNLGLLF 1732
Db 1512 ECNLKFNLS-----FLKLFRARLIKLLRQGITIRILLTWTFFVQSFKALPYVCLLI 1562
QY 1733 MLLFFIFAALGVELFGDLECDETHPCEGLRHATFRNFGMAFLTFRVSTGDNWNGIMKD 1792
Db 1563 AMLFFIYAIIGMQLFGNIGLDHTP---INRHNNFHTFFNALMLLFRSATGESWQEIMLA 1619
QY 1793 TL--RDGD--QESTCVNTVISPIYFVSFVLTAQFVLNVVVIKLVAVLKMHLEESKEAK--- 1844
Db 1620 CLSGKECEGTREPC-GTDVAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSSILGP 1678
QY 1845 ----EEAELEAELE-----LEMKTL-SPQPSPLGSPFLWPG-----VE 1878
Db 1679 HHLDEFVRVWAEYDRAACGRIHYTDMYQMLTLMSP---PLGLKXKCPKVAYKRLVLMN 1734
QY 1879 GPDSPD-----SPKPGALHPAAHARSA-----SHFSLEHPTMQPHTELPGPDL 1922
Db 1735 MPVTEDKTVHFTSTILMGLIRTALQIKLARGGADKQQLDAELRKEIMTIWPHLSQ-KTLDL 1793
QY 1923 L-----TVRKSGVSRTHSL-----PNDSYMCRHGSTAEGPLGHR----- 1956
Db 1794 LVPMTYSDLTVGKIYAAMMIMDYKQSKNKKYKQLQEEQSRTPMFQRMEEASSLPPOIIS 1853
QY 1957 -GWGLPKAQSGVLSVHVSQPADTSYILQLPKDAPHLLQPHSAPTGW-TIPKLPPPGRSPL 2014
Db 1854 STKGLPYLQTGTGPDVDSR-SEFTPLVPLP---PVMFQQGRFSSQGEIHKQRPKELKI 1909
QY 2015 AQR-----PLRRQA-AIRTDSDLVQGLSGSREDLLAEVSPSPPLARAYSFWGQSSTQ 2065
Db 1910 KLEYPHYGHYLPFIEHQGRAVMPRLIE---SAED-----TSPLKRSL-----STF 1952
QY 2066 AQQHSRSHSKISKHMTPPAPCPGPE---PNWKGKP--PETRSSLELDTELSWISGDLPLP 2120

Db 1953 AANHSNS-TWLNEYSLERA---GPEDLYKRWSRRPLRPPSRSS-----N 1992
QY 2121 GGQEEPPSPRDLKKCYSEVAQSCQRRPTFSWLDEQRRHSIAVSCLDGSGQPHLGTDPNSLG 2180
Db 1993 AGSRERGRSRERKHLSPERSVCS-----TGQCAH-----PSQHRGLD-QRLS 2034
QY 2181 GQPLGGPGSRPKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKD-PLASGPP 2238
Db 2035 RSPSPGYSHRPREQVN-SSVSESPVSSSGTSPPKQG---QROLPQTPSKRPLVSYSP 2089
RESULT 15
A37490
voltage-dependent calcium channel alpha 1E - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A37490
R:Soong, T.W.; Stea, A.; Hodson, C.D.; Dubel, S.J.; Vincent, S.R.; Snutch, T.P.
Science 260, 1133-1136, 1993
A:Title: Structure and functional expression of a member of the low voltage-activated ca
A:Reference number: A37490; MUID:93262464; PMID:8388125
A:Accession: A37490
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2222 <SOO>
A:Cross-references: UNIPROT:Q07652; GB:L15453; NID:g310082; PIDN:AAA40855.1; PID:g310083
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIP:132101)
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
Query Match 13.9%; Score 1651.5; DB 2; Length 2222;
Best Local Similarity 23.6%; Pred. No. 1.4e-92;
Matches 591; Conservative 374; Mismatches 831; Indels 707; Gaps 77;
QY 62 FYLSQDSRPRSWCLRTVCNPFMERISMLVILLNCVTLMGER--PCEDIAQDSQRCRILQA 119
Db 21 FIFGEDNIVRKYAKKLIDWPPFEYMLATIIANCIVLALEQHLPEDDKTPMSRR---LEK 77
QY 120 FDDFIFAFFAVEMVVMVALG-IFGKKCYLGDWTNRLDFFVIAGMLEYSLDLQN--VSF 176
Db 78 TBPYFIGIFCFEAGIKIVALGFIFHKGYLRNGWNVDMFIVLSGILATAGTHFNTHVDL 137
QY 177 SAVRTVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFIFGIVGVQLWAGL 236
Db 138 RTLRAVRVLRPLKLVSGIPSLQIVLKSIMKAMVPLLQIGLLLFFAILMFAIIGLEFYSGK 197
QY 237 LRNRCFLPENFSLPLSDLERYYQTEDESPFICSQPRENGMRSCRSVPTLRGDGGGP 296
Db 198 LHRACFMNNSGIL-----EGFDP-----PHPCGVQGC----- 224
QY 297 PCGLDYEAYNSSNTTCVWNQYNTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGW 356
Db 225 PAG--YE-----CKDW-----IGPNDGITQFDNILFAVLTVFQCITMEGW 262
QY 357 VDIMYFVMDA-HSFYNFYIFILLIIVGSSFFMINLCIVVIAIQFSETKQRESQLMREQVR 415
Db 263 TTVLYNTNDALGATWNWLYFIPLIIGSFVNLVGLVLSGEFAKERERV-----ENRRA 317
QY 416 FLSNASTLASFPSEPGSCYEELLKVLVYLKKAARRLAQVSRAAGVRVGLLSSPAPLGGQE 475
Db 318 FMK-----LRRQQOI----- 327
QY 476 TQPSSSCSRSHRRLSVHHLVHHHHHHHHYHLNGTLRAPRASPEIQDRDANGSRRLMLP 535
Db 328 -----ERELNGYRAWI-- 338
QY 536 PPSTPALSAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKYVPTVHT 595
Db 339 ----- 338
QY 596 SPPPETLKEKALVEAASSGPPTLTSLNIPPGPYSSMHKLJETQSTGACQSSCKISSPCL 655

Db 339 ----DKAEVMAEENKNGSALVLRATIKRSRTEAMTRDSSDEHCVDISSVGTPLA 394
QY 656 KADSGACPDSPYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRS 715
Db 395 RASIKSTKVDGASY-----FRHKE-----413
QY 716 LGPDAEPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTSMGIEYHEQPEELTNAL 775
Db 414 -----RLLRISIRHMVKSQVFWIWSLVVALNTACVAIVHNPQWLTHLL 459
QY 776 EISNIVFTSLFALEMLKLLVYGPFGYIKPNYIFDGVIVVISWEIVGQ-----QGGGL 830
Db 460 YYAEFLFLGLLEMSLKMYGMGPRLYTHSSFNCFDFGVTVGSIPEVWVAIFRPGTSFGI 519
QY 831 SVLRTFRLMRVLKLVFLPALQRLVLMKTMNDNVATFCMLLMFLIFISILGMHLFGCK 890
Db 520 SVLRALRLRIFKITYKIASLRNLVSLMSSMKSIISLLFLFLFVVFALLGMQLFGGR 579
QY 891 FASERDGDTLPRKNPDSLLWAIIVTVFQILTQEDWNKVLYNGM-----ASTSSWAALYFI 945
Db 580 F-NFNDG---TPSANEDTFPAAIMTVFQILTEDWNEVMYNGIRSQGVSSGMSAIYFI 635
QY 946 ALMTFGNYVLNLLVAILVEGF-QAEEISK-----REDASQOLSCIQLPVDSSQGDANKSE 1000
Db 636 VLTIFGNYTLNVLAIADNLANAQELTKDEOESEAFNOKHALQAKEV-----SPM 689
QY 1001 SEPDEFSPSLDGDGRKKIAL-----VSLGEHPE 1030
Db 690 SAPNM--PSIERDRRRHHMSMWEPSSHLRERRRRHHMSVWEQRTSQLRRHMQSSQEA 747
QY 1031 LRKSLPPLIHTAATPMS-----LPKS-TSTGLGEALGPASRRRTSSSGSAE 1076
Db 748 LNKEEAPMNPPLNPLNPLNAHPSLYRRPRPIEGLALGLGLEKCEBERISRGSL 807
QY 1077 PGAAHEMKSPPSARSSPHS-----PW-----SAASSWT 1104
Db 808 KGDIGLTSVLDNQSPSLGKREPPWLPRSCHGNCDPTQOETGGETVTVTFEDRARHRQ 867
QY 1105 SRRSRNSLGRAPSLKRRSPSGERRSLLSGEQESQDEEESSEERASPAAGSDHRHRGSL 1164
Db 868 SQRRSHRRVRTEGESASASRSR---SASQERSLDEGVSDGEKEHEPQSSHRSKEPT 923
QY 1165 EREAKSSFDL--PDTLQVP---GL-----HRTASGRGSASEHQDNGKSA 1204
Db 924 IHEERTQDLRRTNSLMVPRGSLVGALDEAETPLVQPOPELEVGDAAALTEQEAEGSSE 983
QY 1205 SGRLA-----RALRPDDPPL-----1219
Db 984 QALLADVQLDVGRGISQSEPDLSCTMTNMDKATTESTSVTVAIPDVDPVLDSTVVNISNK 1043
QY 1220 -DGDDA-----DDEGNLSKGER---VRAWIRALPACYLERSWSAYIFPPQSRFRL 1267
Db 1044 TDGEASPLKEAETKEEEVEKKQKKEKRETKAMVPHS-----SMFIFSTTNPIRK 1096
QY 1268 LCHRIITHKMFHDHVLVIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTV 1327
Db 1097 ACHYIVNLRIFEMCILLVIAASSIALAEDPVLITNSERNKV-LRYFDYVFTGVFTFEMVI 1155
QY 1328 KVALGWCFGEQAYLRSSWNVLGGLVLISVIDI-LVSMVSDSGTKILGMLRVLRLRLTL 1386
Db 1156 KMIDQGLILQGSYFRDLWNILDFVVVVGALVAFALANALGTNKGRIKTIKSLRVLRL 1215
QY 1387 RPLRVISRAQGLKLVETLMSLKPIGNIVVICAPFIIIFGILGVQLFKGKFFVC--QGE 1444
Db 1216 RPLKTIKRLPKLKAVIDCVVTSLKNVFNILIVKLFMFIFAVIAVQLFKGKFFYCTDSSK 1275
QY 1445 DTRN-----ITNKSDECAEASYSR-WVRHKYNFDNLGQALMSLFLASKDGVVDIMYDGLD 1497
Db 1276 DTEKECIGNYVDHEKNKMEVKGREWKRHEFYDNIWALLTLFTVSTGEGWPQVLQHSVD 1335
QY 1498 AVGVDDQPIMHNHNPWMLLYFISFLLIIVAFFVLNMFVGVVFNENFKCRHQHEEEARRREE 1557
Db 1336 VTEEDRGPSSRNMEMSIYVYVVFVFPFFVFVFIIVFALIITF-----QEQQDKMEE 1388

QY 1558 KRLRLEKKRKA-----QCKPY--YSDYSR--FRLLVHLCTSHYLDLFTITGVIGLVV 1608
Db 1389 ---CSLEKNERACIDFAISAKPLTRYMPQNRTHTFYRVWHFVSPSPFEYTIMAMIALNTV 1445
QY 1609 TMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQLDLAIVLLS 1668
Db 1446 VLMKYYASAPWTYELALKYLNIAFTMVFSLECVLKVIAFGFLNFRDNTWIFDITVIGS 1505
QY 1669 IMGITLEEIEVNASLPINPTIIRIMRVLRARVLLKLMKMAVGRALLDVTMQALPQVGNL 1728
Db 1506 ITEIILTDSKLVNTSGFMSFLKLFRA---ARLIKLRQGYTIRILLTWTVFQSFKALPYV 1562
QY 1729 GLLFMLLFFIFAALGVLEFGDLECD-ETHPCEGLGRHATFRNFGMAFLTFRVSTGDWNW 1787
Db 1563 CLLIAMLFFIYAIIGMQVFGNIKLDEESH---INRHNFRSFFGSLMLLFRSATGEAWQ 1618
QY 1788 GIMKDTL--RDCDQESTC-----YNTVISPIYFVSFVLTQAQFVLNVVIAVLMKHL 1836
Db 1619 EIMLSCLGKCEPDTTAPSGQNESERCGLDLAYVYFVSFIFFCSFLMLNLFVAVIMDNF 1678
QY 1837 EESNKEAK-----EEAELEAELE-----LEMKTLSPQPHSPGLSGPFLWPG 1876
Db 1679 EYLTRDSSILGPHHLDDEFVRVWAEYDRAACGRHYTEMYMLTLM-----SPPLGLG 1730
QY 1877 VEGPDSPPSPKPGALHPAAHARSASHFSLEHPTMQPHPTLPDPDLTLVRKSGVSRTHSL 1936
Db 1731 KRCPSKVAYKRLVLMNMPVAEDMTVHFT--STLMALIRTALD---IKIAGGADRQQL- 1783
QY 1937 PNDSYMCRRHGSTAEGPLHRGWGL-----PKAQSGSVLSVHSQPADTSYI-----1981
Db 1784 --DSELQKETLAIWPHLSQKMLDLLVPMPKASDLTVGKIYAAMIMDYVKQSKVKQKORQQ 1841
QY 1982 LQLPKDAP--HLLQPHSAP-----TWGTIPKLPP-----PGRSPLAQRPPL---2019
Db 1842 LEEQKNAPMFQRMPEPSSLPQEIISNAKALPYLQDDPVSGLSGRSGYPMSPLSPQEIFQL 1901
QY 2020 -----RRQAAIRTDSDVQGLGSR-----EDLLAEVSGSPPLARAY 2056
Db 1902 ACMDPADDGQFQEQQSLVVTDPSSMRRSFSTIRDKRNSNSWLEEFMSERSSENTYKSRRR 1961
QY 2057 SFWGQSSTQAQOH-----SRSHSKISKHMTTP-----AP 2085
Db 1962 SY--HSSLRLSAHRLNSDSGHKSDTHRSGRGRGRSKERKHLSPDVSRNCNEERGTQAD 2019
QY 2086 CPGPEPNWKGPPETRS-----SLE-----LDTELISWISGDLPLPPGQGEPPSP 2129
Db 2020 WESPERQSRSPSEGRSQTPNRQGTGSLSESSIPSISDSTPRRSTRQLPP---VPPKP 2075
QY 2130 RDLKKCYVBAQSCORRPTSWLDEQRRHSIAVCLDSGSOPLGTDPSNLGGQPLGGPGS 2189
Db 2076 RPLLSYSSL-----MRHTGGISPPPDGSE-----GGSPLASQAL 2109
QY 2190 RPKKK-LSPPSITIDPPESQGRTP---PSPGICLRRRAPSSD 2228
Db 2110 ESNSACLTESSNSLHPQQGQHPSQHYISEPYLALHEDSHASD 2152

Search completed: November 18, 2004, 13:35:23
Job time : 97.2671 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:06:30 ; Search time 251.833 Seconds
(without alignments)
5177.235 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEDGAGAEESGQPRFSM.....PKXDVLSLGLSSDPADLDP 2266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11815.5	99.3	2377	1 CCAG HUMAN	Q43497 homo sapien
2	11133.5	93.5	2295	2 Q9WUT2	Q9wut2 mus musculus
3	11111	93.3	2288	2 Q9WUB8	Q9wub8 rattus norv
4	10945	91.9	2254	1 CCAG RAT	O54898 rattus norv
5	10945	91.9	2254	2 AAG35186	Aag35186 rattus no
6	10913	91.7	2248	2 Q6PFV8	Q6pfv8 mus musculus
7	10913	91.7	2248	2 AAH57399	Aah57399 mus muscu
8	6573	55.2	1389	2 Q6ZPX4	Q6zpx4 mus musculus
9	6573	55.2	1389	2 BAC98104	Bac98104 mus muscu
10	6217.5	52.2	2359	1 CCAH RAT	Q9eq60 rattus norv
11	6210	52.2	2353	1 CCAH HUMAN	Q95180 homo sapien
12	6176.5	51.9	2365	1 CCAH MOUSE	O88427 mus musculus
13	5496.5	46.2	2223	1 CCAI_HUMAN	Q9p0x4 homo sapien
14	5383	45.2	1835	1 CCAI RAT	Q9z0y8 rattus norv
15	4836	40.6	1994	2 Q7Z6S8	Q7z6s8 homo sapien
16	4200.5	35.3	1762	2 Q7PQV4	Q7pqv4 anopheles g
17	4180	35.1	2893	2 Q9W433	Q9w433 drosophila
18	3855	32.4	1837	2 Q967R4	Q967r4 caenorhabdi
19	3845.5	32.3	1852	2 Q7Z002	Q7z002 caenorhabdi
20	3845.5	32.3	1852	2 AAR25651	Aar25651 caenorhab
21	3828.5	32.2	1844	2 Q7YZR6	Q7yze6 caenorhabdi
22	3828.5	32.2	1844	2 AAR25653	Aar25653 caenorhab
23	3823	32.1	1885	2 Q7Z003	Q7z003 caenorhabdi
24	3823	32.1	1885	2 AAR25652	Aar25652 caenorhab
25	3683.5	30.9	1460	2 Q80TJ2	Q80tj2 mus musculus
26	2925.5	24.6	1418	2 Q7JPB4	Q7jpb4 caenorhabdi
27	2925.5	24.6	1418	2 AAR30210	Aar30210 caenorhab
28	2866	24.1	1942	2 Q869H0	Q869h0 lymnaea sta
29	2089	17.5	1211	2 Q8MQ95	Q8mq95 caenorhabdi
30	1746.5	14.7	2339	1 CCAB_HUMAN	Q00975 homo sapien
31	1740.5	14.6	2333	2 O89089	O89089 rattus norv

32	1732.5	14.6	2327	1 CCAB_MOUSE	O55017 mus musculus
33	1729.5	14.5	2331	2 Q9TTA4	Q9tta4 bos taurus
34	1722	14.5	2336	1 CCAB_RAT	Q02294 rattus norv
35	1712.5	14.4	541	2 Q6PE92	Q6pe92 mus musculus
36	1712.5	14.4	541	2 AAH58206	Aah58206 mus muscu
37	1710	14.4	2339	1 CCAB_RABIT	Q05152 oryctolagus
38	1697.5	14.3	2357	2 Q9PUM6	Q9pum6 gallus gall
39	1697	14.3	2259	1 CCAE_RABIT	Q02343 oryctolagus
40	1689	14.2	1810	2 O44930	O44930 aiptasia pa
41	1688.5	14.2	2295	2 Q923K6	Q923k6 rattus norv
42	1685	14.2	2346	2 Q9PW47	Q9pw47 gallus gall
43	1683	14.1	2332	2 Q9PW45	Q9pw45 gallus gall
44	1681	14.1	2272	1 CCAE_MOUSE	Q61290 mus musculus
45	1666.5	14.0	2312	1 CCAE_HUMAN	Q15878 homo sapien

ALIGNMENTS

RESULT 1
CCAG_HUMAN STANDARD; PRT; 2377 AA.
ID O43497; O43498; Q94770; Q9NYU4; Q9NYU5; Q9NYU6; Q9NYU7; Q9NYU8;
AC Q9NYU9; Q9NYV0; Q9NYV1; Q9UHP0; Q9ULU6; Q9UNG7; Q9Y5T2;
AC Q9Y5T3;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-gated calcium channel alpha subunit Cav3.1) (Cav3.1c) (NBR13).
DE Name=CACNA1G; Synonyms=KIAA1123;
GN Homo sapiens (Human).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 4 AND 5).
RC TISSUE=Brain;
RX MEDLINE=20014446; PubMed=10548410;
RA Mittman S., Guo J., Agnew W.S.;
RT "Structure and alternative splicing of the gene encoding alpha1G, a human brain T calcium channel alpha1 subunit.";
RL Neurosci. Lett. 274:143-146(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=20115462; PubMed=10648811;
RA Cribbs L.L., Gomora J.C., Daud A.N., Lee J.-H., Perez-Reyes E.;
RT "Molecular cloning and functional expression of ca(v)3.1c, a T-type calcium channel from human brain.";
RL FEBS Lett. 466:54-58(2000).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS 1-2 AND 6-13).
RC TISSUE=Brain;
RX MEDLINE=20158909; PubMed=10692398;
RA Monteil A., Chemin J., Bourinet E., Mennessier G., Lory P., Nargeot J.;
RT "Molecular and functional properties of the human alpha1G subunit that forms T-type calcium channels.";
RL J. Biol. Chem. 275:6090-6100(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 14).
RC Kishi F.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 550-2377 FROM N.A. (ISOFORM 13).
RC TISSUE=Brain;
RX MEDLINE=22158633; PubMed=12168954;
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones.";
RL DNA Res. 9:99-106(2002).
RN [6]

FT	TRANSMEM	151	170	S3 of repeat I (Potential). Extracellular (Potential).	
FT	DOMAIN	171	175		
Query Match					
Best Local Similarity 99.3%; Score 11815.5; DB 1; Length 2377;					
Matches 2264; Conservative 1; Mismatches 1; Indels 111; Gaps 2;					
QY	1	MDEEDGAGAEESGQPR	FMRLNDLSGAGRGPGSAEKDPGSADSEAEGLPYPALAPVV	60	
Db	1	MDEEDGAGAEESGQPR	FMRLNDLSGAGRGPGSAEKDPGSADSEAEGLPYPALAPVV	60	
QY	61	FFYLSQDSRPRSWCLRTVCN	PWFERISMLVILLNCVTLGMFRPCEDIAQDSQRCRILQAF	120	
Db	61	FFYLSQDSRPRSWCLRTVCN	PWFERISMLVILLNCVTLGMFRPCEDIAQDSQRCRILQAF	120	
QY	121	DDFIFAFFAVEMVVKMVALGIFGK	KCYLGDWTNRLDFFIVIAGMLEYSLDLQNVFS	SAVR 180	
Db	121	DDFIFAFFAVEMVVKMVALGIFGK	KCYLGDWTNRLDFFIVIAGMLEYSLDLQNVFS	SAVR 180	
QY	181	TVRVLRLPLRAINRVPSMRILVTLL	LDLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240	
Db	181	TVRVLRLPLRAINRVPSMRILVTLL	LDLPLMGNVLLLCFFVFFIFGIVGVQLWAGLLNR	240	
QY	241	CFLPENFSLPLSVDLERY	YQTENEDESPFICSPRENGMRSCRSVPTLRGDGGGPPCGL	300	
Db	241	CFLPENFSLPLSVDLERY	YQTENEDESPFICSPRENGMRSCRSVPTLRGDGGGPPCGL	300	
QY	301	DYEAYNSSNTTCVNWNQYYTNC	SAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM	360	
Db	301	DYEAYNSSNTTCVNWNQYYTNC	SAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM	360	
QY	361	YFVMDAHSFYNFIYFILLII	IVGSFFMINCLVVIATQFSETKQRESQLMREQRVFLSNA	420	
Db	361	YFVMDAHSFYNFIYFILLII	IVGSFFMINCLVVIATQFSETKQRESQLMREQRVFLSNA	420	
QY	421	STLASFSEPGSCYEELLKYLVI	ILRKAARRLAQVSRAAGVRVGLLSSPAPLGQGTQPSS	480	
Db	421	STLASFSEPGSCYEELLKYLVI	ILRKAARRLAQVSRAAGVRVGLLSSPAPLGQGTQPSS	480	
QY	481	SCSRSHRRLSVHHLVHHHHHHH	YHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTP	540	
Db	481	SCSRSHRRLSVHHLVHHHHHHH	YHLNGTTLRAPRASPEIQDRDANGSRRLMLPPPSTP	540	
QY	541	ALSGAPPGAESVHSFYHAD	CHLEPVRCQAPPPRSPSEASGR	TVGSKVYPTVHTSPPE 600	
Db	541	ALSGAPPGAESVHSFYHAD	CHLEPVRCQAPPPRSPSEASGR	TVGSKVYPTVHTSPPE 600	
QY	601	TLKEKALVEVAASSGPPT	LTSLNIPPGPYSSMHKLL	ETQSTGACQSSCKISSPCLKADSG 660	
Db	601	TLKEKALVEVAASSGPPT	LTSLNIPPGPYSSMHKLL	ETQSTGACQSSCKISSPCLKADSG 660	
QY	661	ACGPDSCPYCARAGAGE	VELADREMPDSDSEAVYEFTQ	DAQHSDLRDPHSRRQRS	SLGPDA 720
Db	661	ACGPDSCPYCARAGAGE	VELADREMPDSDSEAVYEFTQ	DAQHSDLRDPHSRRQRS	SLGPDA 720
QY	721	EPSSVLAFWRLICD	TRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI	780	
Db	721	EPSSVLAFWRLICD	TRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI	780	
QY	781	VFTSLFALEMLLKL	LVGPGFYIKNPYNIFDGVI	VISVWEIVGQGGGLSVLRTFRLMR 840	
Db	781	VFTSLFALEMLLKL	LVGPGFYIKNPYNIFDGVI	VISVWEIVGQGGGLSVLRTFRLMR 840	
QY	841	VLKLVRLPALORQL	VLMKTMNDNVATFCMLLM	FIFIFISILGMHLFGCKFASERDGTLL 900	
Db	841	VLKLVRLPALORQL	VLMKTMNDNVATFCMLLM	FIFIFISILGMHLFGCKFASERDGTLL 900	
QY	901	PDRKNFDSL	LLWAI	VTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLV 960	
Db	901	PDRKNFDSL	LLWAI	VTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLV 960	
QY	961	AILVEGFQAE	EISKREDASGQLSCIQLP	VDSQGGDANKSESEPDFFSPSLDGDGDRKKCL 1020	

Db	961	AILVEGFOAEIISKREDASGQLSCIQLPVD	SQGGDANKSESEPDFFSPSLDGDGRKKCL	1020					
Qy	1021	ALVSLGEHP	ELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA	1080					
Db	1021	ALVSLGEHP	ELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGAA	1080					
Qy	1081	HEMKSPPSAR	SSPHSPWSAASWTSSRRSSRNSLGRAPSLKRRSPSGERRSLLS	GEGQESQ 1140					
Db	1081	HEMKSPPSAR	SSPHSPWSAASWTSSRRSSRNSLGRAPSLKRRSPSGERRSLLS	GEGQESQ 1140					
Qy	1141	DEEESSEER	ASPAGSDHRH	RGSLEREAKSSF	LDLPTLQVPLHRTASGRGSA	SEHQDCN 1200			
Db	1141	DEEESSEER	ASPAGSDHRH	RGSLEREAKSSF	LDLPTLQVPLHRTASGRGSA	SEHQDCN 1200			
Qy	1201	GKSASGRLA	RALRPDDPPLD	GGDDADDEGNLSKGERV	RAWIRARLPACYLERDS	WSAYIFP 1260			
Db	1201	GKSASGRLA	RALRPDDPPLD	GGDDADDEGNLSKGERV	RAWIRARLPACCLERDS	WSAYIFP 1260			
Qy	1261	PQSRFRLL	CHRIITHKMF	DHVVLVIIIFLNCITIAMERPKIDPHSAERIFL	TLSNYIFTAV 1320				
Db	1261	PQSRFRLL	CHRIITHKMF	DHVVLVIIIFLNCITIAMERPKIDPHSAERIFL	TLSNYIFTAV 1320				
Qy	1321	FLAEMTVKV	VALGWC	FGEQAYLRSSWN	VDGLLLVLSVIDILVSM	VSDSGTKILGMLRVL 1380			
Db	1321	FLAEMTVKV	VALGWC	FGEQAYLRSSWN	VDGLLLVLSVIDILVSM	VSDSGTKILGMLRVL 1380			
Qy	1381	RLRLTLR	PLRVISRAQ	GLKLVVETIMSSLKPIGNIVVICAPFIIFGILGVQLFKGKFFV	1440				
Db	1381	RLRLTLR	PLRVISRAQ	GLKLVVETIMSSLKPIGNIVVICAPFIIFGILGVQLFKGKFFV	1440				
Qy	1441	CQGEDTR	NI	TNKSDCAEASYRVR	HKYNFDNLGOALMSL	FVLASKDGWVDIMYDGLDAVG 1500			
Db	1441	CQGEDTR	NI	TNKSDCAEASYRVR	HKYNFDNLGOALMSL	FVLASKDGWVDIMYDGLDAVG 1500			
Qy	1501	VDQQPIN	MNHPWMLLYFIS	FLLIVAFVFLNMFVG	VVVENFHKCRHQHEEEARRREKRL 1560				
Db	1501	VDQQPIN	MNHPWMLLYFIS	FLLIVAFVFLNMFVG	VVVENFHKCRHQHEEEARRREKRL 1560				
Qy	1561	RRLEKKRR	-----	-----	-----	-----	KAQCKPYSDYSRFRLLVH	HLCTSHYLDL	FIGTV 1602
Db	1561	RRLEKKRR	NMLDDV	IASGSSASAA	SEAQCKPYSDYSRFRLLVH	HLCTSHYLDL	FIGTV 1620		
Qy	1603	IGLNVVT	MAMEHYQQ	QILDEALKICNYIFTVI	FVLESVFKL	VAFGFRFFQDRWNQ	LDL 1662		
Db	1621	IGLNVVT	MAMEHYQQ	QILDEALKICNYIFTVI	FVLESVFKL	VAFGFRFFQDRWNQ	LDL 1680		
Qy	1663	AI	VLLSIMGITLEEIE	VNASLPINPTIIRIMRVLRIARVLKLL	KMAVGMRA	LLDTVMQAL 1722			
Db	1681	AI	VLLSIMGITLEEIE	VNASLPINPTIIRIMRVLRIARVLKLL	KMAVGMRA	LLDTVMQAL 1740			
Qy	1723	PQVGNL	GLLFMLLFF	IFAALGVELFGDLECD	ETHPC	CEGLGRHATFRNFGMA	FLTLFRVST 1782		
Db	1741	PQVGNL	GLLFMLLFF	IFAALGVELFGDLECD	ETHPC	CEGLGRHATFRNFGMA	FLTLFRVST 1800		
Qy	1783	GDWN	GIMKDTLR	DCDQESTCYNTVISPIYFVS	FVLTAQFVL	VNVVIAVLMKHLEESNKE 1842			
Db	1801	GDWN	GIMKDTLR	DCDQESTCYNTVISPIYFVS	FVLTAQFVL	VNVVIAVLMKHLEESNKE 1860			
Qy	1843	AK	EAELEAELE	LEMKTLSPOPHSPLGSPFL	WPVEGPDSPD	SPKPGALHPAAHARSASH 1902			
Db	1861	AK	EAELEAELE	LEMKTLSPOPHSPLGSPFL	WPVEGPDSPD	SPKPGALHPAAHARSASH 1920			
Qy	1903	FSLEHPT	-----	-----	-----	-----	-----	-----	1909
Db	1921	FSLEHPT	DRQL	FDTISLLIQGSLEWELK	LMDEL	AGPGQPSAFPSAPSLGSD	PQIPLAE 1980		
Qy	1910	-----	-----	-----	-----	-----	-----	-----	1929
Db	1981	MEAL	SLTSEIVSE	BPCS	LALTD	SLPDDMHT	LLLSALESNM	QPHPTLPGP	DLTLTVRKSG 2040
Qy	1930	VS	RTHSLP	NDSYMC	RHGSTAEG	PLGHRGWGLPKA	QSGSVLSVHSQ	PADTSYI	LQLPKDAP 1989
Db	2041	VS	RTHSLP	NDSYMC	RHGSTAEG	PLGHRGWGLPKA	QSGSVLSVHSQ	PADTSYI	LQLPKDAP 2100

QY	1990	HLLQPHSA	PTWTG	TPKLP	PPGRS	PLAQ	RPLRR	QAART	DSL	DVQ	GLS	RED	LLA	EVSGPS	2049
Db	2101	HLLQPHSA	PTWTG	TPKLP	PPGRS	PLAQ	RPLRR	QAART	DSL	DVQ	GLS	RED	LLA	EVSGPS	2160
QY	2050	PPLARAY	FWGQS	STQAQ	HSRSH	SKISK	HMTTP	PAPCP	GPEPN	WGKGP	PETRS	SLELD	TE	2109	
Db	2161	PPLARAY	FWGQS	STQAQ	HSRSH	SKISK	HMTTP	PAPCP	GPEPN	WGKGP	PETRS	SLELD	TE	2220	
QY	2110	LSWISG	DLPLP	GGQEP	SPRDL	KKCYS	VEAQ	SCORR	PTSWL	DEQ	RHS	IAVS	CLDS	GSQ	2169
Db	2221	LSWISG	DLPLP	GGQEP	SPRDL	KKCYS	VEAQ	SCORR	PTSWL	DEQ	RHS	IAVS	CLDS	GSQ	2280
QY	2170	PHLGTDP	NSLGG	QPLGG	PSRP	KKLS	PPSIT	IDPP	ESQGP	RTPPS	PGICL	RRRAP	SSDS	2229	
Db	2281	PHLGTDP	NSLGG	QPLGG	PSRP	KKLS	PPSIT	IDPP	ESQGP	RTPPS	PGICL	RRRAP	SSDS	2340	
QY	2230	KDPLAS	GPPDS	MAASP	SPKDV	LSL	SGLS	SDP	ADLDP	2266					
Db	2341	KDPLAS	GPPDS	MAASP	SPKDV	LSL	SGLS	SDP	ADLDP	2377					
RESULT 2															
Q9WUT2															
ID	Q9WUT2	PRELIMINARY; PRT; 2295 AA.													
AC	Q9WUT2;														
DT	01-NOV-1999	(TrEMBLrel. 12, Created)													
DT	01-NOV-1999	(TrEMBLrel. 12, Last sequence update)													
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)													
DE	Voltage-gated calcium channel, alpha-1-G subunit.														
GN	Name=Cacnalg;														
OS	Mus musculus (Mouse).														
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;														
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.														
OX	NCBI_TaxID=10090;														
RN	[1]														
RP	SEQUENCE FROM N.A.														
RC	TISSUE=Brain;														
RX	MEDLINE=99189326; PubMed=10087148;														
RA	Klugbauer N., Marais E., Lacinova L., Hofmann F.;														
RT	"A T-type calcium channel from mouse brain.";														
RL	Pflugers Arch. 437:710-715(1999).														
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).														
CC	-!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.														
CC	EMBL; AJ012569; CAB40793.1; --														
DR	MGD; MGI:1201678; Cacnalg.														
DR	GO; GO:0005886; C:plasma membrane; IDA.														
DR	GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.														
DR	InterPro; IPR001682; Ca_Na_pore.														
DR	InterPro; IPR002111; Cat_channel_TripL.														
DR	InterPro; IPR002077; Ca_channel_alpha.														
DR	InterPro; IPR005821; Ion_trans.														
DR	InterPro; IPR005820; M+channel_nlg.														
DR	InterPro; IPR005445; TVDCCalpal.														
DR	Pfam; PF00520; Ion_trans; 4.														
DR	PRINTS; PR00167; CACHANNEL.														
DR	PRINTS; PR01629; TVDCCALPAL.														
KW	Calcium channel; Calcium-binding; Ion transport; Ionic channel;														
KW	Transmembrane; Transport; Voltage-gated channel.														
SQ	SEQUENCE 2295 AA; 253957 MW; FE817D054ED26984 CRC64;														
Query Match 93.5%; Score 11133.5; DB 2; Length 2295;															
Best Local Similarity 93.3%; Pred. No. 0;															
Matches 2142; Conservative 32; Mismatches 91; Indels 31; Gaps 5;															
QY	1	MDEEDG	GAGAE	ESGQ	PSFWM	NDLS	GAGG	CPGSA	EKDP	GSAD	SEAE	GLPY	PALAP	VV 60	
Db	1	MDEEDG	GAGAE	ESGQ	PSFWM	NDLS	GAGG	CPGSA	EKDP	GSAD	SEAE	GLPY	PALAP	VV 60	
QY	61	FFYLSQ	DSRPR	SWCL	RTVC	NPFWR	ISML	VILL	NCVT	LMGFR	PCEDI	ACDSQ	RCRIL	QAF 120	
Db	61	FFYLSQ	DSRPR	SWCL	RTVC	NPFWR	ISML	VILL	NCVT	LMGFR	PCEDI	ACDSQ	RCRIL	QAF 120	

QY 1200 NKSASGRLARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACVLERDSWSAYIF 1259
Db 1201 NKSASGRLARTLRADDPPLDGDGDDEGNLSKGERLAWVRARLPACCRERDSWSAYIF 1260
QY 1260 PPQSRFRLLCHRIITHKMFHDVWLVIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTA 1319
Db 1261 PPQSRFRLLCHRIITHKMFHDVWLVIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFTA 1320
QY 1320 VFLAEMTVKVALGCFGEQAYLRSSWNVLGILLVLSVIDILVSMVSDSGTKILGMLRV 1379
Db 1321 VFLAEMTVKVALGCFGEQAYLRSSWNVLGILLVLSVIDILVSMVSDSGTKILGMLRV 1380
QY 1380 LRLRLTLRPLRVISRAQGLKLVVETLMSLLKPIGNIVVICCAFFIIFGILGVQFKGKFF 1439
Db 1381 LRLRLTLRPLRVISRAQGLKLVVETLMSLLKPIGNIVVICCAFFIIFGILGVQFKGKFF 1440
QY 1440 VCOGEDTRNITNKSDCAEASYSYRWRHKYNFDNLGOALMSFLVASKDGVVDIMYDGLDAV 1499
Db 1441 VCOGEDTRNITNKSDCAEASYSYRWRHKYNFDNLGOALMSFLVASKDGVVDIMYDGLDAV 1500
QY 1500 GVDQOPIMNHNPNMLLYFISFLLIIVAFFVLNMFVGVVENFHKRQHQHEEEARRREEKR 1559
Db 1501 GVDQOPIMNHNPNMLLYFISFLLIIVAFFVLNMFVGVVENFHKRQHQHEEEARRREEKR 1560
QY 1560 LRRLEKKRR-----KAQCKPYYSYDSRFRLLVHHLCTSHY 1594
Db 1561 LKRLEKKRRSKEQKQADMLMDVVIASGSSASAASEAQCKPYYSYDSRFRLLVHHLCTSHY 1620
QY 1595 LDLFITGVIGLVNVTMAMEHYQQQIILDEALKICNYIFTVIFLESVFKLVAFGRFRFFQ 1654
Db 1621 LDLFITGVIGLVNVTMAMEHYQQQIILDEALKICNYIFTVIFLESVFKLVAFGRFRFFQ 1680
QY 1655 DRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRAL 1714
Db 1681 DRWNQDLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRAL 1740
QY 1715 LDTVMQALPOVGNLGLLFMLFFIIPAAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAF 1774
Db 1741 LDTVMQALPOVGNLGLLFMLFFIIPAAALGVLEFGDLECDETHPCCEGLGRHATFRNFGMAF 1800
QY 1775 LTLFRVSTGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVIVAVLMK 1834
Db 1801 LTLFRVSTGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVIVAVLMK 1860
QY 1835 HLEESNKEAKEAEAELEAELEEMKTLSPQHPSPGSPFLWPGEVGPDSPPSKPGALHPA 1894
Db 1861 HLEESNKEAKEAEAELEAELEEMKTLSPQHPSPGSPFLWPGEVGVNSPDSKPGAPHTT 1920
QY 1895 AHARSASH-FSLEHPTMQPHTELP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAE 1950
Db 1921 AHIGAASSGFSLEHPTMVPHTEEGVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAE 1980
QY 1951 GPLHGRGWGLPKAQSGSVLSVHSQPADTSYIQLPKDAPHLLQPHSAPTWGTIPKLPPPG 2010
Db 1981 RSLGHRGWGLPKAQSGSVLSVHSQPADTSCILQLPKDAHLLQPHGAPTWGAIPKLPPPG 2040
QY 2011 RSPLAQRLRQAAIRTDSDVQGLGSRREDLLAEVSGSPSPPLARAYSFWGQSSTQAQHS 2070
Db 2041 RSPLAQRLRQAAIRTDSDVQGLGSRREDLLAEVSGSPSPPLTRSSSFWGGSSIQVQORS 2100
QY 2071 RSHSKISKHMTPPACPGPEPNWKGPPETRSSLELDTLSWISGDLPLPGQGEPPSPR 2130
Db 2101 GSQSKVSKHIRLPAPCPGLEPSPWAKDPQETRSSLLELDTLSWISGDL-LPSSQEEPLSPR 2159
QY 2131 DLKKCYSVAEQSCORRPTSWLDEQRRHSIAVSCLDGSGQPHLCTDPNSLGGQPLGGPSR 2190
Db 2160 DLKKCYSVAEQSCORRRPGSWLDEQRRHSIAVSCLDGSGQPHLCPSPSSLGGQPLGGPSR 2219
QY 2191 PKKKLSPPSITIDPPESQGPRTPPSPGICLRRAPSSDSKDPLASGPPDSMAASPPSKD 2250
Db 2220 PKKKLSPPSISIDPPESQGPRTPPSPGICLRRAPSSDSKDPLASGPPDSMAASPPSKD 2279
QY 2251 VLISLGLSSDDPADLDP 2266

Db 2280 ALSLSGLSSDPTDLDP 2295
RESULT 3
Q9WUB8
ID Q9WUB8 PRELIMINARY; PRT; 2288 AA.
AC Q9WUB8;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE T-type calcium channel isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=20081696; PubMed=10615950;
RA Zhuang H., Bhattacharjee A., Hu F., Zhang M., Goswami T., Wang L.,
RA Wu S., Berggren P.O., Li M.;
RT "Cloning of a T-type Ca2+ channel isoform in insulin-secreting
cells";
RL Diabetes 49:59-64 (2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
family.
DR EMBL; AF125161; AAD26858.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR002077; Ca_channel_alpha.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR005445; TVDCCAlphal.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00167; CACHANNEL.
DR PRINTS; PR01629; TVDCCALPHA1.
KW Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KW Transmembrane; Transport; Voltage-gated channel.
SQ SEQUENCE 2288 AA; 253476 MW; B89DBB5A1D81757F CRC64;
Query Match 93.3%; Score 11111; DB 2; Length 2288;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2135; Conservative 35; Mismatches 95; Indels 24; Gaps 5;
QY 1 MDEEDGAGAEESGQPRSFMRNLNLSGAGRGPGSAEKDPGSADSEAEGLPYPALAPVV 60
Db 1 MDEEDGAGAEESGQPRSFMRNLNLSGAGRGPGSAEKDPGSADSEAEGLPYPALAPVV 60
QY 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIACDSQRCRILQAF 120
Db 61 FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLMFRPCEDIACDSQRCRILQAF 120
QY 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVFSAVR 180
Db 121 DDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVFSAVR 180
QY 181 TVRVLRLRAINRVPSMRILVTLLLDLTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
Db 181 TVRVLRLRAINRVPSMRILVTLLLDLTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLNR 240
QY 241 CFLPENFSLPLSVDLERYYQ TENEDESPFCISQPRENMRSCRVP TLRGDGGGPPCGL 300
Db 241 CFLPENFSLPLSVDLERYYQ TENEDESPFCISQPRENMRSCRVP TLRGE GGGPPCSL 300
QY 301 DYEAYNSSNTTCVNWNOY YTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIM 360

Db	1381	VLRLRLRLRPLRVISRAQGLKLVVETLMSSSLKPIGNIWVICCAFFIIFGILGVQLFKGKF	1440
QY	1439	FVCQGEDTRNITNKSDCAEASRWRHXYNFNDNLGQALMSLFVLASKDQWVDIMYDGLDA	1498
Db	1441	FVCQGEDTRNITNKSDCAEASRWRHXYNFNDNLGQALMSLFVLASKDQWVDIMYDGLDA	1500
QY	1499	VGVDQQPIMHNPNWMLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQHEEEARRRREK	1558
Db	1501	VGVDQQPIMHNPNWMLLYFISFLLIIVAFVLMFVGVVVENFHKCRHQHEEEARRRREK	1560
QY	1559	RLRRLEKRR-----KAOCKPYYSYDSRFRLLVHHLCTSHYLDLFT	1600
Db	1561	RLRRLEKRRNMLDDVIASGSSASAASEAOCKPYYSYDSRFRLLVHHLCTSHYLDLFT	1620
QY	1601	GVIGLNVVTMAMEHYQQPILDEALKICNYITFTVIFVLESVFKLVAFGRFRFFQDRWNQL	1660
Db	1621	GVIGLNVVTMAMEHYQQPILDEALKICNYITFTVIFVLESVFKLVAFGRFRFFQDRWNQL	1680
QY	1661	DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRARVLKLLKMAVGMRALDVTMQ	1720
Db	1681	DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRARVLKLLKMAVGMRALDVTMQ	1740
QY	1721	ALPQVGNLGLLFMLFFIPAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRV	1780
Db	1741	ALPQVGNLGLLFMLFFIPAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTFRV	1800
QY	1781	STGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVVIAMKHEESN	1840
Db	1801	STGDNWNGIMKDTLRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVVIAMKHEESN	1860
QY	1841	KEAKEAEAELEMEKTLSPQPHSPGSPFPLWPGVEGSDSPSPKPGALHAAHARS	1900
Db	1861	KEAKEAEAELEMEKTLSPQPHSPGSPFPLWPGVEGSDSPSPKPGAPHTTAHIGAA	1920
QY	1901	SHFSLHPTMQPHPTLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGLHGRG	1957
Db	1921	SGFSLHPTMVPHPEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAEGLHGRG	1980
QY	1958	WGLPKAQSGLSVHSQPADTSTVILQPKDAPHLLQPHSAPTWTGTPKLPFGPSPLAQ	2017
Db	1981	WGLPKAQSGLSVHSQPADTSTVILQPKDAPHLLQPHSAPTWTGTPKLPFGPSPLAQ	2040
QY	2018	PLRRQAIRTDSDLVQGLGSRDLAEVSGPSPPLARAYFWQSSSTQAQQHSHRSKIS	2077
Db	2041	PLRRQAIRTDSDLVQGLGSRDLAEVSGPSPPLARAYFWQSSSTQAQQHSHRSKIS	2100
QY	2078	KHMTTPAPCPGPEPNWGKPPETRSLELDTLSWISGDLPPGGQEEPPSPRDLKKCY	2137
Db	2101	KHIRLPAPCPGLEPSWAKDPPETRSLELDTLSWISGDLPPGGQEEPPSPRDLKKCY	2159
QY	2138	VEAQSCQRRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDPNGLGGQPLGGPSRPPKKLSP	2197
Db	2160	VETQSCRRRPGSWLDEQRRHSIAVSCLDGSGQPHLGTDPNGLGGQPLGGPSRPPKKLSP	2219
QY	2198	PSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPPLASGPPDSMAASPPKDVLSGL	2257
Db	2220	PSISIDPPESQGSRRPPCSPGVCLRRRAPASDSKDPSSVSSPLDSTAASPPKDTLSGL	2279
QY	2258	SSDPADLDP	2266
Db	2280	SSDPTMDP	2288

RESULT 4

CCAG RAT	STANDARD;	PRT;	2254 AA.
ID-CCAG RAT			
AC	O54898;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Voltage-dependent T-type calcium channel alpha-1G subunit (Voltage-gated calcium channel alpha subunit Cav3.1).		
GN	Name=Cacna1g;		

Db	301	DYETYNSSNTTCVNWNYTNCAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM	360
QY	361	YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMRQVRFLSNA	420
Db	361	YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMRQVRFLSNA	420
QY	421	STLASFSEPGSCYEELLKYLVIILRKAARLQAQVRAAGVRVGLLSSPAPLGGQETQPS	480
Db	421	STLASFSEPGSCYEELLKYLVIILRKAARLQAQVRAAGVRVGLLSSPAPLGGQETQPS	480
QY	481	SCSRSHRRLSVHLLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPPSTP	540
Db	481	SCSRSHRRLSVHLLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPPSTP	540
QY	541	ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE	600
Db	541	TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVSGKVYPTVHTSPPE	600
QY	601	TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG	660
Db	601	ILKDKALVEVAPSPGPTLTSLNIPPGPYSSMHKLLETQSTGACHSSCKISSPCLKADSG	660
QY	661	ACGPDSCPYCARAGAGEVELADREMPDSSEAVYEFTQDAQHSDLRDPHS--RRQRS	719
Db	661	ACGPDSCPYCARTGAGEPESADHVPMPDSSEAVYEFTQDAQHSDLRDPHSRRQRS	720
QY	720	AEPSSVLAFWRLLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN	779
Db	721	AEPSSVLAFWRLLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN	780
QY	780	IVFTSLFALEMLLKLIVGPFYIKNPYNIFDGVIVVTSWEIVGQGGGLSVLRTFRM	839
Db	781	IVFTSLFALEMLLKLIVGPFYIKNPYNIFDGVIVVTSWEIVGQGGGLSVLRTFRM	840
QY	840	RVLKLVRLPALQRLVLMKTMNDVATFCMLLMFLIFIPSLGMHLFGCKFASERDGD	899
Db	841	RVLKLVRLPALQRLVLMKTMNDVATFCMLLMFLIFIPSLGMHLFGCKFASERDGD	900
QY	900	LPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL	959
Db	901	LPDRKNFDSLLWAIIVTFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL	960
QY	960	VAILVEGFQAEHISKREDASQGLSCIQLPVDSQGGDANKSESEPDDFFSPSLDGDGRKK	1019
Db	961	VAILVEGFQAEHISKREDASQGLSCIQLPVNSQGGDATKSESEPDDFFSPSLDGDGRKK	1020
QY	1020	LALVSLGEHPELRKSLPLPILIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGA	1079
Db	1021	LALVALGEHAEELRKSLLPPLIIHTAATPMSLPKSSSTGVGEALGSGRRRTSSSGSAEPGA	1080
QY	1080	A-HEMKSPPSARSPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLS	1138
Db	1081	AHEMKSPPSARSPHSPWSAASSWTSRRSRNSLGRAPSLKRSPSGERRSLLS	1140
QY	1139	SQDEEESSEERASGPDHRRHGRSLEREAKSSFDLPDTLQVPLHRTASGRGSASEHQD	1198
Db	1141	SQDEEESSEEDRASGPDHRRHGRSLEREAKSSFDLPDTLQVPLHRTASGRSSASEHQD	1200
QY	1199	CNGKSASGLRALRPDDPPLDGDADDDEGNLSKGERVRAWIRARLPACYLERSWSAYI	1258
Db	1201	CNGKSASGLARTLRDTPQLDGDADDDEGNLSKGERIQAWVRSRLPACCRERSWSAYI	1260
QY	1259	FPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1318
Db	1261	FPQSRFRLLCHRIITHKMFHDHVVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1320
QY	1319	AVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLVLISVIDILVMSVSDSGTKILGMLR	1378
Db	1321	AVFLAEMTVKVALGWCFCGEQAYLRSSWNVDGLVLISVIDILVMSVSDSGTKILGMLR	1380
QY	1379	VLRLRLRLRPLRVISRAQGLKLVVETLMSSSLKPIGNIWVICCAFFIIFGILGVQLFKGKF	1438

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98154730; PubMed=9495342;
RA Perez-Reyes E., Cribbs L.L., Daud A., Lacerda A.E., Barclay J.,
RA Williamson M.P., Fox M., Rees M., Lee J.-H.;
RT "Molecular characterization of a neuronal low-voltage-activated T-type
RL calcium channel.";
RL Nature 391:896-900(1998).
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC entry of calcium ions into excitable cells and are also involved
CC in a variety of calcium-dependent processes, including muscle
CC contraction, hormone or neurotransmitter release, gene expression,
CC cell motility, cell division and cell death. The isoform alpha-1G
CC gives rise to T-type calcium currents. T-type calcium channels
CC belong to the "low-voltage activated (LVA)" group and are strongly
CC blocked by nickel and mibefradil. A particularity of this type of
CC channels is an opening at quite negative potentials and a voltage-
CC dependent inactivation. T-type channels serve pacemaking functions
CC in both central neurons and cardiac nodal cells and support
CC calcium signaling in secretory cells and vascular smooth muscle.
CC They may also be involved in the modulation of firing patterns of
CC neurons which is important for information processing as well as
CC in cell growth processes.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Moderate expression
CC in heart; low expression in placenta, kidney and lung.
CC -!- DOMAIN: Each of the four internal repeats contains five
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC positively charged transmembrane segment (S4). S4 segments
CC probably represent the voltage-sensor and are characterized by a
CC series of positively charged amino acids at every third position.
CC -!- PTM: In response to raising of intracellular calcium, the T-type
CC channels are activated by CaM-kinase II.
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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DR EMBL; AF027984; AAC67372.1; -.
DR PIR; T09053; T09053.
DR RGD; 68942; Cacnal9.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF005445; TVDCCalpha1.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR01629; TVDCCALPHA1.
KW Calcium channel; Calcium-binding; Glycoprotein; Ion transport;
KW Ionic channel; Multigene family; Phosphorylation; Repeat;
KW Transmembrane; Voltage-gated channel.
FT REPEAT 68 398 I.
FT REPEAT 730 968 II.
FT REPEAT 1242 1519 III.
FT REPEAT 1564 1822 IV.
FT DOMAIN 1 80 Cytoplasmic (Potential).
FT TRANSMEM 81 101 S1 of repeat I.
FT DOMAIN 102 119 Extracellular (Potential).
FT TRANSMEM 120 141 S2 of repeat I (Potential).
FT DOMAIN 142 150 Cytoplasmic (Potential).
FT TRANSMEM 151 170 S3 of repeat I.
FT DOMAIN 171 175 Extracellular (Potential).

FT	TRANSMEM	176	193	S4 of repeat I.
FT	DOMAIN	194	213	Cytoplasmic (Potential).
FT	TRANSMEM	214	234	S5 of repeat I (Potential).
FT	DOMAIN	235	370	Extracellular (Potential).
FT	TRANSMEM	371	395	S6 of repeat I.
FT	DOMAIN	396	744	Cytoplasmic (Potential).
FT	TRANSMEM	745	765	S1 of repeat II (Potential).
FT	DOMAIN	766	778	Extracellular (Potential).
FT	TRANSMEM	779	800	S2 of repeat II (Potential).
FT	DOMAIN	801	806	Cytoplasmic (Potential).
FT	TRANSMEM	807	825	S3 of repeat II (Potential).
FT	DOMAIN	826	833	Extracellular (Potential).
FT	TRANSMEM	834	857	S4 of repeat II (Potential).
FT	DOMAIN	858	868	Cytoplasmic (Potential).
FT	TRANSMEM	869	889	S5 of repeat II (Potential).
FT	DOMAIN	890	940	Extracellular (Potential).
FT	TRANSMEM	941	965	S6 of repeat II (Potential).
FT	DOMAIN	966	1251	Cytoplasmic (Potential).
FT	TRANSMEM	1252	1274	S1 of repeat III (Potential).
FT	DOMAIN	1275	1292	Extracellular (Potential).
FT	TRANSMEM	1293	1313	S2 of repeat III (Potential).
FT	DOMAIN	1314	1323	Cytoplasmic (Potential).
FT	TRANSMEM	1324	1343	S3 of repeat III (Potential).
FT	DOMAIN	1344	1357	Extracellular (Potential).
FT	TRANSMEM	1358	1379	S4 of repeat III (Potential).
FT	DOMAIN	1380	1389	Cytoplasmic (Potential).
FT	TRANSMEM	1390	1413	S5 of repeat III (Potential).
FT	DOMAIN	1414	1490	Extracellular (Potential).
FT	TRANSMEM	1491	1516	S6 of repeat III (Potential).
FT	DOMAIN	1517	1578	Cytoplasmic (Potential).
FT	TRANSMEM	1579	1599	S1 of repeat IV (Potential).
FT	DOMAIN	1600	1613	Extracellular (Potential).
FT	TRANSMEM	1614	1635	S2 of repeat IV (Potential).
FT	DOMAIN	1636	1642	Cytoplasmic (Potential).
FT	TRANSMEM	1643	1661	S3 of repeat IV (Potential).
FT	DOMAIN	1662	1675	Extracellular (Potential).
FT	TRANSMEM	1676	1699	S4 of repeat IV (Potential).
FT	DOMAIN	1700	1713	Cytoplasmic (Potential).
FT	TRANSMEM	1714	1734	S5 of repeat IV (Potential).
FT	DOMAIN	1735	1794	Extracellular (Potential).
FT	TRANSMEM	1795	1822	S6 of repeat IV (Potential).
FT	DOMAIN	1823	2254	Cytoplasmic (Potential).
FT	TRANSMEM	290	295	Poly-Gly.
FT	DOMAIN	496	506	Poly-His.
FT	TRANSMEM	1527	1530	Poly-Glu.
FT	SITE	354	354	Calcium ion selectivity and permeability (By similarity).
FT	SITE	924	924	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1465	1465	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1770	1770	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	173	173	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	246	246	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	306	306	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	310	310	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	322	322	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1427	1427	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1430	1430	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1666	1666	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	2254 AA;	250405 MW;	697BBE06360CF0F6 CRC64;

Query Match 91.9%; Score 10945; DB 1; Length 2254;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2107; Conservative 34; Mismatches 101; Indels 36; Gaps 6;

Qy	1	MDEEDGAGAEESGQPRSFMRNLDSLGGRRPGSGAEKDPGSADSEAEGLPYPALAPVV	60
Db	1	MDEEDGAGAEESGQPRSFQNLDSLGGRRPGSGTEKDPGSADSEAEGLPYPALAPVV	60
Qy	61	FFYLSQDSRPRSWCLRTVCNPWFERISMLVILLNCVTGLMFPCEDIACDSQRCRILOAF	120

Db	61	FFYLSQDSRPRSWCLRTVCNPFWRVSMVLVLLNCVTGLMFRPCEDIACDQSQRILQAF	120
Qy	121	DDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRDLDFIIVIAAGMLEYSLDLQNVFSAVR	180
Db	121	DDFIFAFFAVEMVVMVALGIFGKKCYLGDTWNRDLDFIIVIAAGMLEYSLDLQNVFSAVR	180
Qy	181	TVRVLRLRAINRVPMSRILVTLTLLDTPMLGNVLLLCFFVFFIFIGIVGVQVLWAGLLNR	240
Db	181	TVRVLRLRAINRVPMSRILVTLTLLDTPMLGNVLLLCFFVFFIFIGIVGVQVLWAGLLNR	240
Qy	241	CFLPENFSLPLSVDLERYQTENEDESPFCISQPRENGMRSCRVPTRLRGDGGGPPCGL	300
Db	241	CFLPENFSLPLSVDLERYQTENEDESPFCISQPRENGMRSCRVPTRLRGDGGGPPCGL	300
Qy	301	DYEAYNSSNTTCVWNQYTYNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM	360
Db	301	DYETYNSSNTTCVWNQYTYNCSAGEHNPFGKAINFDNIGYAWIAIFQVITLEGWVDIM	360
Qy	361	YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREBQVRFLSNA	420
Db	361	YFVMDAHSFYNFYIFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREBQVRFLSNA	420
Qy	421	STLASFSEPGSCYEBELLKYLVIILKAARLAQVSRAGVRVGLLSSPAPLGGQETQPSS	480
Db	421	STLASFSEPGSCYEBELLKYLVIILKAARLAQVSRAGVRVGLLSSPAPLGGQETQPSS	480
Qy	481	SCSRSHRRLSVHHLVHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTP	540
Db	481	SCTRSHRRLSVHHLVHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTP	540
Qy	541	ALSGAPPGAEVSHSFYHADCHLEBPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPE	600
Db	541	TPSGGPPRGAESVHSFYHADCHLEBPVRCQAPPPRSPSEASGRTVGSGKVYPTVHTSPPE	600
Qy	601	TLKEKALVEVAASSGPPTLTLSLNPYPGYSMMHKLLETQSTGACQSSCKISSPCLKADSG	660
Db	601	ILKDKALVEVAPSPGPPTLTLSFNIPGPFSSMMHKLLETQSTGACHSSCKISSPCKADSG	660
Qy	661	ACGPDSCPCYCARAGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDEHS-RRQRSIGPD	719
Db	661	ACGPDSCPCYARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHSRRRQRSIGPD	720
Qy	720	AEPSSVLAFWRLICDTRKIVDSKYFGGIMIAILLVNTLSMGIEYHQPEELTNALIEISN	779
Db	721	AEPSSVLAFWRLICDTRKIVDSKYFGGIMIAILLVNTLSMGIEYHQPEELTNALIEISN	780
Qy	780	IVFTSLFALEMMLKLLVYGPFGYIKNPYNIPDGVIIVISVWEIVGQGGGLSVLRFELM	839
Db	781	IVFTSLFALEMMLKLLVYGPFGYIKNPYNIPDGVIIVISVWEIVGQGGGLSVLRFELM	840
Qy	840	RVLKLVRLPALQRLVVLMTMDNVATFCMLLMFLIFIFSILGMHLFGCKFASERDGT	899
Db	841	RVLKLVRLPALQRLVVLMTMDNVATFCMLLMFLIFIFSILGMHLFGCKFASERDGT	900
Qy	900	LPDRKNFDSLWAIWTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL	959
Db	901	LPDRKNFDSLWAIWTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL	960
Qy	960	VAILVEGFQAEHIEISKREDASGQLSCIQLPVDSDQGDANKSESEPDFFSPSLDGDGRKKC	1019
Db	961	VAILVEGFQAE-----GDATKSESEPDFFSPSVLDGDGRKKR	997
Qy	1020	LALVSLGEHPELRLKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRTSSSGSAEPGA	1079
Db	998	LALVALGEHAELRLKSLPLLIHTAATPMSHPKSSSTGVGEALGSGRRTSSSGSAEPGA	1057
Qy	1080	A-HEMKSPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE	1138
Db	1058	AHEMKCPPSARSSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE	1117
Qy	1139	SQDEEESSEERASAPGSDHRHSGSLEREAKSFDLPDTLQVPLGLHRTASGRGSASEHQD	1198
Db	1118	SQDEEESSEEDRASAPGSDHRHSGSLEREAKSFDLPDTLQVPLGLHRTASGRSSASEHQD	1177

Qy	1199	CNGKSASGRLARALRPDDPLDGDADDDEGNLSKGERVRAWIRARLPACYLERSWSAYI	1258
Db	1178	CNGKSASGRLARALRTDDPQLDGDNDDEGNLSKGERIQAWRSRLPACCRERDSWSAYI	1237
Qy	1259	FPQOSRFRLLCHRIITHKMFEDHVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1318
Db	1238	FPQOSRFRLLCHRIITHKMFEDHVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1297
Qy	1319	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVSMVSDSGTKILGMLR	1378
Db	1298	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDDLVLISVIDILVSMVSDSGTKILGMLR	1357
Qy	1379	VLRLRLRLPLRVISRAQGLKLVVETILMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF	1438
Db	1358	VLRLRLRLPLRVISRAQGLKLVVETILMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKF	1417
Qy	1439	FVCOGEDTRNITNKSDCAEASRWRVKYNFNQLGQALMSLFLVASKDGVDMIMYDGLDA	1498
Db	1418	FVCOGEDTRNITNKSDCAEASRWRVKYNFNQLGQALMSLFLVASKDGVDMIMYDGLDA	1477
Qy	1499	VGVDQOPIMNHNPMWLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEARRREEK	1558
Db	1478	VGVDQOPIMNHNPMWLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEARRREEK	1537
Qy	1559	RLRLLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLNVVTMA	1611
Db	1538	RLRLLEKKRRSKEQMAEAOCKPYSDYSRFRLLVHHLCTSHYLDLFTITGVIGLNVVTMA	1597
Qy	1612	MEHYQOPQILDEALKICNYITFVIFVLESVFKLVAFGPRRFFQDRWNQDLAIALLSIMG	1671
Db	1598	MEHYQOPQILDEALKICNYITFVIFVLESVFKLVAFGPRRFFQDRWNQDLAIALLSIMG	1657
Qy	1672	ITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDITVMQALPQVGNLGLL	1731
Db	1658	ITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLDITVMQALPQVGNLGLL	1717
Qy	1732	FMLLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK	1791
Db	1718	FMLLFFIFAALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK	1777
Qy	1792	DTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEAEAELEA	1851
Db	1778	DTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVIAVLMKHLEESNKEAEAELEA	1837
Qy	1852	ELELEMKTLSPQSPHSPGLSPFPLWPGVEGPDSPDKPGALHPAAHARSASHFSLEHTMQ	1911
Db	1838	ELELEMKTLSPQSPHSPGLSPFPLWPGVEGVDSTDPKPGAPHTTAHIGAASGFSLEHTMV	1897
Qy	1912	PHPTLPP---GPDLLTVRKSGVSRTHSLPNDSYMCRRHSGSTAEGLPHGRGWGLPKAQSGSV	1968
Db	1898	PHPEEVPLGPDLLTVRKSGVSRTHSLPNDSYMCRRHSGSTAEGLPHGRGWGLPKAQSGSI	1957
Qy	1969	LSVHSQPADTSYILQPKDAPHLLQPHSAPTWTGTIPKLPPPGSPPLAQRPLRQAIRTD	2028
Db	1958	LSVHSQPADTSYILQPKDAPHLLQPHSAPTWTGTIPKLPPPGSPPLAQRPLRQAIRTD	2017
Qy	2029	SLDVQGLGSRREDLLAEVSGSPPLARAYSWGQSSSTQAQQRHSHSKISKHMTTPPAPCPG	2088
Db	2018	SLDVQGLGSRREDLLSEVSGSPCLTRSSSWGSSSIQVQQRSGIQSKVSKHIRLPAPCPG	2077
Qy	2089	PEPNWKGPPETRSSLELDTLSWISGDLPPGGQEPPSPRDLKKCYSEVAQSCQRRPT	2148
Db	2078	LEPSWAKDPPETRSSLELDTLSWISGDLT-PSSQEELFPRLDKKCYSEVETQSCRRRP	2136
Qy	2149	SWLDEQRRHSIAVSCLDSDSGQPHLGTDPNLSGQPLGGPSRPPKKLSPPSITIDPPESQ	2208
Db	2137	FWLDEQRRHSIAVSCLDSDSGQPLCPSPSSILGGQPLGGPSRPPKKLSPPSISIDPPESQ	2196
Qy	2209	GPRTPPSPGICLRRRAPSSDSKDPPLASGPPDMSMAASPPKQDLVLSLGLSSDPADLDP	2266
Db	2197	GSRPSPGICLRRRAPSSDSKDPVSSPLDSTAASPPKKOTLSLGLSSDPTDMDP	2254

RESULT 5									
AAG35186									
ID	AAG35186	PRELIMINARY;	PRT;	2254	AA.				
AC	AAG35186;								
DT	02-MAR-2004	(TrEMBLrel. 27, Created)							
DT	02-MAR-2004	(TrEMBLrel. 27, last sequence update)							
DT	02-MAR-2004	(TrEMBLrel. 27, Last annotation update)							
DE	Calcium channel alpha-1-G subunit.								
OS	Rattus norvegicus (Rat).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.								
OX	NCBI_TaxID=10116;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=brain;								
RX	PubMed=11073957;								
RA	McRory J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G.,								
RA	Baillie D.L., Stea A., Snutch T.P.;								
RT	"Molecular and functional characterization of a family of rat brain T-								
RT	type calcium channels.";								
RL	J. Biol. Chem. 276:3999-4011(2001).								
DR	EMBL; AF290212; AAG35186.2; -.								
SQ	SEQUENCE 2254 AA; 250405 MW; 697BBE06360CF0F6 CRC64;								
Query Match									
Best Local Similarity 91.9%; Score 10945; DB 2; Length 2254;									
Matches 2107; Conservative 34; Mismatches 101; Indels 36; Gaps 6;									
QY	1	MDEEEDGAGAEESGQPRSFMRNLDSGAGRPGGSAEKDPGSADSEAEGLYPALAPVW	60						
Db	1	MDEEEDGAGAEESGQPRSFMTQLNDLSGAGGRQGGSTEXDKDPGSADSEAEGLYPALAPVW	60						
QY	61	FFYLSQDSRPRSWCLRTVCNPNWFERISMLVILLNCVTILGMFRPCEDIACDSQRCRILQAF	120						
Db	61	FFYLSQDSRPRSWCLRTVCNPNWFERVSMVLVILLNCVTILGMFRPCEDIACDSQRCRILQAF	120						
QY	121	DDFIFAFPAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIAGMLEYSLDLQNVSFSAVR	180						
Db	121	DDFIFAFPAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIAGMLEYSLDLQNVSFSAVR	180						
QY	181	TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR	240						
Db	181	TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNR	240						
QY	241	CFLPENFSLPLSVDLERYQYOTENEDESPFICSQPRENGMRSCRSVPTLRDGGGGPPCGL	300						
Db	241	CFLPENFSLPLSVDLEPYQYOTENEDESPFICSQPRENGMRSCRSVPTLRGEGGGPPCSL	300						
QY	301	DYEAYNSSNTTCVNNWQYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM	360						
Db	301	DYETYNSSNTTCVNNWQYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM	360						
QY	361	YFVMDAHSFYNFIFYILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420						
Db	361	YFVMDAHSFYNFIFYILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420						
QY	421	STLASFSEPGSCYEELLKYLVIILRKAARLAQVSRAGVRVGLLSSPAPLGQEQTPSS	480						
Db	421	STLASFSEPGSCYEELLKYLVIILRKAARLAQVSRAGVIRAGLLSSPVARSQEQPQPSG	480						
QY	481	SCSRSHRRLSVHHLVHHHHHHHHYHLNGTILRAPRASPEIQDRDANGSRRLMLPPSTP	540						
Db	481	SCTRSHRRLSVHHLVHHHHHHHHYHLNGTILRVPRASPEIQDRDANGSRRLMLPPSTP	540						
QY	541	ALSGAPPGAESVHSFYHADCHLEPVRCAQPPRSPSEASGRTVGSGKYPTVHTSPPPE	600						
Db	541	TPSGGPPRGAESVHSFYHADCHLEPVRCAQPPRCPSEASGRTVGSGKYPTVHTSPPPE	600						
QY	601	TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG	660						
Db	601	ILKDKALVEVAPSGPPTLTSTFNIPPGPFSSMHKLLETQSTGACHSSCKISSPCKADSG	660						

QY	661	ACGPDSCPYCARAGAVEVELADREMPDSDSEAVYEFTQDAQHSIDLDPHS-RRQRSGLPD	719						
Db	661	ACGPDSCPYCARTGAGEPESADHVMPDSDSEAVYEFTQDAQHSIDLDPHSRRRQRSGLPD	720						
QY	720	AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN	779						
Db	721	AEPSSVLAFWRLICDTFRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISN	780						
QY	780	IVFTSLFALEMLLKLLVYGPFGYIKPNYNIFDGVIVVISWEIVGQGGGLSVLRTFRILM	839						
Db	781	IVFTSLFALEMLLKLLVYGPFGYIKPNYNIFDGVIVVISWEIVGQGGGLSVLRTFRILM	840						
QY	840	RVLKLVRFLEPALQRQLVVLMTMDNVATFCMLLMLFIFIFSTILGMHLFGCKFASERDGT	899						
Db	841	RVLKLVRFLEPALQRQLVVLMTMDNVATFCMLLMLFIFIFSTILGMHLFGCKFASERDGT	900						
QY	900	LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL	959						
Db	901	LPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLL	960						
QY	960	VAILVEGFAEIEISKREDASGQLSCIQLPVDVSQGGDANKSESEPDFFSPSLDGDGRKKC	1019						
Db	961	VAILVEGFAE-----GDATAKSESEPDFFSPSVGDGRKKR	997						
QY	1020	LALVSLGEHPELRKSLPLPLIHTAATPMSLPKSTSTGLGEALGPASRRTSSGSAEPGA	1079						
Db	998	LALVALGEHAELRKSLPLPLIHTAATPMHPKSSSTGVGEALGSGRRRTSSGSAEPGA	1057						
QY	1080	A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE	1138						
Db	1058	AHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQE	1117						
QY	1139	SQDEESSEERASPAGSDHHRHGSLEREAKSSFDLPDTLQVPLHRTASGRGSAEHQD	1198						
Db	1118	SQDEESSEEDRASPAGSDHHRHGSLEREAKSSFDLPDTLQVPLHRTASGRGSAEHQD	1177						
QY	1199	CNGKSASGRLARALRPDDPPLDGDADDDEGNLSKGERVRAWRARLPACYLERDSWSAYI	1258						
Db	1178	CNGKSASGRLARTLRDTPDQDGDNDDEGNLSKGERIQAWVRSLPACORERDSWSAYI	1237						
QY	1259	FPPQSRFRLLCHRIITHKMFHDVVLVIIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFT	1318						
Db	1238	FPPQSRFRLLCHRIITHKMFHDVVLVIIIFLNCITIAMERP KIDPHSAERIFLTLSNYIFT	1297						
QY	1319	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLVLISVIDILVSMVSDSGTKILGMLR	1378						
Db	1298	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLVLISVIDILVSMVSDSGTKILGMLR	1357						
QY	1379	VLRLRLRLPLRVISRAQGLKLVVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKGKF	1438						
Db	1358	VLRLRLRLPLRVISRAQGLKLVVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKGKF	1417						
QY	1439	FVQGEDTRNITNKSDCAEAS YRWRHKYNFEDNLGQALMSLFVLASKDGWVDIMYDGLDA	1498						
Db	1418	FVQGEDTRNITNKSDCAEAS YRWRHKYNFEDNLGQALMSLFVLASKDGWVDIMYDGLDA	1477						
QY	1499	VGVDQQPIMNHNPMWLLYFISFLLIIVAFFVLNMVGVVVENFHKCRQHQQEERREEK	1558						
Db	1478	VGVDQQPIMNHNPMWLLYFISFLLIIVAFFVLNMVGVVVENFHKCRQHQQEERREEK	1537						
QY	1559	RLRRLEKKRR-----KAQCKPYYSYSRFRLLVHHLCTSHYLDLFTIGVIGLVVVTMA	1611						
Db	1538	RLRRLEKKRRSKEQMAEAQCKPYYSYSRFRLLVHHLCTSHYLDLFTIGVIGLVVVTMA	1597						
QY	1612	MEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLDAIVLLSIMG	1671						
Db	1598	MEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGRFRFFQDRWNQDLDAIVLLSIMG	1657						
QY	1672	ITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALDITVMQALPOVGNLGLL	1731						
Db	1658	ITLEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALDITVMQALPOVGNLGLL	1717						
QY	1732	FMLLFFIFAALGVLELFGDLECDETHCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK	1791						

Db	1718	FMLLFFFAALGVFLFDLECDETHPCCEGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMK	1777
QY	1792	DTLRDCDQESTCYNTVTSPIYFVSFVLTAQFVLNVVIAVLMKHLESNKEAKEAELEA	1851
Db	1778	DTLRDCDQESTCYNTVTSPIYFVSFVLTAQFVLNVVIAVLMKHLESNKEAKEAELEA	1837
QY	1852	ELEEMKTLSPQHPSPGLSPFLWPVGEGPDSPPSPKPGALHPAAHARSASHFSLEHPTMQ	1911
Db	1838	ELEEMKTLSPQHPSPGLSPFLWPVGEGVNSDTPKPGAPHTTAHIGAASGFSLEHPTMV	1897
QY	1912	PHPTPELPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGLCHRGWGLPKAQSGSV	1968
Db	1898	PHPEVPVPLPGPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGLCHRGWGLPKAQSGSI	1957
QY	1969	LSVHSQPADTSYIQLPKDAPHLLQPHSAPTWTGTPKLPPPGRSPLAQRLRRQAIRTD	2028
Db	1958	LSVHSQPADTSCILQPKDVHYLLQPHGAPTWGALPKLPPPGRSPLAQRLRRQAIRTD	2017
QY	2029	SLDVQGLGSRDLAEVSGSPPLARAYFWGQSSTQAQOHSRSHSKISKHMTPPAPCPG	2088
Db	2018	SLDVQGLGSRDLSEVSGSPCLTRSSSFVGGSSIQVQQRSGIQSKVSHIRLPAPCPG	2077
QY	2089	PEPNWKGPPETRSSLELDTLSWISGDLPPGGQEBPPSPRDLKKCYVFAQSCQRRPT	2148
Db	2078	LEPSWAKDPETRSSLELDTLSWISGDLPPSSQEEELFPRDLKKCYVFAQSCQRRPG	2136
QY	2149	SWLDEQRHSHIAVSCLDGSGQHILGTDPSNLGGQPLGGPGSRPKKLSPPSITIDPPESQ	2208
Db	2137	FWLDEQRHSHIAVSCLDGSGQPLCPSPSSLGQPLGGPGSRPKKLSPPSISIDPPESQ	2196
QY	2209	GPRTSPSGICLRRRAPSSDKDPLASGPPDSMAASPKKDVLSGLSSDDPADLDP	2266
Db	2197	GSRPPCGVCLRRRAPASDSKDPSSVSSPLDSTAASPKKDTLSGLSSDDPTMDP	2254
RESULT 6			
Q6PFV8			
ID	Q6PFV8	PRELIMINARY;	PRT; 2248 AA.
AC	Q6PFV8;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Cacnalg protein.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=Brain;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Sodergren E.J., Lu X., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		

RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=Brain;		
RA	Strausberg R.;		
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBDJ databases.		
DR	EMBL; BC057399; AAH57399.1; -.		
DR	GO; GO:0005886; C:plasma membrane; IDA.		
DR	GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.		
DR	InterPro; IPR001682; Ca/Na_pore.		
DR	InterPro; IPR002111; Cat_channel_TrpL.		
DR	InterPro; IPR005821; Ion_trans.		
DR	InterPro; IPR005820; M+channel_nlg.		
DR	InterPro; IPR005445; TVDCCAlphal.		
DR	Pfam; PF00520; Ion_trans; 4.		
DR	PRINTS; PR01629; TVDCCALPHAL.		
KW	Ion transport; Ionic channel; Transmembrane; Transport.		
SQ	SEQUENCE 2248 AA; 248888 MW; 332C5A8D9115A64F CRC64;		
Query Match	91.7%;	Score 10913;	DB 2; Length 2248;
Best Local Similarity	92.0%;	Pred. No. 0;	
Matches 2106;	Conservative 30;	Mismatches 89;	Indels 64; Gaps 7;
QY	1	MDEEDGAGAEESGQPRSPMRLNDLSGAGRPGCGSAEKDPGSADSEAEGLPYPALAPVV	60
Db	1	MDEEDGAGAEESGQPRSFQNDLSGAGRQGPSTGKDPGSADSEAEGLPYPALAPVV	60
QY	61	FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF	120
Db	61	FFYLSQDSRPRSWCLRTVCNPFWRISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAF	120
QY	121	DDFTFAFFAVEMVVMVVALGIFGKKCYLGDTWNRLDFFIVIAAGMLEYSLDLQNVFSFSAVR	180
Db	121	DDFTFAFFAVEMVVMVVALGIFGKKCYLGDTWNRLDFFIVIAAGMLEYSLDLQNVFSFSAVR	180
QY	181	TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLCFVFFIFGIVGVQLWAGLLNR	240
Db	181	TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLCFVFFIFGIVGVQLWAGLLNR	240
QY	241	CFLPENFSLPSVDLERYVQTEDESPFICSPRENGMRSCRVPVTLRGDGGGPPCGL	300
Db	241	CFLPENFSLPSVDLEPYVQTEDESPFICSPRENGMRSCRVPVTLRGDGGGPPCGL	300
QY	301	DYEAYNSSNTTCVNNQYTYNCSAGEHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIM	360
Db	301	DYEAYNSSNTTCVNNQYTYNCSAGEHNPFKGAINFNDNIGYAWIAIFQVITLEGWVDIM	360
QY	361	YFVMDAHSFYNIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNA	420
Db	361	YFVMDAHSFYNIYFILLII-----FSETKQRESQLMREQVRFLSNA	403
QY	421	STLASFSEPGSCYEELLYLKYVILRKAARRLAQVSRAAGVRVGLSSPAPLGGQETQPS	480
Db	404	STLASFSEPGSCYEELLYLKYVILRKAARRLAQVSRAAGVRVGLSSPAPLGGQETQPS	463
QY	481	SCSRSHRRLSVHHLVHHHHHHHHHVLGNGTTLRAPRASPEIQDRDANGSRRLMLPPSTP	540
Db	464	SCSRSHRRLSVHHLVHHHHHHHHHVLGNGTTLRVPRASPEIQDRDANGSRWLMLPPSTP	523
QY	541	ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRVSGKVYPTVHTSPDPE	600
Db	524	TPSGGPPRGAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRVSGKVYPTVHTSPDPE	583
QY	601	TLKEKALVEVAASSGPPTLTSLNIPPGYSSMMHKLLETQSTGACQSSCKISSPCLKADSG	660
Db	584	MLKDKALVEVAPSPGPTLTSTFNIPPGPFSSMMHKLLETQSTGACHSSCKISSPCLKADSG	643
QY	661	ACGPDSCPYCARACAGEVELADREMPDSDEAVYEFTQDAQHSDLRDPHSRRQRSLGPD	720
Db	644	ACGPDSCPYCARACAGEPEPESADHEMPDSDEAVYEFTQDAQHSDLRDPHSRRQRSLGPD	703
QY	721	EPSSVLAFWRLICDTRFKIVDSKYFGRGIMTAILVNTLSMGIEYHQPEELTNALEISNI	780
Db	704	EPSSVLAFWRLICDTRFKIVDSKYFGRGIMTAILVNTLSMGIEYHQPEELTNALEISNI	763

QY 781 VFTSLFALEMLLKLVLVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFRLMR 840
Db 764 VFTSLFALEMLLKLVLVGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFRLMR 823
QY 841 VLKLVRFPLALQRLVVLMTMDNVATFCMLLMLEFIFISILGMHLFGCKFASERDGDITL 900
Db 824 VLKLVRFPLALQRLVVLMTMDNVATFCMLLMLEFIFISILGMHLFGCKFASERDGDITL 883
QY 901 PDRKNFDSLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLV 960
Db 884 PDRKNFDSLWAIWTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLV 943
QY 961 AILVEGFQAEIISKREDASQLSCIQLPVDSQGGDANKSESEPFFSPSLDGDGRKKCL 1020
Db 944 AILVEGFQAE-----GDATKSESEPFFSPVDGDGRKKRL 980
QY 1021 ALVSLGHEPELRKSLPLLIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGAA 1080
Db 981 ALVALGEHSELKSLPLLIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGTA 1040
QY 1081 -HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQES 1139
Db 1041 HHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEGQES 1100
QY 1140 QDEEESSEERASPDGSDHRRHGRSLEREAKSSFDPDTPQLVPGHLRTASGRGSASEHQDC 1199
Db 1101 QDEEESSEEDRASPDGSDHRRHGRSLEREAKSSFDPDTPQLVPGHLRTASGRSSASEHQDC 1160
QY 1200 NGKSASGRLARALRPDDPPLDGGDDADDEGNLSKGERVRAWIRARLPACYLERSDSWSAYIF 1259
Db 1161 NGKSASGRLARALRPDDPPLDGGDDDEGNLSKGERLARWARARLPACCRERDSWSAYIF 1220
QY 1260 PQSRFRLLCHRIITHKMFHDHVVLVIIFLNCITIAMERPDKIDPHSAERIFLTLSNYIFTA 1319
Db 1221 PQSRFRLLCHRIITHKMFHDHVVLVIIFLNCITIAMERPDKIDPHSAERIFLTLSNYIFTA 1280
QY 1320 VFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLRV 1379
Db 1281 VFLAEMTVKVVALGWCFCGEQAYLRSSWNVDGLLVLSIVDILVSMVSDSGTKILGMLRV 1340
QY 1380 LRLRLTRLRLRVISRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFF 1439
Db 1341 LRLRLTRLRLRVISRAQGLKLVVETLMSSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFF 1400
QY 1440 VCQGEDTRNITNKSDCAEASRWVRHKYNFNDNLGQALMSLFVLASKDGVVDIMYDGLDAV 1499
Db 1401 VCQGEDTRNITNKSDCAEASRWVRHKYNFNDNLGQALMSLFVLASKDGVVDIMYDGLDAV 1460
QY 1500 GVDQQPMNHNPMWMLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRQHQQEERARRREEKR 1559
Db 1461 GVDQQPMNHNPMWMLLYFISFLLIIVAFVFLNMFVGVVVENFHKCRQHQQEERARRREEKR 1520
QY 1560 LRRLEKKRR-----KAQCKPYYSYSRFRLLVHHLCTSHYLDLFTIG 1601
Db 1521 LKRLKKRRNMLDDVIASSGSASAASEAQCKPYYSYSRFRLLVHHLCTSHYLDLFTIG 1580
QY 1602 VIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQLD 1661
Db 1581 VIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQLD 1640
QY 1662 LAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMRALLDVTMQA 1721
Db 1641 LAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMRALLDVTMQA 1700
QY 1722 LPQVGNLGLLFLMLFFIFAALGVVEFGDLECDETHPC EGLGRHATFRNFGMAFLTILFRVS 1781
Db 1701 LPQVGNLGLLFLMLFFIFAALGVVEFGDLECDETHPC EGLGRHATFRNFGMAFLTILFRVS 1760
QY 1782 TGDWNNGIMKDTLRDCDQESTCYNTVVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNK 1841
Db 1761 TGDWNNGIMKDTLRDCDQESTCYNTVVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNK 1820
QY 1842 EAKEEAELEAELEMKTLSPQPHSPLGSPFLWPVGVEGPDSPDSPKPGALHPAAHARSAS 1901

Db 1821 EAKEEAELEAELEMKTLSPQPHSPLGSPFLWPVGVEGVNSPDSPKPGAPHTTAHIGAAS 1880
QY 1902 H-FSLEHPTMQPHPTLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHRG 1957
Db 1881 SGFSLEHPTMVPHTEEGVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHG 1940
QY 1958 WGLPKAQSGSVLSVHSQPADTSYIQLPKDAPHLLQPHSAPTGWGIPKLPPLPPGRSPLAQ 2017
Db 1941 WGLPKAQSGSVLSVHSQPADTSCILQLPKDAHLLQPHGAPTWGAIPKLPPLPPGRSPLAQ 2000
QY 2018 PLRRQAAIRTDSDLVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKIS 2077
Db 2001 PLRRQAAIRTDSDLVQGLGSRREDLLSEVSGSPCLTRSSSFWGGSSIQVQQRSGSQSKVS 2060
QY 2078 KHMTPPAPCPGPEPNWKGPPETRRSSLELDTLSWISGDLPLPPGQGEPPSPRDLKKCYS 2137
Db 2061 KHIRLPAPCPGLEPSWAKDPQETRSSLDELDTLSWISGDL--PSSQEEPLSPRDLKKCYS 2119
QY 2138 VEAQSCORRPTSWLDEQRRHSIAVSCLDGSGSQPHLGTDPNSNLGGQPLGGSPRKKLSP 2197
Db 2120 VEAQSCRRRPGSWLDEQRRHSIAVSCLDGSGSQPRLCPSSSLGQPLGGSPRKKLSP 2179
QY 2198 PSITIDPPESQGPTPPSPGICLRRRAPSSDSKDPASGPPDSMAASPSPKOVLSLSGL 2257
Db 2180 PSISIDPPESQGPRPPCSPGVCLRRRAPASDSKDPASSPDLSTAASPSPKDALSLSG 2239
QY 2258 SSDPADLDP 2266
Db 2240 SSDPTDLP 2248

RESULT 7

AAH57399
ID AAH57399 PRELIMINARY; PRT; 2248 AA.
AC AAH57399;
DT 02-MAR-2004 (TremBLrel. 27, Created)
DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TremBLrel. 27, Last annotation update)
DE Caenalg protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

QY	2078	KHMTTPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPPGQGEPPSPRDLKKCYS	2137
Db	2061	KHIRLPAPCPGLEPSWAKDPQETRSSLELDTLSWISGDL- PSSQEEPLSPRDLKKCYS	2119
QY	2138	VEAQSCORRPTSWLDEQRRHSIAVSCLDGSGQPHLGTDPNSNLGGQPLGGPSRPKKKLS	2197
Db	2120	VEAQSCRRRPGSWLDEQRRHSIAVSCLDGSGQPRLCPSSSLGGQPLGGPSRPKKKLS	2179
QY	2198	PSITIDPPESQGRTPPSPGICLRRRAPSSDSKDPLASGPPDSMAASPSPKDVL	2257
Db	2180	PSISIDPPESQGRPPCSPGVCLRRRAPASDSKDPASSPDSTAASPSPKDALS	2239
QY	2258	SSDPADLDP	2266
Db	2240	SSDPTDLDP	2248
RESULT 8			
Q6ZPX4			
ID	Q6ZPX4	PRELIMINARY;	PRT; 1389 AA.
AC	Q6ZPX4;		
DT	05-JUL-2004	(TReMBLrel. 27, Created)	
DT	05-JUL-2004	(TReMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TReMBLrel. 27, Last annotation update)	
DE	MKIAA1123	protein (Fragment).	
GN	Name=mKIAA1123;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	PubMed=14621295;		
RA	Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,		
RA	Saga Y., Nagase T., Ohara O., Koga H.;		
RT	"Prediction of the coding sequences of mouse homologues of KIAA gene:		
RT	III. the complete nucleotide sequences of 500 mouse KIAA-homologous		
RT	cDNAs identified by screening of terminal sequences of cDNA clones		
RT	randomly sampled from size-fractionated libraries."		
RL	DNA Res. 10:167-180(2003).		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).		
CC	-!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits		
CC	family.		
DR	EMBL; AK129294; BAC98104.1; -.		
DR	GO; GO:0005886; C:plasma membrane; IDA.		
DR	GO; GO:0005245; F:voltage-gated calcium channel activity; IDA.		
DR	InterPro; IPR001682; Ca/Na_pore.		
DR	InterPro; IPR002111; Cat_channel_TrpL.		
DR	InterPro; IPR002077; Ca_Channel_alpha.		
DR	InterPro; IPR005821; Ion_trans.		
DR	InterPro; IPR005820; M+channel_nlg.		
DR	Pfam; PF00520; Ion_trans; 2.		
DR	PRINTS; PR00167; CACHANNEL.		
KW	Calcium channel; Calcium-binding; Ion transport; Ionic channel;		
KW	Transmembrane; Transport; Voltage-gated channel.		
FT	NON TER 1		
SQ	SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;		
Query Match 55.2%; Score 6573; DB 2; Length 1389;			
Best Local Similarity 92.0%; Pred. No. 1.2e-294;			
Matches 1279; Conservative 25; Mismatches 62; Indels 24; Gaps 5;			
QY	900	LPRKNFDSLLWAIIVTVFOILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL	959
Db	1	LPRKNFDSLLWAIIVTVFOILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLL	60
QY	960	VAILVEGFQAEIISKREDASQLSLCIQLPVDQGGDANKSESEPDFFPSLDGDGRKKC	1019
Db	61	VAILVEGFQAEIIGKREDTSGQLSLCQLPVNSQGGDATKSESEPDFFPSVDGDGRKKR	120
QY	1020	LALVSLGEHPELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSSGSAEPGA	1079

Db	121	LALVALGEHSELKSLPLPLIIHTAATPMSLPKSSSTGVGEALGSGSRRTSSSGSAEPGT	180
QY	1080	A-HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRSPSGERRSLLSGEQE	1138
Db	181	AHEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRSPSGERRSLLSGEQE	240
QY	1139	SQDEEESSEERASPAAGSDHRRHSGSLEREAKSSFDLPDTLQVPLGHLRTASGRGSASEHQD	1198
Db	241	SQDEEESSEEDRASPAAGSDHRRHSGSLEREAKSSFDLPDTLQVPLGHLRTASGRSSASEHQD	300
QY	1199	CNGKSASGRLARALRPDDPPLDGDADDDEGNLSKGERVRAWTRARLPACYLERDSWSAYI	1258
Db	301	CNGKSASGRLARALTLRADDPPLDGDGDDEGNLSKGERLRAWVRARLPACCRERDSWSAYI	360
QY	1259	FPPQSRFRLLCHRIITHKMFHDVVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1318
Db	361	FPPQSRFRLLCHRIITHKMFHDVVVLVIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	420
QY	1319	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLR	1378
Db	421	AVFLAEMTVKVVALGWCFCGEQAYLRSSWNVLDGLLVLSVIDILVSMVSDSGTKILGMLR	480
QY	1379	VLRLRLRLPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKF	1438
Db	481	VLRLRLRLPLRVISRAQGLKLVVETLMSLKPIGNIVVICCAFFIIFGILGVQLFKGKF	540
QY	1439	FVCOGEDTRNITNKSDCAEASVVRVHRKYNFDNLGQALMSLFLVASKDGVWDIMYDGLDA	1498
Db	541	FVCOGEDTRNITNKSDCAEASVVRVHRKYNFDNLGQALMSLFLVASKDGVWDIMYDGLDA	600
QY	1499	VGVDQQPIMNHNPMWLLYFISFLLIVAFFVLNMFVGVVVFVNFHKKRQHOOEERARRREK	1558
Db	601	VGVDQQPIMNHNPMWLLYFISFLLIVAFFVLNMFVGVVVFVNFHKKRQHOOEERARRREK	660
QY	1559	RLRLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHVLDLFT	1600
Db	661	RLRLEKKRRNMLDDVIASSSSASAASEAQCKPYSDYSRFRLLVHHLCTSHVLDLFT	720
QY	1601	GVIGLVVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQL	1660
Db	721	GVIGLVVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVFKLVAFGFRFFQDRWNQL	780
QY	1661	DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGNRALLDTVMQ	1720
Db	781	DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLRIARVLKLLKMAVGNRALLDTVMQ	840
QY	1721	ALPQVGNLGLLFMLLFFIFAALGVLEFGDLECDETHPCBGLGRHATFRNFGMAFLTFRV	1780
Db	841	ALPQVGNLGLLFMLLFFIFAALGVLEFGDLECDETHPCBGLGRHATFRNFGMAFLTFRV	900
QY	1781	STGDNWNGIMKOTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVAVLMKHLEESN	1840
Db	901	STGDNWNGIMKOTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVAVLMKHLEESN	960
QY	1841	KEAKEAELEAELEEMKTLSPQPHSPLGSPFLWPGVEGDPSPDKPGALHPAAHARSA	1900
Db	961	KEAKEAELEAELEEMKTLSPQPHSPLGSPFLWPGVEGVNSPDKPGAPHTTAHIGAA	1020
QY	1901	SH-FSLEHPTMQHPHTPLP---GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHR	1956
Db	1021	SSGFSLEHPTMVPHTEEGPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHR	1080
QY	1957	GWGLPKAQSGSVLSVHSQPADTSYIILQPKDAPHLLQPHSAPTWGTIPKLPPLPPGRSPLAQ	2016
Db	1081	GWGLPKAQSGSVLSVHSQPADTSCILQPKDAHLLQPHGAPTWGAIPKLPPLPPGRSPLAQ	1140
QY	2017	RPLRRQAAIRTDSDLVQGLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQQHSRSHSKI	2076
Db	1141	RPLRRQAAIRTDSDLVQGLGSRREDLLSEVSGSPCLTRSSSFWGGSSIQQVQRSQSQSKV	1200
QY	2077	SKHMTTPAPCPGPEPNWKGPPETRSSLELDTLSWISGDLPPGQGEPPSPRDLKKCY	2136

bb	1201	SKHIRLPAPCPGLEPSWAKDPQETRSSLLELDTLSWISGDLL-PSSQEEPLSPRDLKKCY	1259
yy	2137	SVEAQSCQRRPTSWLDEQRHRSIAVSCLDGSGQPHLGTDPNLSGQPLGGPSRPKKLS	2196
bb	1260	SVEAQSCRRRPGSWLDEQRHRSIAVSCLDGSGQPRLCPSPSSSLGGQPLGGPSRPKKLS	1319
yy	2197	PPSITIDPPESQGPRTPPSPGICLRRRAPSSDKDPLASGPPDSMAASPKKDVLSLSG	2256
db	1320	PPSISIDPPESQGPRPPCPGVCRLRRAPASDKDPSASSPLDSTAASPKKDALSLSG	1379
QY	2257	LSSDPADLDP	2266
db	1380	LSSDPTDLDP	1389
RESULT 9			
BAC98104	PRELIMINARY; PRT; 1389 AA.		
BAC98104			
AC	BAC98104;		
DT	02-MAR-2004 (TrEMBLrel. 27, Created)		
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)		
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)		
DE	MKIAA1123 protein (Fragment).		
EN	MKIAA1123.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,		
RA	Saga Y., Nagase T., Ohara O., Koga H.;		
RA	"Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:		
RT	III. The Complete Nucleotide Sequences of 500 Mouse KIAA-homologous		
RT	cDNAs Identified by Screening of Terminal Sequences of cDNA Clones		
RT	Randomly Sampled from Size-fractionated Libraries.";		
RT	DNA Res. 10:167-180(2003).		
RL	EMBL; AK129294; BAC98104.1; --		
DR	NON TER 1		
FT	SEQUENCE 1389 AA; 153067 MW; DA31535CA3C03B10 CRC64;		
SQ			
Query Match 55.2%; Score 6573; DB 2; Length 1389;			
Best Local Similarity 92.0%; Pred. No. 1.2e-294;			
Matches 1279; Conservative 25; Mismatches 62; Indels 24; Gaps 5;			
QY	900	LPDRKNFSLWAIIVTFQILTQEDWNKVLNGMASTSSWAAIFYALMTFGNYVLENLL	959
Db	1	LPDRKNFDSLWAIIVTFQILTQEDWNKVLNGMASTSSWAAIFYALMTFGNYVLENLL	60
QY	960	VAILVEGFQAEISKREDASGQLSCIQLPVDSQGGDANKSEPDFFPSLSDGDGRKKC	1019
Db	61	VAILVEGFQAEITGKREDTSGQLSCIQLPVNSQGGDATKSESEPDFFPSVVDGDRKKR	120
QY	1020	LALVSLGEHPELRKSLPLPIIHTAATPMVSLPKSTSTGLGEALGPASRRRTSSSGSAEPGA	1079
Db	121	LALVALGEHSELKSLPLPIIHTAATPMVSLPKSSSTGVGEALGSGSRRTSSSGSAEPGT	180
QY	1080	A-HEMKSPPSARSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE	1138
Db	181	AHEMKSPPSARSPHSPWSAASSWTSRRSRNSLGRAPSLKRRSPSGERRSLLSGEGQE	240
QY	1139	SQDEEESSEERASGSDHRRHRSGLERAKSSFDLPDTLQVPGHLRTASGRGSASEHQD	1198
Db	241	SQDEEESSEEDRASGSDHRRHRSGLERAKSSFDLPDTLQVPGHLRTASGRSSASEHQD	300
QY	1199	CNGKSASGRLARALRPDDPPLDGDADDGNNLSKGERVRAWIRALPACYLERSWSAYI	1258
Db	301	CNGKSASGRLARTLRADDPPLDGDGDDGNNLSKGERLRAWVRARLPACRRERDSWSAYI	360
QY	1259	FPPQSRFRLLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	1318
Db	361	FPPQSRFRLLCHRIITHKMFHDHVVLVIIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFT	420

QY	1319	AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGGLLVLSVIDILVSMVSDSGTKILGMLR	1378
Db	421	AVFLAEMTVKVALGWCFCGEQAYLRSSWNVLGGLLVLSVIDILVSMVSDSGTKILGMLR	480
QY	1379	VRLRLRTLRLPLRVISRAQGLKLVVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKGKF	1438
Db	481	VRLRLRTLRLPLRVISRAQGLKLVVETLMSLLKPIGNIVVICCAFFIIFGILGVQLFKGKF	540
QY	1439	FVCGEDTRNITNKSDCAEASRWVRHKYNFNLGQALMSLFLVASKDGVVDIMYDGLDA	1498
Db	541	FVCGEDTRNITNKSDCAEASRWVRHKYNFNLGQALMSLFLVASKDGVVDIMYDGLDA	600
QY	1499	VGVDQOPIMNHNPMWLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREK	1558
Db	601	VGVDQOPIMNHNPMWLLYFISFLLIIVAFFVLNMFVGVVVENFHKCRHQHEEEARRREK	660
QY	1559	RLRLLEKKRR-----KAQCKPYSDYSRFRLLVHHLCTSHYLDLFT	1600
Db	661	RLKRLKRRNLMLDDVIASGSSASAASEAQCKPYSDYSRFRLLVHHLCTSHYLDLFT	720
QY	1601	GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVKLVAFGFRFFQDRWNQL	1660
Db	721	GVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVLESVKLVAFGFRFFQDRWNQL	780
QY	1661	DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMRAALLDTVMQ	1720
Db	781	DLAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMRAALLDTVMQ	840
QY	1721	ALPQVGNLGLLMLFFIFAALGVLELFGDLECEDETHPCGLGRHATFRNFGMAFLTLPV	1780
Db	841	ALPQVGNLGLLMLFFIFAALGVLELFGDLECEDETHPCGLGRHATFRNFGMAFLTLPV	900
QY	1781	STGDNWNGIMKDLTRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESN	1840
Db	901	STGDNWNGIMKDLTRDCQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESN	960
QY	1841	KEAKEEALEAELEEMKTLSPHSPGLSPFLWPVGVEGSDSPDKPGALHPAAHARSA	1900
Db	961	KEAKEEALEAELEEMKTLSPHSPGLSPFLWPVGVEGSDSPDKPGAPHTTAHIGAA	1020
QY	1901	SH-FSLEHTMQPHPTLP--GPDLLTVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGHR	1956
Db	1021	SSGFSLEHTMQVPHTEEGVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGR	1080
QY	1957	GWGLPKAQSGSVLSVHSQPADTSYLQPKDAPHLLOPHSAPTWTGTPKLPPLPPGRSPLAQ	2016
Db	1081	GWGLPKAQSGSVLSVHSQPADTSYLQPKDAPHLLOPHSAPTWTGTPKLPPLPPGRSPLAQ	1140
QY	2017	RPLRRQAARTDSDLVQGLSGREDLLAEVSGPPPLARAYFWGQSSTQAQOHSRSHSKI	2076
Db	1141	RPLRRQAARTDSDLVQGLSGREDLLAEVSGPPPLARAYFWGQSSTQAQOHSRSHSKI	1200
QY	2077	SKHMTPPAPCPGPEPNWKGPPETFRSSLELDTLSWISGDLPPGGQEEPPSPRDLKKCY	2136
Db	1201	SKHIRLPAPCPGLEPSWAKDPQETRSSLLELDTLSWISGDLPPGGQEEPPSPRDLKKCY	1259
QY	2137	SVEAQSCQRRPTSWLDEQRHRSIAVSCLDGSGSQPHLGTDPNLSGQPLGGPSRPKKLS	2196
Db	1260	SVEAQSCRRRPGSWLDEQRHRSIAVSCLDGSGQPRLCPSPSSSLGGQPLGGPSRPKKLS	1319
QY	2197	PPSITIDPPESQGPRTPPSPGICLRRRAPSSDKDPLASGPPDSMAASPKKDVLSLSG	2256
Db	1320	PPSISIDPPESQGPRPPCPGVCRLRRRAPASDKDPSASSPLDSTAASPKKDALSLSG	1379
QY	2257	LSSDPADLDP	2266
Db	1380	LSSDPTDLDP	1389

RESULT 10
CCAH_RAT
ID CCAH_RAT STANDARD; PRT; 2359 AA.

QY 109 CDSQRCRILQAFDDFIAPFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAMLEYS 168
Db 128 CRSEKCSILEAFDDFIAPFAVEMVVMVALGIFGKKCYLGDTWNRLDFFIVIAMMEYS 187
QY 169 LDQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTPMLGNVLLCFVFFIFGIV 228
Db 188 LDGHNVSLSAIRTVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLCFVFFIFGIV 247
QY 229 GVQLWAGLLRNRCFLPENFSLPLSVD-LERYQQTENEDESPFICSPRENGMRSCRSVPT 287
Db 248 GVQLWAGLLRNRCFLDSAFVNNNLTLFLRPPYQTEGEENPFICSSRRDNGMKCSHIP 307
QY 288 ---LRDGGGGPPCGLDYEA-----NSSNTTCVNNQYNTNCSAGEHNPFGKAINF 337
Db 308 RREL-----VQCTLGWEAYQQAEDGGAGRNACINNNQYNNVCRSGEFNPHGAINF 361
QY 338 DNIYAWIAFQVITILEGWVDIMYFVMDAHSFYNFIFILLIIVGSFFMINCLVVIATQ 397
Db 362 DNIYAWIAFQVITILEGWVDIMYFVMDAHSFYNFIFILLIIMGSFFMINCLVVIATQ 421
QY 398 FSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLYLVLILRKAARLAQVSRA 457
Db 422 FSETKQRENQLMREQVARYLSNDSTLASFSEPGSCYEELLYKVGHIFRKYKRRSLRLYAR 481
QY 458 AGVRVGLLSSP-APLGGQETQPSSSCSRSHRR-LSVHVLV-HHHHHHHHHYHLNGTTLRA 514
Db 482 WQSRWRKVDPSSTVHGQ--GPGRRPRRAGRRTASVHVLVYHHHHHHHHYHFSHGPPRR 539
QY 515 PRASPEIQDRDANGSRRLM--LPPSTPALSGAPPGAESVHSFYHADCHLEPVRCQAPP 572
Db 540 P--SPE----PGAGDNLVRACAPSPSPGHGPP-DSESVHSIYHADCHVEGPQERARV 592
QY 573 PRSPSEASGRVSGS---KVYPTVHTSPPETLKEKALVEVAASSGPPTLTSLNIP--- 625
Db 593 AHSIATAASLKASGLGTWNYPTI---LPSGTVNSKG---GTSSRPKGLRGAGAPGA 645
QY 626 -----PGPYSSMHKLETOSTGACQS-----SKISSPCLKADSGACGPDSCPYC 670
Db 646 HSPLSLGSRPYEKIQDVVGEQGLGRASSHLSGLSVPCPLSP--QAGTLTCELKSCPYC 703
QY 671 ARA-GAGEVELADREMPDSDSEAVYEBTQDAQHSDLRDP-----HS--RRQBSL 716
Db 704 ASALEDPFEPFSGSESGSDAHSVYFTQDVRHGDGRDPVQOPHEVGTGPHSNERRRTP 763
QY 717 GPDAEPSSVLAFWRLICDTRFKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALE 776
Db 764 RKASQPGGIGHLWASFGKLRRIVDSKYFNRGIMAAILVNTLSMGVEYHEQPEELTNALE 823
QY 777 ISNIVFTSLFALMLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLRTF 836
Db 824 ISNIVFTSMFALEMLKLLACGPLGYIRNPYNIFDGVIVVISVWEIVGQADGGQSVLRTF 883
QY 837 RLMRVLKLVRFLPALQRLVLMKTMNVATFCMLLMFIFIFISILGMHLFGCKFASERD 896
Db 884 RLLRVLKLVRFLPALRRQLVLMRTMDNVATFCMLLMFIFIFISILGMHLFGCKFSLKTD 943
QY 897 -GDTLPDRKNFDSLLWAIIVTVFQILTQEDWNKVLYNGMASTSSWAAALYFIALMTFGNYVL 955
Db 944 SGDTVPDRKNFDSLLWAIIVTVFQILTQEDWNVLYNGMASTSSWAAALYFVALMTFGNYVL 1003
QY 956 FNLLVAILVEGFQABEISKREDASGQLSCIQLPVDQSGGDANKSESEPDFSPSLDGDGD 1015
Db 1004 FNLLVAILVEGFQAE-----GDATRSDDTDKSTQLEGDFD 1040
QY 1016 RKKCL-----ALVSLGEHPELRKSLPLIHTAATPMSLPKSTSTGLGEALGPAS 1066
Db 1041 KLRLDRATEMKMYSIAVTPNGHLEGRGSLPPPLIHTAATPMPTPKS-SPNLDVAHALLD 1099
QY 1067 RRTSSGSAEPGAHAHEMKSPPSARSSPHSPWSAASSWTSSRSSNSLGRAPSLKRRSPSG 1126
Db 1100 SRRSSGSDVPQLG-DQKSLASLRSSPCTPWGPNAGSAGSSRSSNSLGRAPSLKRRNQCG 1158

QY 1127 ERRSLLSGEGQESQDEHESSEERAS-----PAGSDHRRHSGSLEREAKSFDL-- 1174
Db 1159 ERESLLSGEGKGSTDD--AEDSRPSTGTHPGASPGPRATPLRRAESLDH--RSTLDLCP 1214
QY 1175 --PDTLQVPLHRTASGRGSAHQDCNGKSGASGLARALRPDDPPLDDDDADDEGNLSK 1232
Db 1215 PRPAALLPTKFH-----DCNGQMVALPSEFFLRIDSHKEDAAEFDDDDIEDSC 1261
QY 1233 GERVRAWIRARLPACYLERDSWSAYIFPPQSRPRLCHRITTHKMFHDHVVLVIFLNCIT 1292
Db 1262 CFRLHKVLEPYAPQWCRSRESWALYLFPPQNRRLRVSCQKIAHKMFHDHVVLVIFLNCIT 1321
QY 1293 IAMERP KIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAVLRSSWNVLDGL 1352
Db 1322 IALERPDIIDPGSTERAFLSVSNYIFTAIFVVEVMVMKVVALGLLWGEHAYLQSSWNVLDGL 1381
QY 1353 LVLLISVIDILVSMVSDSGTKILGMLRVLRLRLRLRPLRVISRAOGLKLVVETLMSSLKPI 1412
Db 1382 LVLVSLVDIIVAMASAGGAKILGVLRVVRLLRPLRVISRAPGLKLVVETLISSLRPI 1441
QY 1413 GNIVVICCAFFIIFGILGVQIFKGFVFCQGEDTRNTKSDCAEASRYWRHKNYFDNL 1472
Db 1442 GNIVLICCAFFIIFGILGVQIFKGFYCEGTDTRNTTKAECHAAHYRWRHKNYFDNL 1501
QY 1473 GOALMSLFLVASKDGVIMVDGLDAVGVDQOQPMNHNPMWMLLYFISFLLIIVAFFVLNMF 1532
Db 1502 GOALMSLFLVSSKDGWVIMYDGLDAVGIDQOQPVQNHNPWMLLYFISFLLIIVSEFFVLNMF 1561
QY 1533 VGVVVENPHKCRHQHEEEARRRREKRLRRLEKRRKAQCKPYSDYSRFRLLVHHLCTS 1592
Db 1562 VGVVVENPHKCRHQHEAEEARRRREKRLRRLEKRRKAQCKPYSDYSRFRLLVHHLCTS 1621
QY 1593 HYLDLFTITGVIGLVNVTMAMEHYQQOQILDEALKICNYIFTVIFVLESVFKLVAFGFRF 1652
Db 1622 HYLDLFTITFICLVNVTMSMEHYNQPKSLDEALKYCNVYFTIVFVFEAALKLVAFGFRF 1681
QY 1653 FQDRWNQDLAIIVLLSIMGITTEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMR 1712
Db 1682 FKDRWNQDLAIIVLLSIMGIALEEIEMNAALPINPTIIRIMRVLRIRARVLKLLKMAVGMR 1741
QY 1713 ALLDTVMQALPOVGNLGLLFFMLFFFAALGVLEFGDLECDETHPCCEGLGRHATERNFGM 1772
Db 1742 ALLDTVVQALPOVGNLGLLFFMLFFIYAAALGVLEFGRLCECEDNPFCEGLSRHATFTNFGM 1801
QY 1773 AFLTLFRVSTGDNWNGIMKDTLRDC---DOESTCYNTVISPIYFVSFVLTAQFVLNVVI 1829
Db 1802 AFLTLFRVSTGDNWNGIMKDTLRCTREDKCHLSYLPALSPYFVTFMLVAQFVLNVVV 1861
QY 1830 AVLMKHLEESNKEAEAEAELEAELEEMKTLSPQPHSPLGSPFLWPVGVEGPDSPDPRKG 1889
Db 1862 AVLMKHLEESNKEAREDAEMDAEIELEM----- 1889
QY 1890 ALHPAAHARSASHFSLEHPTMQPHPT--ELPG-----PDLLTVRKSGVSRTHSLPNDSYM 1942
Db 1890 -----AQGSTAQPPPTAQESQGTQDTPNLLVVRKVSVRMLSLPNDSYM 1934
QY 1943 CRHGSTAEGPLGHRGWGLP-----KAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHS 1996
Db 1935 FRPVAPAAAPHSH-----PLQEVEMETVYTGPTVSAHSPPLEPRASFQVPSAA-----S 1982
QY 1997 APTWGTIP--KLPPPG--RSPLAQRLRQAAIRTDSLD--VQGLGSRREDLLAEVSGPSP 2050
Db 1983 SPARVSDPLCALSPRGTPRSLSLRILCQEAHSESGLEKGVDDVGG--DSIPDYTEPAE 2040
QY 2051 PLARAYSFVG-----QSSTQAQQHRSRSHSKISKHMTTPPAPCPGPEFNWKGPPET 2100
Db 2041 NMSTSQASTGAPRSPPCSPRPASVRTRKHFTGQRCISSR--PPT-----LGGDEA 2088
QY 2101 RSSLELDTLSWISGDLIP-----PGQEBPP-----SPDLKKCYSVAEQSCQR 2145
Db 2089 EAADPADEEVSHITSSAHPWPATEPHSPESAPTASPVKGTMGSGRDRFRFCSDAQSF 2148
QY 2146 RPTSWLDEQRRHSIAVSCLDSDSGSQPHLGTDPNSLGGQPLG-----GPGSRPKKLSPP 2198

Db 2149 KP-GRPDAQRWSSVE---LDNG-ESHLES-----GEVGRASELEPALGSRKKKMSPP 2197
QY 2199 SITIDPP-ESQPRTPPSP---GICLRRRAPSDSK-----DPLASGPP 2238
Db 2198 CISIEPPTKDEGSSRPAAEGGNTLRRRTSCAAALHRCDCPEPTGPGTGDPVAKGER 2257
QY 2239 DSMAASPSPKDVLSGLSSDPADL 2264
Db 2258 WGQA---SCRAEHLTVPNFAFEPLDM 2280

RESULT 11
CCAH HUMAN
ID -CCAH_HUMAN STANDARD; PRT; 2353 AA.
AC O95180; O95802; Q8WWI6; Q96QI6; Q96RZ9; Q9NYY4; Q9NYY5;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2) (Low-voltage-activated calcium channel alpha1 3.2 subunit).
DE Name=CACNA1H;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Heart;
RX MEDLINE=98333998; PubMed=9670923;
RA Cribbs L.L., Lee J.-H., Yang J., Satin J., Zhang Y., Daud A.N., Barclay J., Williamson M.P., Fox M., Rees M., Perez-Reyes E.;
RA "Cloning and characterization of alpha1H from human heart, a member of the T-type Ca2+ channel gene family.";
RL Circ. Res. 83:103-109(1998).
RN [2]
RP REVISIONS.
RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thyroid carcinoma;
RX MEDLINE=99127945; PubMed=9930755;
RA Williams M.E., Washburn M.S., Hans M., Urrutia A., Brust P.F., Prodanovich P., Harpold M.M., Stauderman K.A.;
RA "Structure and functional characterization of a novel human low-voltage activated calcium channel.";
RT J. Neurochem. 72:791-799(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21096910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K., Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J., Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Testis;
RX MEDLINE=21864207; PubMed=11751928; DOI=10.1074/jbc.M105345200;
RA Jagannathan S., Punt E.L., Gu Y., Arnoult C., Sakas D., Barratt C.L., Publicover S.J.;
RA "Identification and localization of T-type voltage-operated calcium channel subunits in human male germ cells. Expression of multiple isoforms.";
RL J. Biol. Chem. 277:8449-8456(2002).
RN [6]
RP SEQUENCE OF 86-817 FROM N.A.
RA Cobley V.E.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [7]

RP SEQUENCE OF 424-661 AND 838-2373 FROM N.A. (ISOFORM 1).
RA Mittman S., Agnew W.S.;
RT "Organization and alternative splicing of CACNA1H.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=AlH-a;
CC IsoId=O95180-1; Sequence=Displayed;
CC Name=2; Synonyms=AlH-b;
CC IsoId=O95180-2; Sequence=VSP 000949;
CC -!- TISSUE SPECIFICITY: Expressed in kidney, liver, heart, brain.
CC Isoform 2 seems to be testis-specific.
CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.
CC -!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by Cam-kinase II.
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.
CC -!- CAUTION: AT-AC pre mRNA splicing gives rise to the isoform 1 shown in this entry. The additional 20 amino acids found in the Ref.4 and Ref.6 sequences are due to a misunderstanding of the real type of splicing mechanism involved.
CC -----
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CC -----
DR EMBL; AF051946; AAC67239.3; -
DR EMBL; AF073931; AAD17668.1; -
DR EMBL; AE006466; AAK61268.1; ALT_SEQ.
DR EMBL; AJ420779; CAD12646.1; -
DR EMBL; AL031703; CAC42094.1; ALT_SEQ.
DR EMBL; AF223562; AAF60162.1; -
DR EMBL; AF223563; AAF60163.1; -
DR Genew; HGNC:1395; CACNA1H.
DR MIM; 607904; -
DR GO; GO:0005891; C:voltage-gated calcium channel complex; TAS.
DR GO; GO:0008332; F:low voltage-gated calcium channel activity; TAS.
DR GO; GO:0006936; P:muscle contraction; TAS.
DR GO; GO:0007520; P:myoblast fusion; TAS.
DR GO; GO:0008016; P:regulation of heart rate; TAS.
DR GO; GO:0006810; P:transport; TAS.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR005445; TVDCCALpha1.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR01629; TVDCCALPHA1.
KW Alternative splicing; Calcium channel; Calcium-binding; Glycoprotein;

KW	Ion transport; Ionic channel; Multigene family; Phosphorylation;		
FT	Repeat; Transmembrane; Voltage-gated channel.		
FT	REPEAT	87	422
FT	REPEAT	779	1018
FT	REPEAT	1281	1558
FT	REPEAT	1602	1863
FT	DOMAIN	1	100
FT	TRANSMEM	101	119
FT	DOMAIN	120	139
FT	TRANSMEM	140	160
FT	DOMAIN	161	169
FT	TRANSMEM	170	184
FT	DOMAIN	185	193
FT	TRANSMEM	194	212
FT	DOMAIN	213	232
FT	TRANSMEM	233	253
FT	DOMAIN	254	394
FT	TRANSMEM	395	419
FT	DOMAIN	420	793
FT	TRANSMEM	794	814
FT	DOMAIN	815	827
FT	TRANSMEM	828	849
FT	DOMAIN	850	855
FT	TRANSMEM	856	874
FT	DOMAIN	875	882
FT	TRANSMEM	883	906
FT	DOMAIN	907	917
FT	TRANSMEM	918	938
FT	DOMAIN	939	990
FT	TRANSMEM	991	1015
FT	DOMAIN	1016	1290
FT	TRANSMEM	1291	1313
FT	DOMAIN	1314	1331
FT	TRANSMEM	1332	1352
FT	DOMAIN	1353	1362
FT	TRANSMEM	1363	1382
FT	DOMAIN	1383	1396
FT	TRANSMEM	1397	1418
FT	DOMAIN	1419	1428
FT	TRANSMEM	1429	1452
FT	DOMAIN	1453	1529
FT	TRANSMEM	1530	1555
FT	DOMAIN	1556	1616
FT	TRANSMEM	1617	1637
FT	DOMAIN	1638	1651
FT	TRANSMEM	1652	1673
FT	DOMAIN	1674	1680
FT	TRANSMEM	1681	1699
FT	DOMAIN	1700	1713
FT	TRANSMEM	1714	1737
FT	DOMAIN	1738	1751
FT	TRANSMEM	1752	1772
FT	DOMAIN	1773	1835
FT	TRANSMEM	1836	1863
FT	DOMAIN	1864	2353
FT	TRANSMEM	520	530
FT	DOMAIN	1107	1110
FT	TRANSMEM	1583	1586
FT	SITE	378	378
FT	SITE	974	974
FT	SITE	1504	1504
FT	SITE	1808	1808
FT	CARBOHYD	192	192
FT	CARBOHYD	271	271

Query Match 52.2%; Score 6210; DB 1; Length 2353;
Best Local Similarity 56.6%; Pred. No. 1.1e-277;
Matches 1364; Conservative 216; Mismatches 526; Indels 302; Gaps 59;

QY	7	GAGAEESGQP-RSEMRINDLSGAGRPGPGSAEKDPGSADSEAEGLPYPALAPVVFYLS	65
Db	27	GASPESPGAPGREAGERSEL-GVSPSESP-AAERGAELGADEEQRPVPAATAATVFFCIG	84
QY	66	QDSRPRSCLRTVCNPFERISMLVILLNCVTLGMRPCEDIACDSQRCRILQAFDDFIF	125
Db	85	QTRPRSCLRLVCNPFVHVSMLVIMLNCVTLGMRPCEDVECGSERCNILEAFDAFIF	144
QY	126	AFFAVEMVVKMVALGIFGKKCYLGDWTNRDLDFIIVAGMLEYSLDLQNVSFSAVRTVRVL	185
Db	145	AFFAVEMVIKVALGLFGQCYLGDWTNRDLDFIIVAGMMEYSLDGHNVSLSAIRTVRVL	204
QY	186	RPLRAINRVPSMRILVTLILLDTLPLMGNVLLLCFFVFFIFIGVQVQWAGLNRNRCFLPE	245
Db	205	RPLRAINRVPSMRILVTLILLDTLPLMGNVLLLCFFVFFIFIGVQVQWAGLNRNRCFLDS	264
QY	246	NFSLPLSVD-LERYYQTENEDESPFICSQPRENGMPCRSVP---TLRGDGGGPPCGGLD	301
Db	265	AFVRNNLTFLRPYYQTEEGENPFICSSRRDNGMKCSHIPGRREL------MPCTLG	318
QY	302	YEAYN-----SSNTTCVNNQYNTNCSSAGEHNPKGAINFDNIGYAWIAIFQVITLE	354
Db	319	WEAYTQPAEGVGAARNACINWNQYNNVCRSGDSNPHNGAINFDNIGYAWIAIFQVITLE	378
QY	355	GWVDIMYFVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQUMREQRV	414
Db	379	GWVDIMYVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQUMREORA	438
QY	415	RFLSNASTLASFSEPGSCYEELLYLVYILRKAARLQVSRRAAGVRVGLLSSPAPLGGQ	474
Db	439	RHLSNDSTLASFSEPGSCYEELLYVGHIFRKVKRRSLRLYARWQSRWKVDPFSAVQGG	498
QY	475	ETQPSSSCSRSRHR-LSVHHLV-HHHHHHHHHLGNTGLRAPRASPEIQDRDANGSRRL	532
Db	499	--GPGHRQRRAGRHTASVHHLVHHHHHHHHHHSFGSRPRPPEPGACD-----TRLV	551
QY	533	MLPPPSTPALSGAPPGAESVHSFYHADCHLE--PVRQCAPPPSPSEASGR-TVGSCKV	589
Db	552	RAGAPPPSPGRGPPDAESVHSIYHADCHIEGPOERARVAHAATAAASLRLATGLGTM	611
QY	590	-YPTV-----HTSP-----PPETLKEKALVEVAASSGPPTLTSLNIPPGPY	629
Db	612	NYPTILPSGVSGKSGTSPGPKGWAGGPPGT-----GGHGPLSLNS---PDPY	657
QY	630	SSMHKLLETQSTGACQS-----SCKISSPCLKADSGACGDDSCPYCARA-GAGEVELA	681
Db	658	EKIPHVVGHEGLQAPGHLVSLVPCPLPSP--PAGTLTCELKSCPYCTRALEDPEGELS	715
QY	682	DREMPDSDSEAVYEFTQDAQHSDLRDP-----HSSRRQSLGPDAPSSV	725
Db	716	GSESGSDSGRGVYEFTQDVRHGRWDPTPRPRATDTPGPGSPQRAAQRAAPGEPGWM	775
QY	726	LAFWRLICDTERKIVDSKYFGRGIMAILVNTLSMGIEYHEQBELTNALEISNIVFTSL	785
Db	776	GRLWVTFSGKLRRIVDSKYFSRGIMAILVNTLSMGVEYHEQBELTNALEISNIVFTSM	835
QY	786	FALEMLLKLVLVYGPFGYKPNYNIYFDGVIIVISVWEIVGQGGGLSVLRTFLMRVLKLV	845
Db	836	FALEMLLKLACGLPLGYIRPNYNIYFDGIIIVISVWEIVGQADGGLSVLRTFLRLVLKLV	895
QY	846	RFLPALQRLVVLKMTMDNVATFCMLLMFIFIPFISILGMHLFGCKFASERD-GDTLPDRK	904
Db	896	RFLPALRRQLVVLKMTMDNVATFCMLLMFIFIPFISILGMHLFGCKFSLKTDGTVDPDRK	955
QY	905	NFDSLLWAIYTVFQILTQEDWNKVLNGMASTSSWAALFYIALMTFGNYVLFNLLVAILV	964
Db	956	NFDSLLWAIYTVFQILTQEDWNVVLNGMASTSSWAALFYVALMTFGNYVLFNLLVAILV	1015
QY	965	EGFQAEIISKREDASGQLSCIQLPVDVDSQGDANKSESEDPFFPSLDGD-----GD	1015
Db	1016	EGFQAE-----GDANRSDTDEKTSVHFEEDFHKLRELQTTTE	1052
QY	1016	RKCLALVSLGEHPELRKSLPLPLIIHTAATPMSLPKSTSTGLGEALGPASRRRTSSGSA	1075

Db 1053 LKMCSLAVTPNGHLEGRGSLSPPLIMCTAATPMPTKSSPFLDAPSLPDSRRGSSSGD 1112
QY 1076 EPGAHEMKSPSPSRSPHSPWSAASSWTSSRRSNLSGRAPSLKRRSPSGERRSLLSGE 1135
Db 1113 PP--LGDQKPPASLRSSPCAPWGPSPGAWSSRRSSWSLGRAPSLKRRGQCGERESLLSGE 1170
QY 1136 QGESQDEESESSEERASPA--GSDHRHRGSLEREAKSSFOLDPDTL-----QVPLGH--- 1184
Db 1171 KGKSTDDE--AEDGRAAPGPRATPLRRAESLDPRPLRPAALPPTKCRDRDQGVVALPSDF 1228
QY 1185 --RTASGRGSAEHQDCNGKSAASGRLARALRPDDPPLDGDADDEGNLSKGERVRAMTRA 1242
Db 1229 FLRIDSHREDAAELDDDDSDSCCLRLHKVLEPKP-----QWCBS 1268
QY 1243 RLPACYLERDSWYIFPPQSRFRLLCHRIITHKMFHDHVLVLIPLNCITIAMERPKIDP 1302
Db 1269 -----REAWALYLFSPQNRFRVSCQVITHKMFHDHVLVFLNLCVTIALERPDIIDP 1320
QY 1303 HSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSWNVLGGLLVLSVIDIL 1362
Db 1321 GSTERVFLSVSNYIFTAIFVAEMVKVVALGLLSGEHAYLOQSSWNLLDGLLVLSLVDIV 1380
QY 1363 VSMVSDSGTKILGWLRLRLRLTLRLRVLISRAQGLKLVETLMSSLKPIGNIVVICAF 1422
Db 1381 VAMASAGGAKILGVLRLRLRLTLRLRVLISRAPGLKLVETLISSLRPIGNIVLICAF 1440
QY 1423 FIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASRWRVKYNFNDLQALMSLFVL 1482
Db 1441 FIIFGILGVQLFKGKFFYCEGPDTRNISTKAQCRAAHYRWRVKYNFNDLQALMSLFVL 1500
QY 1483 ASKDGWVDIMYDGLDVGVDQOPIMNHNPMWMLLYFISFLLIYAFFVLNMFVGVVVENFHK 1542
Db 1501 SSKDGWVNIMYDGLDVGVDQOPVQVHNPMWMLLYFISFLLIYFVFLNMFVGVVVENFHK 1560
QY 1543 CRHQHEEEARRREEKRLRLEKKRR-----KAQCKPYYSYDSRFRLLVHLCCTSHYLD 1596
Db 1561 CRHQHEAEARRREEKRLRLRRLRRRSTFPSPQAORRPPYADYSPTRRSIHSLCTSHYLD 1620
QY 1597 LFITGVIGLNVVTMAMEHYQQOQIJDALKICNYIFTVIFVLESVEKLVAFGRFRFPQDR 1656
Db 1621 LFITFIICVNVITMSMEHYNQPKSLDEALKYCNVFTIVVFEAALKLVAFGRFRFFKDR 1680
QY 1657 WNQLDAIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKMAVGMRALLD 1716
Db 1681 WNQLDAIVLLSLMGITLEEIEMSAALPINPTIIRIMRVLIARVLKLLKMATGMRALLD 1740
QY 1717 TVMQALPQVGNLGLLFLMLFFIYFALGVLELFGDLECDETHPCCEGLGRHATFRNFGMAFLT 1776
Db 1741 TVVQALPQVGNLGLLFLMLFFIYAAALGVLELFGRLCESDNPCEGLSRHATFNFGMAFLT 1800
QY 1777 LFRVSTGDNWNGIMKDTLRDC--DQESTCYNTVISPIYFVSFVLTAQFVLNVVAVLM 1833
Db 1801 LFRVSTGDNWNGIMKDTLRECSREDKHCLSYLPALSPYFVFTVLVAQFVLNVVAVLM 1860
QY 1834 KHLEESNKEAKEEALEAELEEMKTLSPQPHSPGLSPFLWPGVEGPDSP---DSPKPGA 1890
Db 1861 KHLEESNKEAREDAELDAEIELEM-----AQPGSARRVDADR-- 1899
QY 1891 LHPAAHARSASHFSLEHPTMQPHPTELPG-----PDLLTVRKSGVSRTHSLPNDSYMCRHG 1946
Db 1900 -----FLPQESPGARDAPNLV-ARKVSVSRMLSLPNDSYMFRPV 1937
QY 1947 STAEGP-----LGHRGWGLPKAQSGSVLSVHSQPADTSYIQLPKDAPHLLQPHSA 1997
Db 1938 VPASAPHRPRLQEVEMETYAGTP---LGSVASVHSPPAESCASLQIP-----LAVSSPA 1989
QY 1998 PTWGTIPKLPPPG--RSPLAQRLRRQAAIRTDSDLDVQGLGRESDDL--AEVSGPSP--P 2051
Db 1990 RSGEPLHALSPRGTA RSPSLSRLLCRQEAHVTDSELGK-IDSPRDTLDRPEPGEKTPVRP 2048
QY 2052 LARAYFWG--QSSTQAQHSRSHSKISKHMTTPAPCPGPEPNWGKGPPTRSSLELDTE 2109

Db 2049 VTQGGSLQSPPRSPRPASVTRKHTFGQRCVSSRPAAPGGE-----EAEASDPADEE 2100
QY 2110 LSWISGDLPL-----PGQEEPP---SPRDLKKCYVEAQSCORRPTSWLDEQRRHSIA 2160
Db 2101 VSHITSSACPMQPTAEPHGPEASPVAGGERDLRLLYSVDAQGFLDKP-GRADEQWRPSAE 2159
QY 2161 VSCLDSGSQPHLCTDPNSNLGGQPLGGPSRPPKKLSPPSITIDPP-ESQGPRTPPSP--- 2216
Db 2160 LGSGEPEGEAKWGP-----AEP--ALGARRKKMSPPCISVEPPAEDEGSARPSAE 2212
QY 2217 GICLRRRAP-----SDSKDPL-----ASGPPDSMA---ASPSKKDVLSSLGLSSDPAD 2263
Db 2213 STTLRRRTPSCEATPHRDSLEPTEGSGAGGDPAAKGERWGOASCRAEHLTVPSFAFEPLD 2272
QY 2264 L-----DP 2266
Db 2273 LGVPSGDP 2280

RESULT 12

CCAH_MOUSE
ID CCAH_MOUSE STANDARD; PRT; 2365 AA.
AC O88427; Q9JKU5;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE voltage-dependent T-type calcium channel alpha-1H subunit (Voltage-gated calcium channel alpha subunit Cav3.2).
GN Name=Cacnalh;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Mittman S.;
RT "Exon organization of mouse Cacnalh.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1823-1952 FROM N.A.
RC STRAIN=C57BL/6J;
RA Cribbs L.L., Lee J.-H., Yang J., Daud A.N., Perez-Reyes E.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1H gives rise to T-type calcium currents. T-type calcium channels belong to the "low-voltage activated (LVA)" group and are strongly blocked by nickel and mibefradil. A particularity of this type of channels is an opening at quite negative potentials, and a voltage-dependent inactivation. T-type channels serve pacemaking functions in both central neurons and cardiac nodal cells and support calcium signaling in secretory cells and vascular smooth muscle. They may also be involved in the modulation of firing patterns of neurons which is important for information processing as well as in cell growth processes.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one positively charged transmembrane segment (S4). S4 segments probably represent the voltage-sensor and are characterized by a series of positively charged amino acids at every third position.
CC -!- PTM: In response to raising of intracellular calcium, the T-type channels are activated by CaM-kinase II.
CC -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

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CC -----

DR EMBL; AF226868; AAK21607.2; -
DR EMBL; AY026385; AAK21607.2; JOINED.
DR EMBL; AF051947; AAC67240.1; -
DR MGD; MGI:1928842; Cactnalh.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR005445; TVDCCAlphal.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR01629; TVDCCALPHA1.
KW Calcium channel; Glycoprotein; Ion transport; Ionic channel;
KW Multigene family; Phosphorylation; Repeat; Transmembrane;
KW Voltage-gated channel.
FT REPEAT 87 422 I.
FT REPEAT 776 1015 II.
FT REPEAT 1292 1569 III.
FT REPEAT 1613 1874 IV.
FT DOMAIN 1 100 Cytoplasmic (Potential).
FT TRANSMEM 101 119 S1 of repeat I (Potential).
FT DOMAIN 120 139 Extracellular (Potential).
FT TRANSMEM 140 160 S2 of repeat I (Potential).
FT DOMAIN 161 169 Cytoplasmic (Potential).
FT TRANSMEM 170 184 S3 of repeat I (Potential).
FT DOMAIN 185 193 Extracellular (Potential).
FT TRANSMEM 194 212 S4 of repeat I (Potential).
FT DOMAIN 213 232 Cytoplasmic (Potential).
FT TRANSMEM 233 253 S5 of repeat I (Potential).
FT DOMAIN 254 394 Extracellular (Potential).
FT TRANSMEM 395 419 S6 of repeat I (Potential).
FT DOMAIN 420 790 Cytoplasmic (Potential).
FT TRANSMEM 791 811 S1 of repeat II (Potential).
FT DOMAIN 812 824 Extracellular (Potential).
FT TRANSMEM 825 846 S2 of repeat II (Potential).
FT DOMAIN 847 852 Cytoplasmic (Potential).
FT TRANSMEM 853 871 S3 of repeat II (Potential).
FT DOMAIN 872 879 Extracellular (Potential).
FT TRANSMEM 880 903 S4 of repeat II (Potential).
FT DOMAIN 904 914 Cytoplasmic (Potential).
FT TRANSMEM 915 935 S5 of repeat II (Potential).
FT DOMAIN 936 987 Extracellular (Potential).
FT TRANSMEM 988 1012 S6 of repeat II (Potential).
FT DOMAIN 1013 1301 Cytoplasmic (Potential).
FT TRANSMEM 1302 1324 S1 of repeat III (Potential).
FT DOMAIN 1325 1342 Extracellular (Potential).
FT TRANSMEM 1343 1363 S2 of repeat III (Potential).
FT DOMAIN 1364 1373 Cytoplasmic (Potential).
FT TRANSMEM 1374 1393 S3 of repeat III (Potential).
FT DOMAIN 1394 1407 Extracellular (Potential).
FT TRANSMEM 1408 1429 S4 of repeat III (Potential).
FT DOMAIN 1430 1439 Cytoplasmic (Potential).
FT TRANSMEM 1440 1463 S5 of repeat III (Potential).
FT DOMAIN 1464 1540 Extracellular (Potential).
FT TRANSMEM 1541 1566 S6 of repeat III (Potential).
FT DOMAIN 1567 1627 Cytoplasmic (Potential).
FT TRANSMEM 1628 1648 S1 of repeat IV (Potential).
FT DOMAIN 1649 1662 Extracellular (Potential).
FT TRANSMEM 1663 1684 S2 of repeat IV (Potential).
FT DOMAIN 1685 1691 Cytoplasmic (Potential).
FT TRANSMEM 1692 1710 S3 of repeat IV (Potential).
FT DOMAIN 1711 1724 Extracellular (Potential).
FT TRANSMEM 1725 1748 S4 of repeat IV (Potential).
FT DOMAIN 1749 1762 Cytoplasmic (Potential).
FT TRANSMEM 1763 1783 S5 of repeat IV (Potential).
FT DOMAIN 1784 1846 Extracellular (Potential).
FT TRANSMEM 1847 1874 S6 of repeat IV (Potential).
FT DOMAIN 1875 2365 Poly-His.
FT DOMAIN 521 531

FT	DOMAIN	1594	1597	Poly-Arg.
FT	SITE	378	378	Calcium ion selectivity and permeability (By similarity).
FT	SITE	971	971	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1515	1515	Calcium ion selectivity and permeability (By similarity).
FT	SITE	1819	1819	Calcium ion selectivity and permeability (By similarity).
FT	CARBOHYD	192	192	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	271	271	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	1477	1477	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	1823	1825	GIM -> ARG (in Ref. 2).
FT	CONFLICT	1914	1914	D -> E (in Ref. 2).
FT	CONFLICT	1945	1947	APA -> LIQ (in Ref. 2).
FT	CONFLICT	1952	1952	S -> A (in Ref. 2).
FT	CONFLICT	1953	2351	Missing (in Ref. 2).
SQ	SEQUENCE	2365 AA;	261944 MW;	9A8A17570C210596 CRC64;

Query Match

Best Local Similarity

Matches 1365; Conservative 235; Mismatches 528; Indels 285; Gaps 61;

QY	2	DEEDGAGAEESGQPSRFMRNDLS-GAGGRP---GPGS---AEKDPGS---AD---SEA	48
Db	9	DEVTVPLGASPSA-PAAPVRASPASPGVPGREEQSGSSSVLAPESPGTECGADLGADEE	67
QY	49	EGLPYPALAPVVFYLSQDSRRPSWCLRTVCNPFWRISMLVILLNCVTLMFRPCEIDIA	108
Db	68	QVPYPALAAATVFFCLGQTTTPRSWCLRLVCNPFWEHISMLVIMLNCVTLMFRPCEIDVE	127
QY	109	CDSQRCRIILQAFDDFIFAFFAVEMVVMVALGIFGKKCYLGDVTNRLDFFIVIAGMLEYS	168
Db	128	CRSERCILLEAFDDFIFAFFAVEMVVMVALGIFGKKCYLGDVTNRLDFFIVMAGMMEYS	187
QY	169	LDLQNVFSAVRTVRVLRPLRINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIV	228
Db	188	LDGHNVSLSAIRTVRVLRLRINRVPSMRILVTLLDTPMLGNVLLLCFFVFFIFGIV	247
QY	229	GVQLWAGLLNRNRCFLPENFSLPLSD-LERYQOTENEDESPFICSPRENGMRSCSVPT	287
Db	248	GVQLWAGLLNRNRCFLDSAFVRNNLTFLRPYYQTEEGEENPFICSSRRDNGMKCSHIPS	307
QY	288	---LRGDGGGPPCGLDYEAY-----NSSNTTCVNMNQQYTNCSAGEHNPFGKAINF	337
Db	308	RRELRL-----VQCTLGWEAYGQQAEDGGAGRNACINWQYVNCVRSGEFNPNGAINF	361
QY	338	DNIGYAWIALFQVITLEGWVDIMYVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQ	397
Db	362	DNIGYAWIALFQVITLEGWVDIMYVMDAHSFYNYFIYFILLIIVGSFFMINCLVVIATQ	421
QY	398	FSETKQRESQIMREQVRFLSNASTLASFSEPGSCYEELKVLVYLKKAARRLAQVSR	457
Db	422	FSETKQRENQIMREQVRFLSNASTLASFSEPGSCYEELKVLVYLKKAARRLAQVSR	481
QY	458	AGVRVGLLSSP-APLGGQETQPSSCSRSHRR-LSVHHLV-HHHHHHHHHYHNGTLRA	514
Db	482	WQSRWRKKVDPSSSTLHGQ--GPRRRPRRAGRRTASVHHLVHHHHHHHHYHFGGPRR	539
QY	515	PRASPEIQDRDANGSRRLM--LPPSPALSGAPPGAESVHSFYHADCHLEPVRCAQPP	572
Db	540	P--SPE---PGAGDTRLVRACVPPSPSPGHGPP--DSESVHSIYHADCHVEGPQERAR	592
QY	573	PRSPSEASGRITVSGS--KVYPTV-----HTSPPTLTKKALVEAASSGPPTL	619
Db	593	AHTIATAASLKASGLGTMTNYPTILPSGAVNSKSTSSRPKGLR-----SAGTPGA	643
QY	620	TS---LNI-PPGPYSSMHKLLETQSTGACQS-----SKTISPCLKADSGACGPDSCP	668
Db	644	TAHSPLSLGSPPYEKIQHVVGEQGLGRASSHLSGLSVPCPLSP--QAGTLTCELKSCP	701
QY	669	YCARA-GAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDP-----HSRRQR	714

FT

Db 702 YCASALEDPFEFFSGSGSDAHDGVYEFQDVRHGD CRDPVQQPHEGGTPGHGNERWRP 761

Qy 715 SLGPDABPSSVLAFWRLICDTRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNA 774

Db 762 PLRTASQPGGLRLWASFSSKLRRIVDSKYFNRGIMAAAILVNTLSMGVEYHEQPDELTA 821

Qy 775 LEISNIVFTSLFALEMLLKLIVYGPFGYIKNPYNIFDGVIVVISVWEIVGQGGGLSVLR 834

Db 822 LEISNIVFTSMFALEMLLKLACGPLGIYIRPNYINIFDGIIVVISVWEIVGQADGGLSVLR 881

Qy 835 TFRIMRVLKLVRFLPALQRQLVVLMTKMDNVATFCMLLMLFIFIESILGMHLFGCKFASE 894

Db 882 TFRLLRVLKLVRFLPALRRQLVVLMTMDNVATFCMLLMLFIFIESILGMHLFGCKFSLK 941

Qy 895 RD-GDTLPDRKNFDSLIIWAIIVTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNY 953

Db 942 TDSGDTVDRKNFDSLIIWAIIVTVFQILTQEDWNVLYNGMASTSSWAALYFVALMTFGNY 1001

Qy 954 VLFNLLVAILVEGQABEISKREDASGQLSCIQLPVDQSOGGDANKSESEPDFFSPLDGD 1013

Db 1002 VLFNLLVAILVEGQAB-----GDATRSDTDEKDTSTHLEED 1038

Qy 1014 GDRKK-----CLALVSLGEHPELPKSLPLPIIHTAATPMSLPKSTSTGLGEALG 1063

Db 1039 FDKLRDVRATEMKMYSLAVTPNG-HLEGRGSLPPPLITHAATPMPTPKS-SPHLDMAHT 1096

Qy 1064 PASRRTSSGSAEPGAAHEMKSPPSARSPHSPWSAASSWTSSRRSSNSLGRAPSLKRRS 1123

Db 1097 LLDSSRSSGSDVPQLG-DQKSLASLRSSPCAPWGPNSAGSSRRSSWSNSLGRAPSLKRRS 1155

Qy 1124 PSGERRLLSGEGQESQDEE-ESSEERERASPAGSDHRHRGSLEREA-----KSSFDL--- 1174

Db 1156 QCGERESLLSGEGKGSTDEAEDSRPNSGTHPGASPGPRATPLRRAESLGRSTMDLCP 1215

Qy 1175 -PDTLQVPLHRTASGRGSASEHQDCNGKSASGRLARALRPDDPPLDGGDDADDEGNLSKG 1233

Db 1216 RPATL-LP-----TKFRDCNGQMVALPSEFFLRIDSHKEDAAEFDDDDIEDSCC 1262

Qy 1234 ERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIIIFLNCITI 1293

Db 1263 FRLHKVLEYPAPQWCSSRESWALYLFPPQNRRLRVSCQKVIAHKMFHDVVLVFI LNCITI 1322

Qy 1294 AMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAYLRSSWNVL DGLL 1353

Db 1323 ALERPDIDPGSTERAFLSVSNYIFTAIFVVEMMVKVVALGLLWGEHAYLQSSWNVL DGLL 1382

Qy 1354 VLISVIDILVSMVSDSGTKILGMLRVLRLLRTLRLPLRVISRAQGLKLVVETLMSSLKPIG 1413

Db 1383 VLVSLVDIIVAVASAGGAKILGVLRLVRLRLRTLRLPLRVISRAPGLKLVVETLISLRPIG 1442

Qy 1414 NIVVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKSDCAEASRYWRVKYNFDNLG 1473

Db 1443 NIVLICCAFFIIFGILGVQLFKGKYCEGTDTRNITTKAECHAAHYRWRRKYNFDNLG 1502

Qy 1474 QALMSLFLASKDGVIMYDGLDVAVGVDQQPIMHNPWMLLYFISFLLIIVAFVFLNMFV 1533

Db 1503 QALMSLFLVSSKDGWVIMYDGLDVAVGIDQQVPQVQNHNPWMLLYFISFLLIIVSFFVLNMFV 1562

Qy 1534 GVUVNFHKCRHQHEEEARRREKRRLRLEKRR-----KAQCKPYYSYSRFRLLVH 1587

Db 1563 GVUVNFHKCRHQHEAEEARRREKRRLRRLERRRRSTFPNPEAQRPPYVADYSHTRRSIH 1622

Qy 1588 HLCSTHYLDLFTIGVIGLVNVTMAMEHYQQQILDEALKICNYIFTVIFVLESVKLVAF 1647

Db 1623 SLCTSHYLDLFTIICLVNVTMSMEHYNQPKSLDEALKYCNYVFTIVFPEAAKLKLVAF 1682

Qy 1648 GFRFPQDRWNQLDLAIIVLLSIMGITLEEIEVNASLPINPTIIRIMRVLIARVLKLLKM 1707

Db 1683 GFRFPKDRWNQLDLAIIVLLSIMGIALEEIEEMNAALPINPTIIRIMRVLIARVLKLLKM 1742

Qy 1708 AVGMRALLDVTMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLRHATF 1767

Db 1743 ATGMRALLDVTVQALPQVGNLGLLFMLLFFIYAALGVELFGRLECSEDNPNCEGLSRHATF 1802

Qy 1768 RNFGMAFLTFRVSTGDNWNGIMKDTLRDC---DOESTCYNTVISPIYFVSFVLTAQFVL 1824

Db 1803 TNFGMAFLTFRVSTGDNWNGIMKDTLRCTREDKHCLSYLPALSPYFVTFVLVAQFVL 1862

Qy 1825 VNVVIAVLMKHLBESNKEAKEEALEAELELEM-KTSLSPQSPHSPGLSPFLWPVGVEGPDSP 1883

Db 1863 VNVVAVLMKHLBESNKEAREDAEMDAEIELEIAQGSTAQPPSTAQES-----QGT-D-P 1915

Qy 1884 DSPKPGALHPAAHARSASHFSLEHPTMOPHTLPGLPDLTLVRKSGVSRTHSLPNDSYM 1943

Db 1916 DT-----PNULLVVRKVSVRMLSLPNDSYM 1941

Qy 1944 RHGSTAEGPLGHRGWGLP-----KAQSGSVLSVHSQPADTSTYLQPKDAPHLLOPHSA 1997

Db 1942 RPVAPAAAPHSH-----PLOEVEMETVTGPVTSAHSPSLEPRTSFQVPSAASSPARA-SD 1995

Qy 1998 PTWGTIPKLPPPCRSPLAQRPLRRQAIRTDLSLDVQGLGSRREDLLAEVSGSPPLARAYS 2057

Db 1996 PLCALSPRDTF--RSLSLRILYRQEAHMAESLEGQIDDAEDGIPDYTEPAENISMSQA 2053

Qy 2058 FWG-----QSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSILELD 2107

Db 2054 PLGTLRSPPCSPRPASVTRKHTFGQHCISSR--PPT-----LGGDDAEADPAD 2101

Qy 2108 TELSWSIGDLLP---PGGQEEPP-----SPRDLKKCYSEVAQSCORRPTSWLD 2152

Db 2102 EEVSHITSSAHPWPATEPHSPSEASTASPAKGTGVSGRDHRFCSDVAQSFLDKP-CRPD 2160

Qy 2153 EORRHSAIVCLDSGSOPLHGTDPNLSGGQPL-GGPGSRPKKLSPPSITIDPP-ESQGP 2210

Db 2161 AQRWSSVE---LDNG-DGHLESGEVRARASELEPALGARKKKMSPPCISIDPTEDEGS 2216

Qy 2211 RTPPSP---GICLRRRAPSSDSK-----DPLASGPPDSMAASPSPKKDV 2251

Db 2217 SRPPAAEGGNTTLRRRTSPCEAALHRDCPESTEGTGTGDPVAKGERWGQA---SCRAEH 2273

Qy 2252 LSLSGLSDDPADL 2264

Db 2274 LTVPNFAFEPLDM 2286

RESULT 13

CCAI HUMAN

ID _CCAI_HUMAN STANDARD; PRT; 2223 AA.

AC Q9P0X4; O95504; Q7Z6S9; Q8NFX6; Q9NZC8; Q9UH15; Q9ULH30; Q9ULU9;

AC Q9UNE6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Voltage-dependent T-type calcium channel alpha-1I subunit (Voltage-gated calcium channel alpha subunit Cav3.3) (Ca(v)3.3).

DE gated calcium channel alpha subunit Cav3.3) (Ca(v)3.3).

GN Name=CACNA1I; Synonyms=KIAA1120;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Brain;

RX MEDLINE=99381950; PubMed=10454147;

RA Mittman S., Guo J., Emerick M.C., Agnew W.S.;

RT "Structure and alternative splicing of the gene encoding alpha1I, a human brain T calcium channel alpha subunit."

RL Neurosci. Lett. 269:121-124(1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RC TISSUE=Brain;

RX MEDLINE=20287513; PubMed=10749850; DOI=10.1074/jbc.C000090200;

RA Monteil A., Chemin J., Leuranguer V., Altier C., Mennessier G.,

RA Bourinet E., Lory P., Nargeot J.;

RT "Specific properties of T-type calcium channels generated by the human alpha1I subunit.";


```
RL J. Biol. Chem. 275:16530-16535 (2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT VAL-1040.
RC TISSUE=Brain;
RX MEDLINE=22074770; PubMed=12080115;
RA Gomora J.C., Murbartian J., Arias J.M., Lee J.-H., Perez-Reyes E.;
RT "Cloning and expression of the human T-type channel Ca(v)3.3: insights
RT into prepulse facilitation.";
RL Biophys. J. 83:229-241 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495 (1999).
RN [5]
RP SEQUENCE OF 1200-2223 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirose M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA Ohara O.;
RT "Characterization of cDNA clones selected by the GeneMark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336 (1999).
CC -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC entry of calcium ions into excitable cells and are also involved
CC in a variety of calcium-dependent processes, including muscle
CC contraction, hormone or neurotransmitter release, gene expression,
CC cell motility, cell division and cell death. Isoform alpha-11
CC gives rise to T-type calcium currents. T-type calcium channels
CC belong to the "low-voltage activated (LVA)" group and are strongly
CC blocked by nickel and mibefradil. A particularity of this type of
CC channels is an opening at quite negative potentials, and a
```


FT	DOMAIN	142	148	Cytoplasmic (Potential).	
FT	TRANSMEM	149	168	S3 of repeat I (Potential).	
FT	DOMAIN	169	173	Extracellular (Potential).	
FT	TRANSMEM	174	191	S4 of repeat I (Potential).	
FT	DOMAIN	192	211	Cytoplasmic (Potential).	
FT	TRANSMEM	212	232	S5 of repeat I (Potential).	
FT	DOMAIN	233	377	Extracellular (Potential).	
FT	TRANSMEM	378	398	S6 of repeat I (Potential).	
FT	DOMAIN	399	640	Cytoplasmic (Potential).	
FT	TRANSMEM	641	661	S1 of repeat II (Potential).	
FT	DOMAIN	662	676	Extracellular (Potential).	
FT	TRANSMEM	677	697	S2 of repeat II (Potential).	
FT	DOMAIN	698	702	Cytoplasmic (Potential).	
FT	TRANSMEM	703	721	S3 of repeat II (Potential).	
FT	DOMAIN	722	729	Extracellular (Potential).	
FT	TRANSMEM	730	753	S4 of repeat II (Potential).	
FT	DOMAIN	754	764	Cytoplasmic (Potential).	
FT	TRANSMEM	765	785	S5 of repeat II (Potential).	
FT	DOMAIN	786	841	Extracellular (Potential).	
FT	TRANSMEM	842	862	S6 of repeat II (Potential).	
FT	DOMAIN	863	1166	Cytoplasmic (Potential).	
FT	TRANSMEM	1167	1187	S1 of repeat III (Potential).	
FT	DOMAIN	1188	1209	Extracellular (Potential).	
FT	TRANSMEM	1210	1230	S2 of repeat III (Potential).	
FT	DOMAIN	1231	1244	Cytoplasmic (Potential).	
Query Match 46.2%; Score 5496.5; DB 1; Length 2223; Best Local Similarity 51.3%; Pred. No. 8.2e-245; Matches 1241; Conservative 217; Mismatches 527; Indels 435; Gaps 60;					
QY	31	RPGGSAEKDPSADSEAG----	LPYPALAPVVFYLSQDSRPRSWCLRTVCNPFERI	86	
Db	25	QGPSPSPSPSGLEEPLDGDADPHVPHDLAPIAFFCLRQTSPRNWC	IKMVCPNPFECV	84	
QY	87	SMVLVILNCVTLMGMRPCEDIA	CDSDQRILQAFDDFIAPFAVEMVVMVALGIFGKKC	146	
Db	85	SMVLVILNCVTLMGYQPCDDMDCLSDRCKILQVDDFI	FFAMEMVLKMVALGIFGKKC	144	
QY	147	YLGDTWNRLDFFIVIA	GMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLD	206	
Db	145	YLGDTWNRLDFFIVMAGMVEYSLDLQINLSA	IRTVRVLRPLKAINRVPSMRILVNLLD	204	
QY	207	TPLMLGNVLLLCFFVFFIF	IGVGVQLWAGLLRNRCFLPENFSLPLSVDLERYQTENEDE	266	
Db	205	TPLMLGNVLLLCFFVFFIF	IGVGVQLWAGLLRNRCFLEENFTIQGDVALPPYQPEEDDE	264	
QY	267	SPFICSPRENGMRSCRSVP	TLRGDGGGPPCGL-----DYEAYNSSNTT--CVWNWQ	318	
Db	265	MPFICSLSGDNGIMGCHEIP	PLEKEQ---GRECCLSKDDVYDFGAGRQDLNAGSLCVWNWR	321	
QY	319	YYTNC	SAGEHNPFKGAINF	DNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILL	378
Db	322	YYNVC	RTGSANPHKGAINF	DNIGYAWIVIFQVITLEGWVEIMYVMDAHSFYNFIYFILL	381
QY	379	IIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLK		438	
Db	382	IIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYEEIFQ		440	
QY	439	YLVVILRKAARRLAQVSRAGVRVGLLS	SPAPLGQETQPSSSCSRSHRRLSVHHLVHHH	498	
Db	441	YVCHILRKAKR-----	RALGLYQALQSRRALGPEAPAKP-----GPH	480	
QY	499	HHHHHHYH----	LGNGTLRAPRASPEIQDRDAN-GSRRLM-LPPPSTPALSAPPGGAESV	553	
Db	481	AKEPRHYH	GKTKQG-----DEGRHLGSRHCQTLHGPA	SP-----GNDHSGRE--	523
QY	554	HSFYHADCHLEPVRCQAPPPSPSEASGR	TVGSGKVYPTVHTSPPPETLKBKALVEVAAS	613	
Db	524	-----LC--	POHSPLDATPHIL-----VQIPATL-----	546	
QY	614	SGPPTLTSLNIPPGPYSSMHKLL	LETQSTGACQSSCKISSPCLKADSGACGPDSCPYCAR-	672	
Db	547	-----	-----ASDPASCPCQCHE	559	

QY	673	-----AGAGEVELADREMP	SDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAEPSSVL-	726		
Db	560	DGRRPSGLGSTD-SQEGSG	SGSSAGGE--DEADGDGARSSSEDGASSELGKEEEEEQAD	616		
QY	727	-----AFWRLICD	TFRKIVDSKYFGRGIMAILVNTLSMGIEYHEQPEELTNALEISN	779		
Db	617	GAVWLCGDVWRETRAK	LRGIVDSKYFNRGIMAILVNTVSMGIEHHEQPEELTNILEICN	676		
QY	780	IVFTSLFALEMLLKL	LVYGPFGYIKPNYNIFDGVIVVISWEIVGQGGGLSVLRTFRML	839		
Db	677	VVFTSMFALEMLKL	AAFGLFDYLRNPYNIFDSIIIVISWEIVGQADGGLSVLRTFRLL	736		
QY	840	RVLKLVRF	LALQRLVVLMTMDNVATFCMLLMFLIFIFSILGMHLFGCKFASERD-GD	898		
Db	737	RVLKLVRF	MPALRRQLVVLMTMDNVATFCMLLMFLIFIFSILGMHIFGCKFSLRTDTGD	796		
QY	899	TLPRKNFDSLL	WAIWTVFQILTQEDWNKVLYNGMASTSSWAALFYIALMTFGNYVLFNL	958		
Db	797	TVPRKNFDSLL	WAIWTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMTFGNYVLFNL	856		
QY	959	LVAILVEGFQAE	ISKREDASGQLSCIQLPVD	SQGGDANKSESEPDFFSPS-----	1009	
Db	857	LVAILVEGFQAE	-----GDANRSYDDEQSSSNIEEFDKIQE	893		
QY	1010	-LDGDGRKKCLALV	SLGEHPBELRKSLLPPLIIHTAATPMSLPKSTSTGLGEALGPASRR	1068		
Db	894	GLDSSGD	PKLCPIPMTPNGH-----LDP-----SLPLGGHLGPAGAAGPAPRL	936		
QY	1069	T-----SSSGSAEP	GAAHEMKSPSARSPPSHSPWSAASSWTSSRRSSNLGR	1115		
Db	937	SLQDP	MLVALGSRKSSVMSLGRMSYDQ	RLSSSRSSYYGPWGRSAAWASRRSSWN----	992	
QY	1116	APSLKRRSPSGERR	SLLSGE-GQESQDEEESSEE--ERAS	PAGSDH-----	1158	
Db	993	--SLKH	KPPSAEHESLLSAERGGGARVCEVAADGPPRAAPLHTPHAHHIIHGHPLAHRH	1050		
QY	1159	-RHRS	GLEREAKSSFDPDLTQVPLHRTASGR--GSASEHODCNGKSASGRLARALRPD	1215		
Db	1051	RHRR	TLSDNRDSDVLAELVPAVGAHPRAAWRAAGPAPGHEDCNGRMPSIAKDVFTKMG	1110		
QY	1216	DPPLD	GDDADDEGNLSKGERVRAWIRARLPACYLERDSWSAYIFPPQSRFRLLCHRIITH	1275		
Db	1111	DRGDRGED-EEE	IDYTLCFVRKMDVYKPDWC	CEVREDWSVYLFSPENRRFRVLCQTIIAH	1169	
QY	1276	KMFDH	VVLVIIFLNCITIAMERP	KIDPHSAERIFLTLNSYIFTAVFLAEMTVKVVALGWC	1335	
Db	1170	KLFDY	VVLAFIFLNCITIALERP	QIEAGSTERIFLTVSNYIFTAIFVGEMTLKVVS	LGLY	1229
QY	1336	FGEQAYLR	SSWNVLDGLLVLSVIDILVMSVDSG	TKILGMRLVRLRLRLRPLRVISRA	1395	
Db	1230	FGEQAYLR	SSWNVLDGFLVFVSIIDI	VVSLASAGGAKILGVLRLRLRLRPLRVISRA	1289	
QY	1396	QGLKLV	VETLMSLKPIGNI	VVICCAFFIIFGILGVQLFKGKFFVCQGEDTRNITNKS	SDC	1455
Db	1290	PGLKLV	VETLISLKPIGNI	VVICCAFFIIFGILGVQLFKGKFYHCLGVDTRNITNR	SDC	1349
QY	1456	AEASYR	WVRHKYNFDNLGOALMSL	FVLASKDGVWDIMYDGLD	AVGDQQIPMHNHPWMLL	1515
Db	1350	MAANYR	WVRHKYNFDNLGOALMSL	FVLASKDGVWNIMYNGLD	AVAVDQQPVTHNHPWMLL	1409
QY	1516	YFIS	FLLI	VAFVFLNMFVGVVNFHFKCRHQHEEARRRREKRLRREKKRKAQCKPY	1575	
Db	1410	YFIS	FLLI	VSFFVLNMFVGVVNFHFKCRHQHEEARRRREKRLRREKKRKAQRLPY	1469	
QY	1576	YSDY	SRFRLLVHHLCTSHYLD	LDFITGVIGLVNVTMAMEHYQQPQILDEALKICNYIFTVI	1635	
Db	1470	YATY	CHTRLLIHS	MCTSHYLDIFITFIICLVNVTMSLEHYNQPTSLETAL	KYCNYMFTTV	1529
QY	1636	FVLES	VFKLVAFGRFRFFQDRWNQ	LDLAILVLLSIMGITLEEIEVNASLPINPTIIRMRV	1695	
Db	1530	FVLEAV	LKLVAFGLRRFFKDRWNQ	LDLAILVLSVMGITLEEIEINAAALPINPTIIRMRV	1589	

FT TRANSMEM 172 S4 of repeat I (Potential).
FT DOMAIN 190 Cytoplasmic (Potential).
FT TRANSMEM 230 S5 of repeat I (Potential).
FT DOMAIN 210 Extracellular (Potential).
FT TRANSMEM 371 S6 of repeat I (Potential).
FT DOMAIN 397 Cytoplasmic (Potential).
FT TRANSMEM 599 S1 of repeat II (Potential).
FT DOMAIN 620 Extracellular (Potential).
FT TRANSMEM 633 S2 of repeat II (Potential).
FT DOMAIN 655 Cytoplasmic (Potential).
FT TRANSMEM 661 S3 of repeat II (Potential).
FT DOMAIN 680 Extracellular (Potential).
FT TRANSMEM 688 S4 of repeat II (Potential).
FT DOMAIN 712 Cytoplasmic (Potential).
FT TRANSMEM 723 S5 of repeat II (Potential).
FT DOMAIN 744 Extracellular (Potential).
FT TRANSMEM 796 S6 of repeat II (Potential).
FT DOMAIN 821 Cytoplasmic (Potential).
FT TRANSMEM 1126 S1 of repeat III (Potential).
FT DOMAIN 1149 Extracellular (Potential).
FT TRANSMEM 1167 S2 of repeat III (Potential).
FT DOMAIN 1188 Cytoplasmic (Potential).
FT TRANSMEM 1198 S3 of repeat III (Potential).
FT DOMAIN 1218 Extracellular (Potential).
FT TRANSMEM 1232 S4 of repeat III (Potential).
FT DOMAIN 1254 Cytoplasmic (Potential).
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FT DOMAIN 1288 Extracellular (Potential).
FT TRANSMEM 1365 S6 of repeat III (Potential).
FT DOMAIN 1391 Cytoplasmic (Potential).
FT TRANSMEM 1445 S1 of repeat IV (Potential).
FT DOMAIN 1466 Extracellular (Potential).
FT TRANSMEM 1467 S2 of repeat IV (Potential).
FT TRANSMEM 1481 Cytoplasmic (Potential).
FT TRANSMEM 1503 S3 of repeat IV (Potential).
FT TRANSMEM 1510 S4 of repeat IV (Potential).
FT DOMAIN 1529 Cytoplasmic (Potential).
FT TRANSMEM 1543 S5 of repeat IV (Potential).
FT DOMAIN 1567 Extracellular (Potential).
FT TRANSMEM 1581 S6 of repeat IV (Potential).
FT DOMAIN 1602 Cytoplasmic (Potential).
FT TRANSMEM 1665 Extracellular (Potential).
FT DOMAIN 1693 S6 of repeat IV (Potential).
FT SITE 355 Cytoplasmic (Potential).
FT Calcium ion selectivity and permeability (By similarity).
FT Calcium ion selectivity and permeability (By similarity).
FT Calcium ion selectivity and permeability (By similarity).
FT Calcium ion selectivity and permeability (By similarity).
FT N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 171 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 242 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 309 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1301 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1304 N-linked (GlcNAc. . .) (Potential).
FT CONFLICT 193 M -> L (in Ref. 3).
FT CONFLICT 291 C -> V (in Ref. 3).
FT CONFLICT 394 V -> L (in Ref. 3).
FT CONFLICT 406 E -> N (in Ref. 3).
FT CONFLICT 485 C -> S (in Ref. 3).
FT CONFLICT 512 D -> Y (in Ref. 3).
FT CONFLICT 558 S -> R (in Ref. 3).
FT CONFLICT 683 G -> S (in Ref. 3).
FT CONFLICT 691 F -> S (in Ref. 3).
FT CONFLICT 739 MH -> ID (in Ref. 3).
FT CONFLICT 833 C -> Y (in Ref. 3).
FT CONFLICT 846 F -> L (in Ref. 3).
FT CONFLICT 856 S -> R (in Ref. 3).
FT CONFLICT 905 L -> R (in Ref. 3).
FT CONFLICT 913 M -> YW (in Ref. 3).
FT CONFLICT 936 W -> G (in Ref. 3).
FT CONFLICT 996 A -> R (in Ref. 3).
FT CONFLICT 1060 I -> M (in Ref. 3).

FT CONFLICT 1094 1094 D -> CC (in Ref. 3).
FT CONFLICT 1197 1198 SS -> TD (in Ref. 3).
FT CONFLICT 1229 1231 Missing (in Ref. 3).
FT CONFLICT 1422 1422 K -> Y (in Ref. 3).
FT CONFLICT 1623 1625 FGM -> SAR (in Ref. 3).
FT CONFLICT 1656 1656 S -> T (in Ref. 3).
FT CONFLICT 1737 1737 P -> A (in Ref. 3).
SQ SEQUENCE 1835 AA; 205348 MW; E6025E0F1BE80CCA CRC64;

Query Match
Best Local Similarity 45.2%; Score 5383; DB 1; Length 1835;
Matches 1139; Conservative 184; Mismatches 344; Indels 336; Gaps 38;

QY 27 GAGRPGPSAEKDPGSADSEAE-----LPYPALAPVVFVLSQDSRPSRWCRLRTVCNPW 82
Db 19 GITEQPGPRSPPPPPGLEEPLGTNPDPVPHDLPAPVAFCLRTTSPRNWCIKMCVNPW 78

QY 83 FERISMLVILLNCVTLMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVVKMVALGIF 142
Db 79 FECVSMVLVILLNCVTLMGYQPCDDMECLSDRCKILQVFDFFIFFAMEMVLKMVALGIF 138

QY 143 GKCYLGTWNRLDFFIVIAGLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVT 202
Db 139 GKCYLGTWNRLDFFIVMAGMVEYSLDLQNLNSAIRTVRVLRLKAINRVPSMRILVN 198

QY 203 LLLDTLPMGLNVLLLCFFVFFIGIVGVQLWAGLLNRNCFLPENFSLPLSVDLERYQTE 262
Db 199 LLLDTLPMGLNVLLLCFFVFFIGIIGVQLWAGLLNRNCFLEENFTIQGDVALPPYQPE 258

QY 263 NEDESPFICSQPRENGMRSCRSVPTLRGDGGGGPPCGL-----DYEAYNSSNTT--CV 314
Db 259 EDDEMPFICSLTGDNGIMGCHIEIPPLKEQ---GRECCSKDDVDYDFGAGRODLNASGLCV 315

QY 315 NWNQYVYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGVVDIMYFVMDAHSFYNFYI 374
Db 316 NWNRYNVCRVTGNANPHKGAINFDNIGYAWIVIFQVITLEGVVEIMYVMDAHSFYNFYI 375

QY 375 FILLIIVGSFFMINCLVVIATQFSETKQRESQLMRQVRFLSNASTLASFSEPGSCYE 434
Db 376 FILLIIVGSFFMINCLVVIATQFSETKQREHRLMLEQRQRYLS-SSTVASYAEPGDCYE 434

QY 435 ELKYLVLVILKKAARLQAQVSRAGVRVGLLSPPAPLGGQETQPSSSCSRSHRRLSVHHL 494
Db 435 EIFQYVCHILRKAKRRALGLYQALQNR-----ISAILASD-----PSSCPHCQHEA 523

QY 495 VHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPGGAESVH 554
Db 462 -----RQAMG-----PGTPA--PAKPGP----- 477

QY 555 SFVHADCHLEPVRCQAPPPRSPSEASGRTVSGKVVYPTVHTSPPTLKEKALVEVAASS 614
Db 478 ---HAK---EPSHCKLCPRHSPLD-----PTPHTLVQP----- 504

QY 615 GPPTLTSLNIPPGPYSSMHKLLLETQSTGACOSSCKISSPCLKADSGACGPDSCPYCAR-- 672
Db 505 -----ISAILASD-----PSSCPHCQHEA 523

QY 673 ----AGAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPDAPSSVLA- 727
Db 524 GRRPSGLGSTD-SGQEGSGSGSAEAEANGDG---LQSSDGVSSDLGKEEEDGAAR 578

QY 728 ----FWRLICDTRFKIVDSKYFGRGIMIAITLVNTLSMGIEYHEQEPELTNALEISNVFT 783
Db 579 LCGDVWRETRKKLRGLVDSKYFNRGIMMALLVNTVSMGIEHHEQEPELTNILEICNVVFT 638

QY 784 SLFALEMLLLKLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGLSVLRTFRLMRVLK 843
Db 639 SMFALEMILKLAAPGLFDYLRNPYNIFDSIIVISWEIVGQADGGLSVLRTFRLLRVLK 698

QY 844 LVRFPLALQRLVVLMTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPD 902
Db 699 LVRFMPALRRQLVVLMTMDNVATFCMLLMLFIFIFSILGMHLFGCKFSLRTDGTDPD 758

[illegible]

Db 1748 APCRSGGAGAGG-DTSHLCRH 1769

RESULT 15

Q7Z6S8 PRELIMINARY; PRT; 1994 AA.

AC Q7Z6S8; 25, Created)

DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE DJ172B20.1 (Calcium channel, voltage-dependent, alpha 1I subunit)

DE (Fragment).

GN Name=CACNA1I;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Phillips S.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AL022319; CAD92537.1; --

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005261; F:cation channel activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR001682; Ca/Na pore.

DR InterPro; IPR002111; Cat_channel_trpL.

DR InterPro; IPR000345; Cyt_c_heme_BS.

DR InterPro; IPR005821; Ion_trans.

DR InterPro; IPR005820; M+channel_nlg.

DR Pfam; PF00520; Ion_trans; 4.

DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.

KW Ion transport; Ionic channel; Transmembrane; Transport.

FT NON TER 1

SQ SEQUENCE 1994 AA; 220004 MW; A5EFAE5FA32DCF76 CRC64;

Query Match 40.6%; Score 4836; DB 2; Length 1994;

Best Local Similarity 49.8%; Pred. No. 2e-214;

Matches 1117; Conservative 188; Mismatches 484; Indels 456; Gaps 55;

QY 197 MRILVTLLDTPMLGNVLLLCFFVFFIFIGVGVOLWAGLLRNRCFLPENFSLPLSVDL 256

DB 1 MRILVNLLDTPMLGNVLLLCFFVFFIFIGVGVOLWAGLLRNRCFLEENFTIQGDVALP 60

QY 257 RYQTEDESPFICQPRENGMRSCRSVPTLRDGGGGPPCGL-----DYEAYNSSN 310

DB 61 PYYQPEEDDEMPFICSLSGDNGIMGCHEIPPLKEQ---GRECLSKDDVDFGAGRQDLN 117

QY 311 TT--CVNWNQYNTCSAGEHNPFKGAINFEDNIGYAWIAIFQVITLEGWVDIMYFVMDAHS 368

DB 118 ASGLCVNWNRYNVCRGTSANPHKGAINFEDNIGYAWIVIFQVITLEGWVEIMYVMDAHS 177

QY 369 FYNFIYFILLIIVGSFFMINCLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSE 428

DB 178 FYNFIYFILLIIVGSFFMINCLVVIATQFSETKQREHRIMLEQRQRYLS-SSTVASYAE 236

QY 429 PGSCYEBELLKYLVIYILRKAARRLAQVSRAGVRVGLISSLAPLGGQETQFSSSCSRSHRR 488

DB 237 PGDCYEEIFQYVCHILRKAKR-----RALGLYQALQSRRLALG----- 274

QY 489 LSVHILVHHHHHHHHYHLGNGLTRAPRASPEIQDRDANGSRRLMLPPSTPALSGAPPG 548

DB 275 -----PEAFA--PAKPG 284

QY 549 GAESVHSFYHADCHLEPVRCQAPPPRSPSEASGRTVGSGKVPYTVHTSPPPETLKEKALV 608

DB 285 P-----HAK--EPRHYQLCPQHSPLDATPHTL-----VQPIPAIL----- 317

QY 609 EVAASSGPPTLTSLNIPDPGPYSSMHKLLLETQSTGACQSSCKISSPCLKADSGACGPDSCP 668

DB 318 -----ASDPASCP 325

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: November 18, 2004, 13:14:41 ; Search time 40.3132 Seconds
(without alignments)
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 66318000 residues
Total number of hits satisfying chosen parameters: 478139
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	11862.5	99.7	2273	3	US-09-426-998-5
2	6315.5	53.1	1207	4	US-09-398-522-52
3	6211	52.2	2353	3	US-08-984-709A-50
4	5492.5	46.1	2175	3	US-09-404-650-2
5	5492.5	46.1	2175	4	US-09-935-541-2
6	5484	46.1	2188	3	US-09-404-650-4
7	5484	46.1	2188	4	US-09-935-541-4
8	5366	45.1	1835	3	US-09-404-650-5
9	5366	45.1	1835	4	US-09-935-541-5
10	1750.5	14.7	2343	3	US-09-268-163-4
11	1749	14.7	2337	3	US-08-713-118-2
12	1749	14.7	2337	3	US-09-452-007-2
13	1748.5	14.7	2339	1	US-08-455-543A-47
14	1748.5	14.7	2339	2	US-08-223-305C-47
15	1746.5	14.7	2339	3	US-09-268-163-6
16	1743	14.6	2237	1	US-08-455-543A-48
17	1743	14.6	2237	2	US-08-223-305C-48
18	1741	14.6	2237	3	US-09-268-163-8
19	1722	14.5	2336	3	US-09-268-163-10
20	1632.5	13.7	1873	1	US-08-435-675B-4
21	1622.5	13.6	1873	1	US-08-336-257A-7
22	1619.5	13.6	1984	3	US-08-836-325-10
23	1619.5	13.6	1984	4	US-09-457-571-10
24	1619.5	13.6	1985	4	US-09-495-714C-6
25	1616	13.6	1872	6	5386025-6
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29	1607.5	13.5	2516	3	US-08-895-590-2	Sequence 2, Appli
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31	1601	13.4	1977	4	US-09-495-714C-4	Sequence 4, Appli
32	1601	13.4	2509	2	US-08-149-097D-35	Sequence 35, Appli
33	1587	13.3	2016	4	US-09-514-907A-2	Sequence 2, Appli
34	1587	13.3	2016	4	US-09-896-994-2	Sequence 2, Appli
35	1586	13.3	1969	3	US-08-836-325-16	Sequence 16, Appli
36	1586	13.3	1969	4	US-09-457-571-16	Sequence 16, Appli
37	1586	13.3	2016	3	US-09-634-920-4	Sequence 4, Appli
38	1586	13.3	2016	4	US-09-840-125-4	Sequence 4, Appli
39	1583	13.3	1977	4	US-09-976-594-757	Sequence 757, App
40	1583	13.3	1977	4	US-09-919-039-367	Sequence 367, App
41	1573.5	13.2	1912	4	US-09-495-714C-2	Sequence 2, Appli
42	1569.5	13.2	1968	1	US-08-455-543A-45	Sequence 45, Appli
43	1569.5	13.2	1968	2	US-08-223-305C-45	Sequence 45, Appli
44	1560.5	13.1	2161	1	US-08-455-543A-51	Sequence 51, Appli
45	1560.5	13.1	2161	2	US-08-223-305C-51	Sequence 51, Appli

ALIGNMENTS

RESULT 1
US-09-426-998-5
; Sequence 5, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 5
; LENGTH: 2273
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-426-998-5

Query Match	99.7%	Score 11862.5;	DB 3;	Length 2273;
Best Local Similarity	99.4%	Pred. No. 0;		
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			Indels	7;
			Gaps	1;
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Db	1	MDEEDGAGAEESGQPRSFMRNLDSGAGRPGPSAEKDPGSADSEAEGLPYPALAPVV	60	
QY	61	FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLGMFRPCEDIAQDSQRCRILQAF	120	
Db	61	FFYLSQDSRPRSWCLRTVCNPFERISMLVILLNCVTLGMFRPCEDIAQDSQRCRILQAF	120	
QY	121	DDFIFAFFAVEMVVKWVALGIFGKCYLGDTWNRLDFFIVIAQMLEYSLDLQNVFSFSAVR	180	
Db	121	DDFIFAFFAVEMVVKWVALGIFGKCYLGDTWNRLDFFIVIAQMLEYSLDLQNVFSFSAVR	180	
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Db	181	TVRVLRLRAINRVPSMRILVTLLDTPMLGNVLLCFFVFFIFGIVGVQLWAGLLNR	240	
QY	241	CFLPENFSLPSVDLERYVQTEDESPFICSPRENGMRSCRSVPTLRGDGGGPPCGL	300	
Db	241	CFLPENFSLPSVDLERYVQTEDESPFICSPRENGMRSCRSVPTLRGDGGGPPCGL	300	
QY	301	DYEAYNSSNTTCVNNQYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM	360	
Db	301	DYEAYNSSNTTCVNNQYTNCSAGEHNPFGAINFDNIGYAWIAIFQVITLEGWVDIM	360	

QY 361 YFVMDAHSFYNIYFIILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
Db 361 YFVMDAHSFYNIYFIILLIIVGSPFMINCLVVIATQFSETKQRESQLMREQVRFLSNA 420
QY 421 STLASFSEPGSCYEELLKYLVIYILRKAARRLAQVRAAGVRVGLLSSPAPLGGQETQPS 480
Db 421 STLASFSEPGSCYEELLKYLVIYILRKAARRLAQVRAAGVRVGLLSSPAPLGGQETQPS 480
QY 481 SCRSRRLSVHHLVHHHHHHHHYHLGNGTIRAPRASPEIQDRDANGSRRLMLPPSTP 540
Db 481 SCRSRRLSVHHLVHHHHHHHHYHLGNGTIRAPRASPEIQDRDANGSRRLMLPPSTP 540
QY 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPSPSEASGRTVSGKVYPTVHTSPPE 600
Db 541 ALSGAPPGGAESVHSFYHADCHLEPVRCQAPPSPSEASGRTVSGKVYPTVHTSPPE 600
QY 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
Db 601 TLKEKALVEVAASSGPPTLTSLNIPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSG 660
QY 661 ACPDSCPCYCARAGAVEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPD 720
Db 661 ACPDSCPCYCARAGAVEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHSRRQRSLGPD 720
QY 721 EPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
Db 721 EPSSVLAFWRLICDTRKIVDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNI 780
QY 781 VFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFLMR 840
Db 781 VFTSLFALEMLKLLVYGPFGYIKNPYNIFDGVIVVISWEIVGQGGGLSVLRTFLMR 840
QY 841 VLKLVRLPALQRLVLMKTMNDNVATFCMLLMFIFISILGMHLEFGCKFASERDGD 900
Db 841 VLKLVRLPALQRLVLMKTMNDNVATFCMLLMFIFISILGMHLEFGCKFASERDGD 900
QY 901 PDRKNFDSILLWAIIVTFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLV 960
Db 901 PDRKNFDSILLWAIIVTFQILTOEDWNKVLYNGMASTSSWAALYFIALMTFGNYVLFNLV 960
QY 961 AILVEGQAEIISKREDASGQSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKCL 1020
Db 961 AILVEGQAEIISKREDASGQSCIQLPVDSQGGDANKSESEPDFFSPSLDGDGRKKCL 1020
QY 1021 ALVSLGEHPELKSLLPPLIIHTAATPMSLPKSTGTGLGEALGPASRRRTSSGSAEPGAA 1080
Db 1021 ALVSLGEHPELKSLLPPLIIHTAATPMSLPKSTGTGLGEALGPASRRRTSSGSAEPGAA 1080
QY 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEQESQ 1140
Db 1081 HEMKSPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRSLLSGEQESQ 1140
QY 1141 DEEESSEERASPDHHRHRSGLEREAKSSFDLPDTLQVPLHRTASGRGSAEHQDCN 1200
Db 1141 DEEESSEERASPDHHRHRSGLEREAKSSFDLPDTLQVPLHRTASGRGSAEHQDCN 1200
QY 1201 GKSASGRALARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERSWSAYIFP 1260
Db 1201 GKSASGRALARALRPDDPPLDGDADDEGNLSKGERVRAWIRARLPACYLERSWSAYIFP 1260
QY 1261 PQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
Db 1261 PQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV 1320
QY 1321 FLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVL 1380
Db 1321 FLAEMTVKVALGWCFCGEQAYLRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVL 1380
QY 1381 RLLRTLRLRVISRAQGLKLVWETLMSLKPIGNIWWICCAFFIIFGILGVQFKGFFV 1440
Db 1381 RLLRTLRLRVISRAQGLKLVWETLMSLKPIGNIWWICCAFFIIFGILGVQFKGFFV 1440

QY 1441 CQGEDTRNITNKSDCAEASRYWRVHRKYNFNDLQALMSLFVLASKDGVWDIMYDGLDAVG 1500
Db 1441 CQGEDTRNITNKSDCAEASRYWRVHRKYNFNDLQALMSLFVLASKDGVWDIMYDGLDAVG 1500
QY 1501 VDQOPIMNHNPMMLLYFISFLLIVAFVLMNFMVGVVVENFHKRQHQHEEEARRREKRL 1560
Db 1501 VDQOPIMNHNPMMLLYFISFLLIVAFVLMNFMVGVVVENFHKRQHQHEEEARRREKRL 1560
QY 1561 RLLEKKRR-----KAOCKPYYSYSRFRLLVHHLCTSHYLDLFTITVIGLNVVTWAME 1613
Db 1561 RLLEKKRRSKEKQMAEAOCKPYYSYSRFRLLVHHLCTSHYLDLFTITVIGLNVVTWAME 1620
QY 1614 HYQOPQILDALKICNYIFTVIFVLESVKLVAFGFRFFQDRWNQDLDAIVLLSIMGIT 1673
Db 1621 HYQOPQILDALKICNYIFTVIFVLESVKLVAFGFRFFQDRWNQDLDAIVLLSIMGIP 1680
QY 1674 LEEIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMERALLDTVMQALPOVGNLGLLFM 1733
Db 1681 LEQIEVNASLPINPTIIRIMRVLRIRARVLKLLKMAVGMERALLDTVMQALPOVGNLGLLFM 1740
QY 1734 LLFFIFAALGVELFGDLECDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1793
Db 1741 LLFFIFAALGVELFGDLECDETHPCGLGRHATFRNFGMAFLTLFRVSTGDNWNGIMKDT 1800
QY 1794 LRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVAVLMKHLEESNKEAEAELEAEL 1853
Db 1801 LRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIVAVLMKHLEESNKEAEAELEAEL 1860
QY 1854 ELEMKTLSPOPHSPGLSPFLWPGEVGPDSKPKGALHPAAHARSASHFSLEHPTMQPH 1913
Db 1861 ELEMKTLSPOPHSPGLSPFLWPGEVGPDSKPKGALHPAAHARSASHFSLEHPTMQPH 1920
QY 1914 PTELPGPDLTLTVRKSGVSRTHSLPNDSYMCRHGTAEGPLHGRGWGLPKAQSGSVLSVHS 1973
Db 1921 PTELPGPDLTLTVRKSGVSRTHSLPNDSYMCRHGTAEGPLHGRGWGLPKAQSGSVLSVHS 1980
QY 1974 QPADTSYILQPKDAPHLLQPHSAPTWTGTIPKLPPGRSPPLAQRLRQAAIRTDSDLVQ 2033
Db 1981 QPADTSYILQPKDAPHLLQPHSAPTWTGTIPKLPPGRSPPLAQRLRQAAIRTDSDLVQ 2040
QY 2034 GLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQOHSRSHSKISKHMTTPPAPCPGPEPNW 2093
Db 2041 GLGSRREDLLAEVSGSPPLARAYSFWGQSSTQAQOHSRSHSKISKHMTTPPAPCPGPEPNW 2100
QY 2094 GKGPPESTRSSLELDELTSWISGDLPLPPGGQEEPPSPRDLKKCYVEAQSCQRRPTSWLDE 2153
Db 2101 GKGPPESTRSSLELDELTSWISGDLPLPPGGQEEPPSPRDLKKCYVEAQSCQRRPTSWLDE 2160
QY 2154 QRRHSIAVSCDSGSPHLGTDPSNLGGQPLGGPSRPPKILSPPSITIDPPESQGPRT 2213
Db 2161 QRRHSIAVSCDSGSPHLGTDPSNLGGQPLGGPSRPPKILSPPSITIDPPESQGPRT 2220
QY 2214 PSPGICLRRRAPSSDSKDPPLASGPPDSMAASPPKDVLSLGLSSDPADLDP 2266
Db 2221 PSPGICLRRRAPSSDSKDPPLASGPPDSMAASPPKDVLSLGLSSDPADLDP 2273

RESULT 2
US-09-398-522-52
; Sequence 52, Application US/09398522
; Patent No. 6783933
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNALG POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHUI590
; CURRENT APPLICATION NUMBER: US/09/398,522
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1207
; TYPE: PRT

